



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 17, 2020 – 03:17 PM BST

PDB ID : 6JLL
Title : XFEL structure of cyanobacterial photosystem II (2F state, dataset1)
Authors : Suga, M.; Shen, J.R.
Deposited on : 2019-03-06
Resolution : 2.15 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

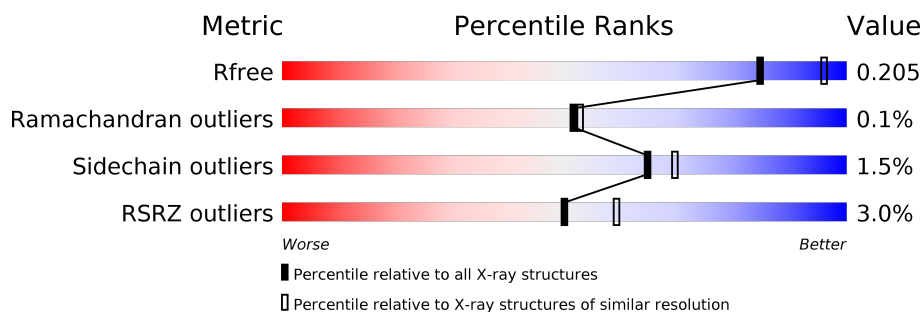
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



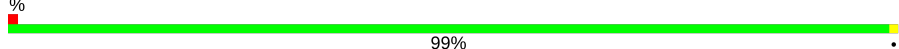
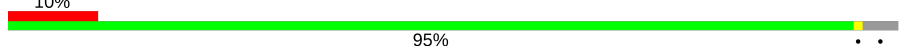
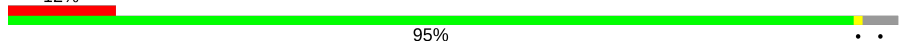


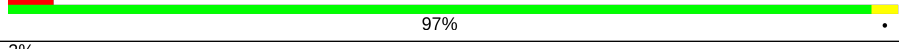
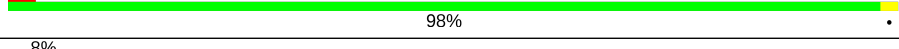
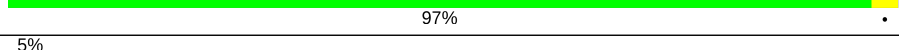
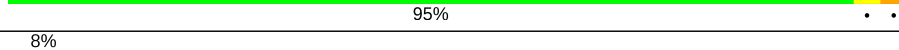
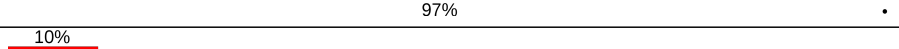
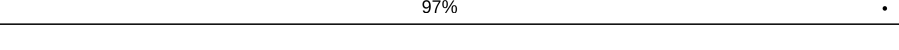
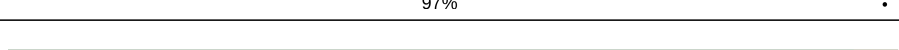
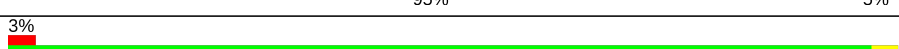

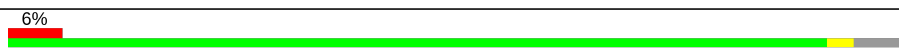
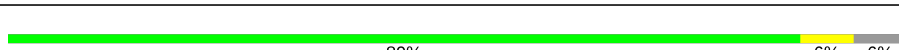
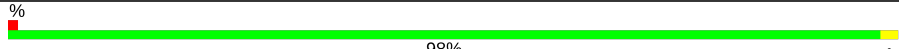
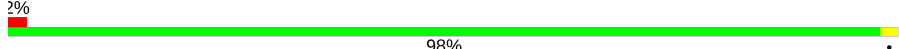


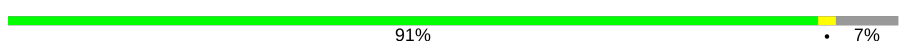
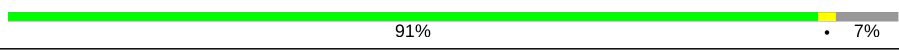
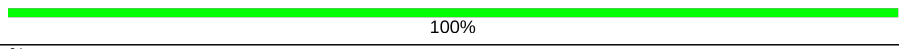
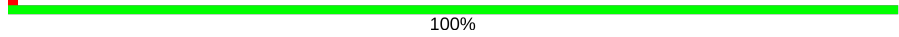

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1479 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	344	<div> <div style="width: 97%;"></div> <div>97%</div> </div>
1	a	344	<div> <div style="width: 96%;"></div> <div>96%</div> </div>
2	B	505	<div> <div style="width: 99%;"></div> <div>99%</div> </div>
2	b	505	<div> <div style="width: 99%;"></div> <div>99%</div> </div>
3	C	455	<div> <div style="width: 98%;"></div> <div>98%</div> </div>
3	c	455	<div> <div style="width: 99%;"></div> <div>99%</div> </div>
4	D	342	<div> <div style="width: 99%;"></div> <div>99%</div> </div>

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Mol	Chain	Length	Quality of chain
4	d	342	% 
5	E	84	10% 
5	e	84	12% 
6	F	44	7% 
6	f	44	5% 
7	H	65	5% 
7	h	65	3% 
8	I	38	8% 
8	i	38	5% 
9	J	39	8% 
9	j	39	10% 
10	K	37	
10	k	37	
11	L	37	3% 
11	l	37	3% 
12	M	36	6% 
12	m	36	
13	O	244	% 
13	o	244	2% 
14	T	32	3% 
14	t	32	
15	U	104	
15	u	104	
16	V	137	
16	v	137	% 

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Mol	Chain	Length	Quality of chain
17	Y	30	
17	y	30	
18	X	40	
18	x	40	
19	Z	62	
19	z	62	
20	R	34	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	A	405	X	-	-	-
24	CLA	A	406	X	-	-	-
24	CLA	A	407	X	-	-	-
24	CLA	A	410	X	-	-	-
24	CLA	B	602	X	-	-	-
24	CLA	B	603	X	-	-	-
24	CLA	B	604	X	-	-	-
24	CLA	B	605	X	-	-	-
24	CLA	B	606	X	-	-	-
24	CLA	B	607	X	-	-	-
24	CLA	B	608	X	-	-	-
24	CLA	B	609	X	-	-	-
24	CLA	B	610	X	-	-	-
24	CLA	B	611	X	-	-	-
24	CLA	B	612	X	-	-	-
24	CLA	B	613	X	-	-	-
24	CLA	B	614	X	-	-	-
24	CLA	B	615	X	-	-	-
24	CLA	B	616	X	-	-	-
24	CLA	B	617	X	-	-	-
24	CLA	C	501	X	-	-	-
24	CLA	C	502	X	-	-	-
24	CLA	C	503	X	-	-	-
24	CLA	C	504	X	-	-	-
24	CLA	C	505	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	C	506	X	-	-	-
24	CLA	C	507	X	-	-	-
24	CLA	C	508	X	-	-	-
24	CLA	C	509	X	-	-	-
24	CLA	C	510	X	-	-	-
24	CLA	C	511	X	-	-	-
24	CLA	C	512	X	-	-	-
24	CLA	C	513	X	-	-	-
24	CLA	D	402	X	-	-	-
24	CLA	D	403	X	-	-	-
24	CLA	a	409	X	-	-	-
24	CLA	a	410	X	-	-	-
24	CLA	a	412	X	-	-	-
24	CLA	b	611	X	-	-	-
24	CLA	b	612	X	-	-	-
24	CLA	b	613	X	-	-	-
24	CLA	b	614	X	-	-	-
24	CLA	b	615	X	-	-	-
24	CLA	b	616	X	-	-	-
24	CLA	b	617	X	-	-	-
24	CLA	b	618	X	-	-	-
24	CLA	b	619	X	-	-	-
24	CLA	b	620	X	-	-	-
24	CLA	b	621	X	-	-	-
24	CLA	b	622	X	-	-	-
24	CLA	b	623	X	-	-	-
24	CLA	b	624	X	-	-	-
24	CLA	b	625	X	-	-	-
24	CLA	b	626	X	-	-	-
24	CLA	c	505	X	-	-	-
24	CLA	c	506	X	-	-	-
24	CLA	c	507	X	-	-	-
24	CLA	c	508	X	-	-	-
24	CLA	c	509	X	-	-	-
24	CLA	c	510	X	-	-	-
24	CLA	c	511	X	-	-	-
24	CLA	c	512	X	-	-	-
24	CLA	c	513	X	-	-	-
24	CLA	c	514	X	-	-	-
24	CLA	c	515	X	-	-	-
24	CLA	c	516	X	-	-	-
24	CLA	c	517	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	d	401	X	-	-	-
24	CLA	d	402	X	-	-	-
24	CLA	d	403	X	-	-	-

2 Entry composition [i](#)

There are 41 unique types of molecules in this entry. The entry contains 55675 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Photosystem II protein D1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	54	0
			3014	1963	496	537	18			
1	a	334	Total	C	N	O	S	0	56	0
			3010	1964	494	534	18			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	279	PRO	ARG	See sequence details	UNP P51765
a	279	PRO	ARG	See sequence details	UNP P51765

- Molecule 2 is a protein called Photosystem II CP47 reaction center protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	504	Total	C	N	O	S	0	10	0
			4021	2639	667	702	13			
2	b	503	Total	C	N	O	S	0	12	0
			4022	2644	664	701	13			

- Molecule 3 is a protein called Photosystem II CP43 reaction center protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	451	Total	C	N	O	S	0	14	0
			3553	2322	592	626	13			
3	c	455	Total	C	N	O	S	0	20	0
			3641	2382	606	639	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	19	ASN	-	See sequence details	UNP D0VWR7
C	20	SER	-	See sequence details	UNP D0VWR7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	21	ILE	-	See sequence details	UNP D0VWR7
C	22	PHE	-	See sequence details	UNP D0VWR7
c	19	ASN	-	See sequence details	UNP D0VWR7
c	20	SER	-	See sequence details	UNP D0VWR7
c	21	ILE	-	See sequence details	UNP D0VWR7
c	22	PHE	-	See sequence details	UNP D0VWR7

- Molecule 4 is a protein called Photosystem II D2 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	341	Total	C	N	O	S	0	16	0
			2849	1884	469	483	13			
4	d	341	Total	C	N	O	S	0	16	0
			2849	1884	469	483	13			

- Molecule 5 is a protein called Cytochrome b559 subunit alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	81	Total	C	N	O	0	2	0
			668	436	107	125			
5	e	81	Total	C	N	O	0	2	0
			670	439	107	124			

- Molecule 6 is a protein called Cytochrome b559 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	34	Total	C	N	O	S	0	0	0
			275	187	45	42	1			
6	f	32	Total	C	N	O	S	0	0	0
			257	175	43	38	1			

- Molecule 7 is a protein called Photosystem II reaction center protein H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	65	Total	C	N	O	S	0	1	0
			519	346	85	86	2			
7	h	65	Total	C	N	O	S	0	0	0
			511	341	82	86	2			

- Molecule 8 is a protein called Photosystem II reaction center protein I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	38	Total	C	N	O	S	0	0	0
			314	211	48	54	1			
8	i	38	Total	C	N	O	S	0	0	0
			314	211	48	54	1			

- Molecule 9 is a protein called Photosystem II reaction center protein J.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	38	Total	C	N	O	S	0	0	0
			272	182	42	47	1			
9	j	39	Total	C	N	O	S	0	0	0
			280	187	43	48	2			

- Molecule 10 is a protein called Photosystem II reaction center protein K.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	K	37	Total	C	N	O	0	0	0
			293	204	43	46			
10	k	37	Total	C	N	O	0	0	0
			293	204	43	46			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	33	LEU	PHE	See sequence details	UNP P19054
K	39	TRP	VAL	See sequence details	UNP P19054
k	33	LEU	PHE	See sequence details	UNP P19054
k	39	TRP	VAL	See sequence details	UNP P19054

- Molecule 11 is a protein called Photosystem II reaction center protein L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	L	37	Total	C	N	O	S	0	1	0
			309	207	48	53	1			
11	l	37	Total	C	N	O	S	0	1	0
			309	207	48	53	1			

- Molecule 12 is a protein called Photosystem II reaction center protein M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	34	Total	C	N	O	S	0	1	0
			274	184	40	49	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	m	34	Total	C	N	O	S	0	0	0
			269	179	40	49	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	8	LEU	PHE	See sequence details	UNP P12312
m	8	LEU	PHE	See sequence details	UNP P12312

- Molecule 13 is a protein called Photosystem II manganese-stabilizing polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	O	243	Total	C	N	O	S	0	8	0
			1903	1191	315	392	5			
13	o	243	Total	C	N	O	S	0	5	0
			1891	1183	315	388	5			

- Molecule 14 is a protein called Photosystem II reaction center protein T.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	T	30	Total	C	N	O	S	0	1	0
			264	185	36	41	2			
14	t	30	Total	C	N	O	S	0	1	0
			264	185	36	41	2			

- Molecule 15 is a protein called Photosystem II 12 kDa extrinsic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	U	97	Total	C	N	O		0	0	0
			774	491	129	154				
15	u	97	Total	C	N	O		0	0	0
			774	491	129	154				

- Molecule 16 is a protein called Cytochrome c-550.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	V	137	Total	C	N	O	S	0	2	0
			1085	689	181	211	4			
16	v	137	Total	C	N	O	S	0	1	0
			1077	684	178	211	4			

- Molecule 17 is a protein called Photosystem II reaction center protein Ycf12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Y	29	Total	C	N	O	S	0	0	0
			215	142	37	33	3			
17	y	29	Total	C	N	O	S	0	0	0
			215	142	37	33	3			

- Molecule 18 is a protein called Photosystem II reaction center protein X.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	X	39	Total	C	N	O	S	0	0	0
			287	191	46	50				
18	x	38	Total	C	N	O	S	0	0	0
			281	188	45	48				

- Molecule 19 is a protein called Photosystem II reaction center protein Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	Z	62	Total	C	N	O	S	0	0	0
			479	328	72	77	2			
19	z	62	Total	C	N	O	S	0	0	0
			479	328	72	77	2			

- Molecule 20 is a protein called Photosystem II protein Y.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	30	Total	C	N	O	S	98	0	0
			239	163	41	35				

- Molecule 21 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
21	A	1	Total	Fe	0	1
			2	2		
21	a	1	Total	Fe	0	1
			1	1		

- Molecule 22 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

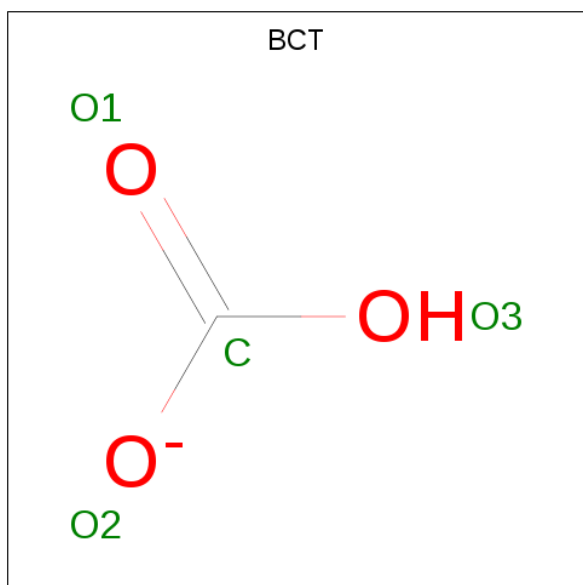
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	2	Total	Cl	0	2
			4	4		
22	v	1	Total	Cl	0	0
			1	1		

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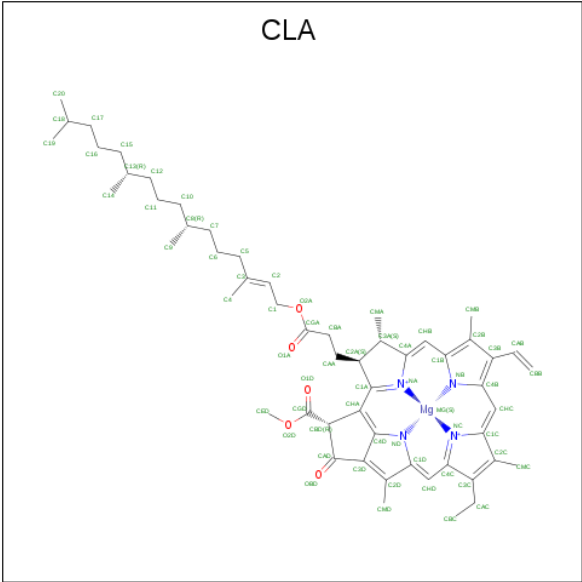
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	a	2	Total	Cl	0	2
			4	4		
22	U	1	Total	Cl	0	0
			1	1		

- Molecule 23 is BICARBONATE ION (three-letter code: BCT) (formula: CHO_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
23	A	1	Total	C	O	0	1
			8	2	6		
23	a	1	Total	C	O	0	1
			8	2	6		

- Molecule 24 is CHLOROPHYLL A (three-letter code: CLA) (formula: $\text{C}_{55}\text{H}_{72}\text{MgN}_4\text{O}_5$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
24	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
24	B	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	B	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	B	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	B	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	B	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	B	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	C	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	D	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	D	1	Total 65	C 55	Mg 1	N 4	O 5	0	0

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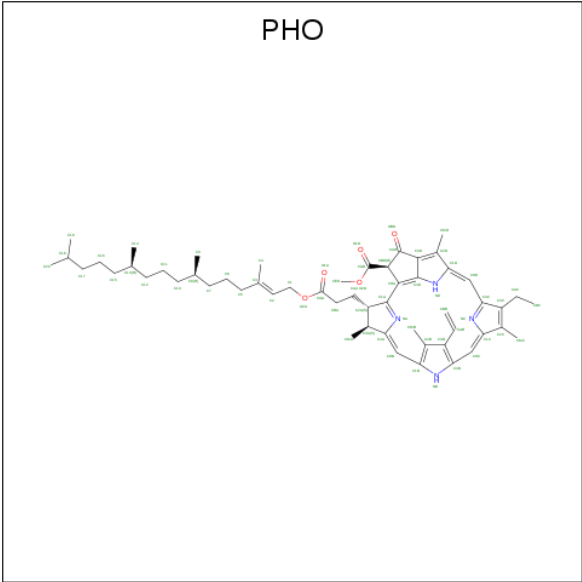
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
24	a	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	a	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	a	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	c	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
24	c	1	Total 65	C 55	Mg 1	N 4	O 5	0	0

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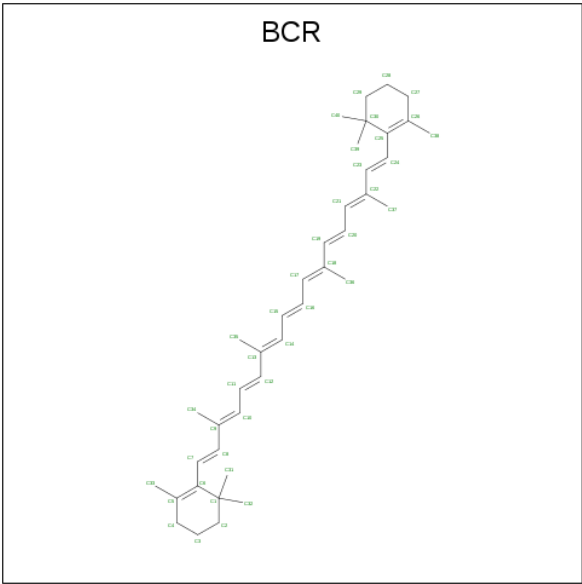
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
24	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 25 is PHEOPHYTIN A (three-letter code: PHO) (formula: C₅₅H₇₄N₄O₅).



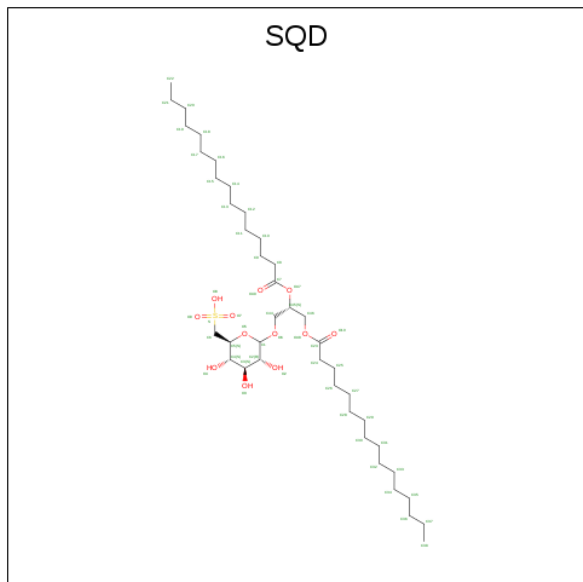
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
25	A	1	Total	C	N	O	0	0
			64	55	4	5		
25	A	1	Total	C	N	O	0	1
			128	110	8	10		
25	a	1	Total	C	N	O	0	0
			64	55	4	5		
25	a	1	Total	C	N	O	0	1
			128	110	8	10		

- Molecule 26 is BETA-CAROTENE (three-letter code: BCR) (formula: C₄₀H₅₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	A	1	Total C 40 40	0	0
26	B	1	Total C 40 40	0	0
26	B	1	Total C 40 40	0	0
26	B	1	Total C 40 40	0	0
26	C	1	Total C 40 40	0	0
26	C	1	Total C 40 40	0	0
26	D	1	Total C 40 40	0	0
26	H	1	Total C 40 40	0	0
26	K	1	Total C 40 40	0	0
26	T	1	Total C 40 40	0	0
26	Y	1	Total C 40 40	0	0
26	a	1	Total C 40 40	0	0
26	b	1	Total C 40 40	0	0
26	b	1	Total C 40 40	0	0
26	b	1	Total C 40 40	0	0
26	c	1	Total C 40 40	0	0
26	c	1	Total C 40 40	0	0
26	d	1	Total C 40 40	0	0
26	h	1	Total C 40 40	0	0
26	k	1	Total C 40 40	0	0
26	t	1	Total C 40 40	0	0
26	y	1	Total C 40 40	0	0

- Molecule 27 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula: $C_{41}H_{78}O_{12}S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
27	A	1	Total	C	O	S	0	0
			54	41	12	1		
27	A	1	Total	C	O	S	0	0
			54	41	12	1		
27	B	1	Total	C	O	S	0	0
			54	41	12	1		
27	F	1	Total	C	O	S	0	0
			43	30	12	1		
27	a	1	Total	C	O	S	0	0
			54	41	12	1		
27	a	1	Total	C	O	S	0	0
			54	41	12	1		
27	b	1	Total	C	O	S	0	0
			54	41	12	1		
27	f	1	Total	C	O	S	0	0
			43	30	12	1		

- Molecule 28 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



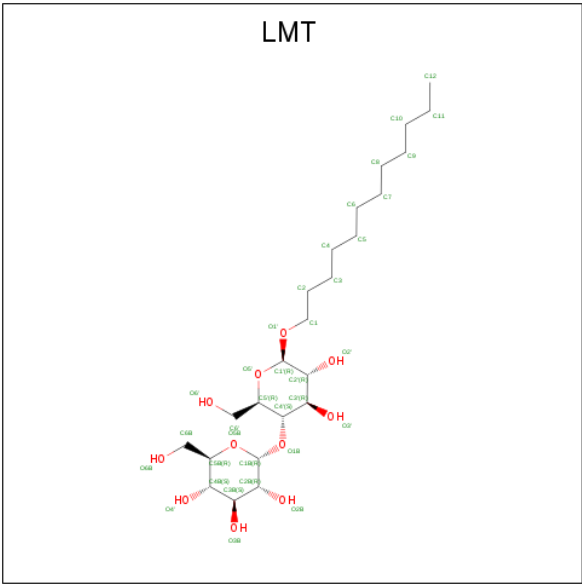
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
28	A	1	Total	C	O	0	0
			6	3	3		
28	A	1	Total	C	O	0	0
			6	3	3		
28	A	1	Total	C	O	0	0
			6	3	3		
28	B	1	Total	C	O	0	0
			6	3	3		
28	B	1	Total	C	O	0	0
			6	3	3		
28	B	1	Total	C	O	0	0
			6	3	3		
28	B	1	Total	C	O	0	0
			6	3	3		
28	B	1	Total	C	O	0	0
			6	3	3		
28	C	1	Total	C	O	0	0
			6	3	3		
28	C	1	Total	C	O	0	0
			6	3	3		
28	O	1	Total	C	O	0	0
			6	3	3		
28	T	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
28	T	1	Total	C	O	0	0
			6	3	3		
28	V	1	Total	C	O	0	0
			6	3	3		
28	V	1	Total	C	O	0	0
			6	3	3		
28	V	1	Total	C	O	0	0
			6	3	3		
28	V	1	Total	C	O	0	0
			6	3	3		
28	a	1	Total	C	O	0	0
			6	3	3		
28	a	1	Total	C	O	0	0
			6	3	3		
28	b	1	Total	C	O	0	0
			6	3	3		
28	b	1	Total	C	O	0	0
			6	3	3		
28	b	1	Total	C	O	0	0
			6	3	3		
28	b	1	Total	C	O	0	0
			6	3	3		
28	b	1	Total	C	O	0	0
			6	3	3		
28	c	1	Total	C	O	0	0
			6	3	3		
28	c	1	Total	C	O	0	0
			6	3	3		
28	f	1	Total	C	O	0	0
			6	3	3		
28	o	1	Total	C	O	0	0
			6	3	3		
28	t	1	Total	C	O	0	0
			6	3	3		
28	v	1	Total	C	O	0	0
			6	3	3		
28	v	1	Total	C	O	0	0
			6	3	3		
28	v	1	Total	C	O	0	0
			6	3	3		

- Molecule 29 is DODECYL-BETA-D-MALTOSIDE (three-letter code: LMT) (formula: C₂₄H₄₆O₁₁).



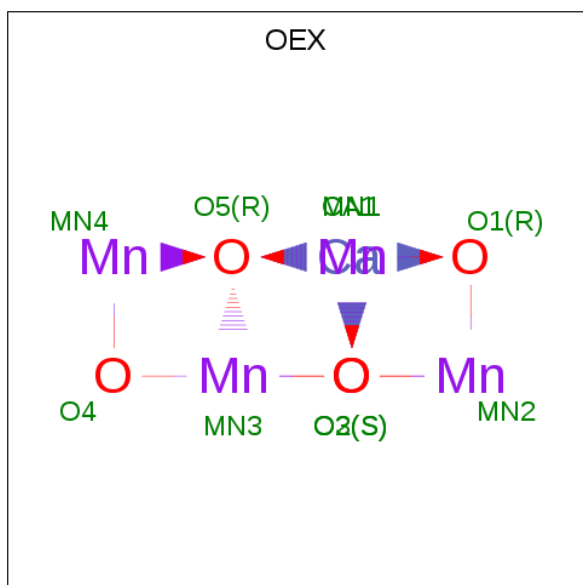
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
29	A	1	Total	C	O	0	0
			35	24	11		
29	B	1	Total	C	O	0	0
			25	19	6		
29	C	1	Total	C	O	0	0
			35	24	11		
29	D	1	Total	C	O	0	0
			35	24	11		
29	F	1	Total	C	O	0	0
			35	24	11		
29	M	1	Total	C	O	0	0
			35	24	11		
29	M	1	Total	C	O	0	0
			35	24	11		
29	M	1	Total	C	O	0	0
			35	24	11		
29	T	1	Total	C	O	0	0
			25	19	6		
29	a	1	Total	C	O	0	0
			35	24	11		
29	a	1	Total	C	O	0	0
			35	24	11		
29	b	1	Total	C	O	0	0
			25	19	6		

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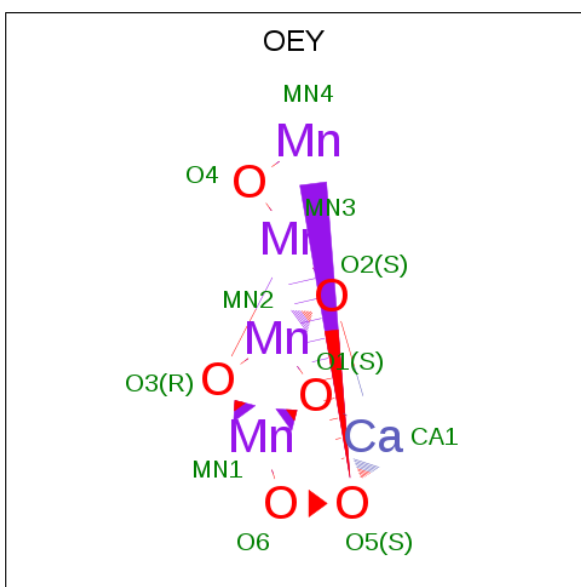
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
29	f	1	Total	C	O	0	0
			35	24	11		
29	m	1	Total	C	O	0	0
			35	24	11		

- Molecule 30 is CA-MN4-O5 CLUSTER (three-letter code: OEX) (formula: CaMn_4O_5).



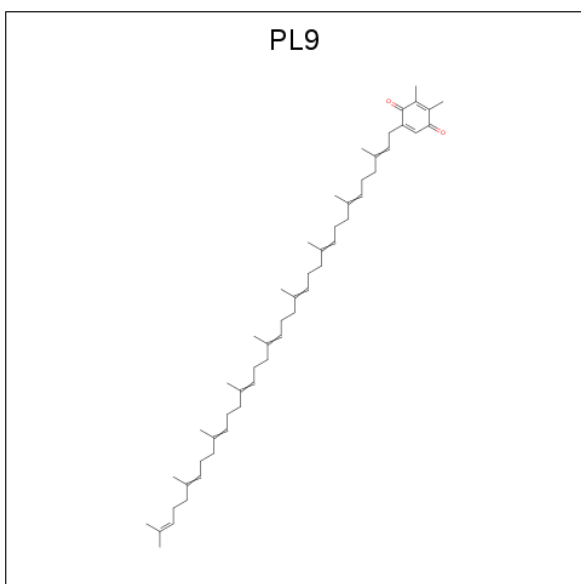
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
30	A	1	Total	Ca	Mn	O	0	1
			10	1	4	5		
30	a	1	Total	Ca	Mn	O	0	1
			10	1	4	5		

- Molecule 31 is CA-MN4-O6 CLUSTER (three-letter code: OEY) (formula: CaMn_4O_6).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
31	A	1	Total	Ca	Mn	O	0	1
			11	1	4	6		
31	a	1	Total	Ca	Mn	O	0	1
			11	1	4	6		

- Molecule 32 is 2,3-DIMETHYL-5-(3,7,11,15,19,23,27,31,35-NONAMETHYL-2,6,10,14,18,22,26,30,34-HEXATRIACONTANONAENYL-2,5-CYCLOHEXADIENE-1,4-DIONE-2,3-DIMETHYL-5-SOLANESYL-1,4-BENZOQUINONE (three-letter code: PL9) (formula: $C_{53}H_{80}O_2$).



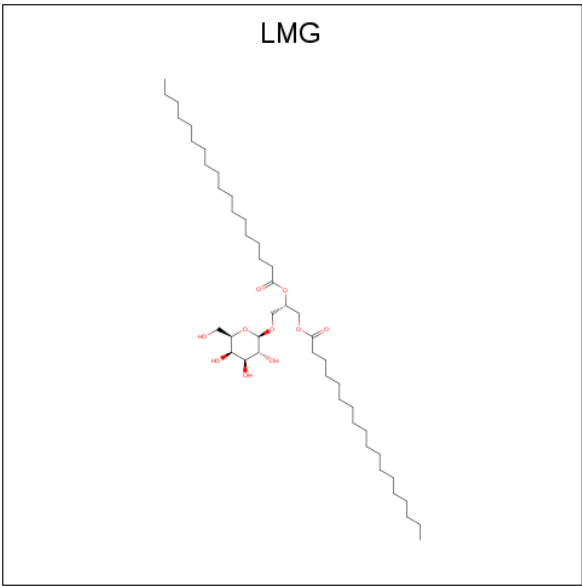
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
32	A	1	Total	C	O	0	1
			110	106	4		
32	D	1	Total	C	O	0	1
			110	106	4		
32	a	1	Total	C	O	0	1
			110	106	4		
32	d	1	Total	C	O	0	1
			110	106	4		

- Molecule 33 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
33	J	1	Total	C		0	0
			10	10			
33	i	1	Total	C	O	0	0
			40	35	5		
33	D	2	Total	C	O	0	0
			57	51	6		
33	B	1	Total	C	O	0	0
			33	28	5		
33	I	1	Total	C	O	0	0
			40	35	5		
33	C	1	Total	C	O	0	0
			34	29	5		
33	a	1	Total	C	O	0	0
			30	25	5		
33	c	1	Total	C	O	0	0
			32	27	5		
33	A	1	Total	C	O	0	0
			28	23	5		
33	j	1	Total	C		0	0
			10	10			
33	X	1	Total	C	O	0	0
			18	16	2		
33	d	3	Total	C	O	0	0
			71	63	8		
33	m	1	Total	C		0	0
			10	10			
33	b	1	Total	C	O	0	0
			33	28	5		
33	M	1	Total	C		0	0
			10	10			

- Molecule 34 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (three-letter

code: LMG) (formula: C₄₅H₈₆O₁₀).

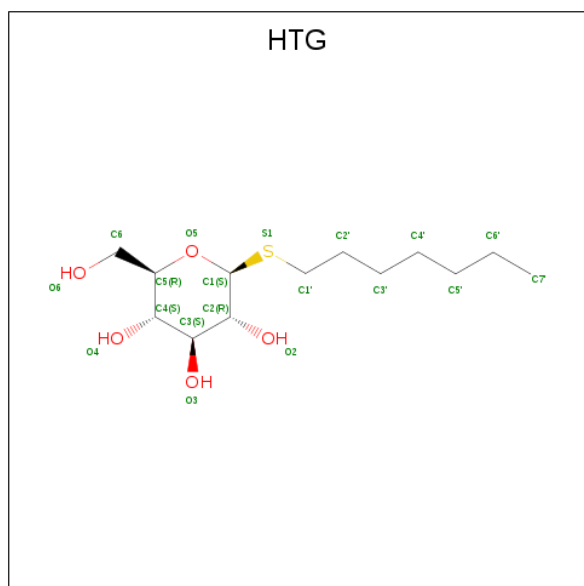


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
34	A	1	Total	C	O	0	0
			51	41	10		
34	B	1	Total	C	O	0	0
			51	41	10		
34	C	1	Total	C	O	0	0
			51	41	10		
34	C	1	Total	C	O	0	0
			51	41	10		
34	D	1	Total	C	O	0	0
			51	41	10		
34	Z	1	Total	C	O	0	0
			37	27	10		
34	a	1	Total	C	O	0	0
			51	41	10		
34	b	1	Total	C	O	0	0
			51	41	10		
34	c	1	Total	C	O	0	0
			51	41	10		
34	c	1	Total	C	O	0	0
			51	41	10		
34	j	1	Total	C	O	0	0
			51	41	10		
34	z	1	Total	C	O	0	0
			39	29	10		

- Molecule 35 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	B	1	Total Ca 1 1	0	0
35	C	1	Total Ca 1 1	0	0
35	c	2	Total Ca 2 2	0	0
35	f	1	Total Ca 1 1	0	0
35	o	1	Total Ca 1 1	0	0
35	O	1	Total Ca 1 1	0	0
35	b	1	Total Ca 1 1	0	0
35	F	1	Total Ca 1 1	0	0

- Molecule 36 is heptyl 1-thio-beta-D-glucopyranoside (three-letter code: HTG) (formula: $C_{13}H_{26}O_5S$).



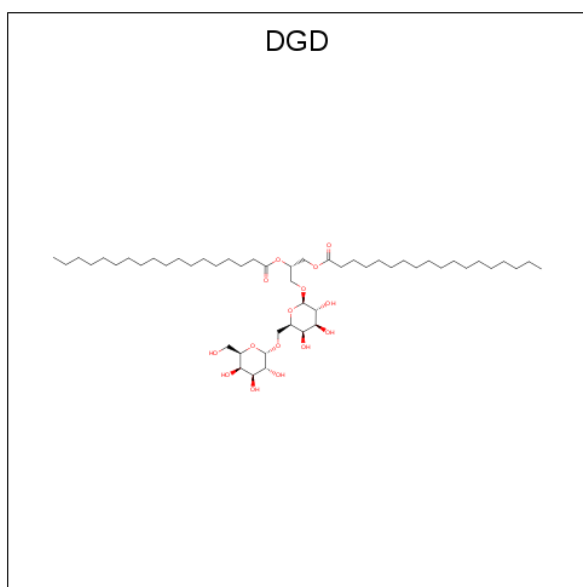
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	B	1	Total C O S 19 13 5 1	0	0
36	B	1	Total C O S 19 13 5 1	0	0
36	B	1	Total C O S 19 13 5 1	0	0

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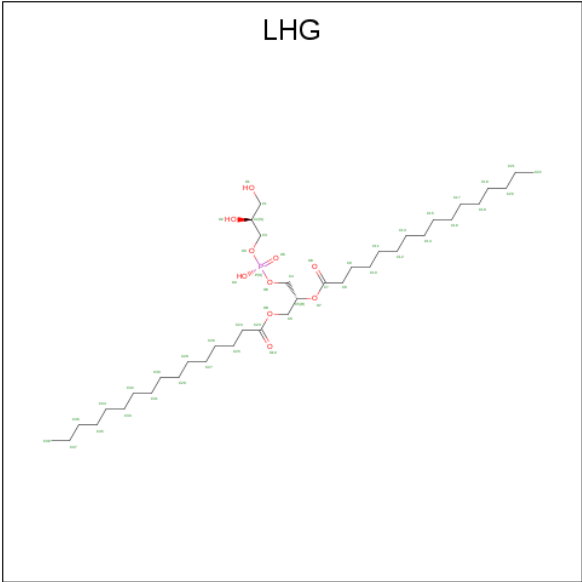
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
36	B	1	Total	C	O	S	0	0
			19	13	5	1		
36	B	1	Total	C	O	S	0	0
			19	13	5	1		
36	C	1	Total	C	O	S	0	0
			19	13	5	1		
36	C	1	Total	C	O	S	0	0
			19	13	5	1		
36	H	1	Total	C	O	S	0	0
			16	10	5	1		
36	V	1	Total	C	O	S	0	0
			19	13	5	1		
36	b	1	Total	C	O	S	0	0
			19	13	5	1		
36	b	1	Total	C	O	S	0	0
			19	13	5	1		
36	b	1	Total	C	O	S	0	0
			19	13	5	1		
36	b	1	Total	C	O	S	0	0
			19	13	5	1		
36	b	1	Total	C	O	S	0	0
			19	13	5	1		
36	c	1	Total	C	O	S	0	0
			19	13	5	1		
36	c	1	Total	C	O	S	0	0
			19	13	5	1		
36	d	1	Total	C	O	S	0	0
			16	10	5	1		

- Molecule 37 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (three-letter code: DGD) (formula: C₅₁H₉₆O₁₅).



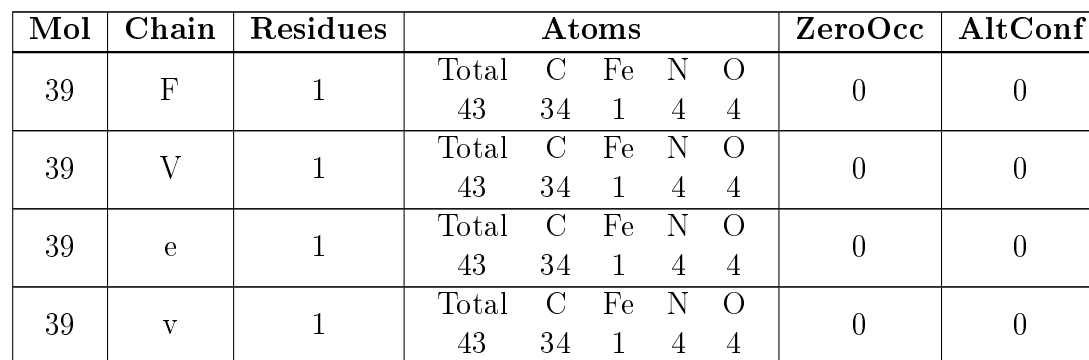
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
37	C	1	Total	C	O	0	0
			62	47	15		
37	C	1	Total	C	O	0	0
			62	47	15		
37	C	1	Total	C	O	0	0
			62	47	15		
37	D	1	Total	C	O	0	0
			52	42	10		
37	H	1	Total	C	O	0	0
			62	47	15		
37	c	1	Total	C	O	0	0
			62	47	15		
37	c	1	Total	C	O	0	0
			62	47	15		
37	c	1	Total	C	O	0	0
			62	47	15		
37	e	1	Total	C	O	0	0
			62	47	15		
37	h	1	Total	C	O	0	0
			62	47	15		

- Molecule 38 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (three-letter code: LHG) (formula: $C_{38}H_{75}O_{10}P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
38	D	1	Total	C	O	P	0	0
			49	38	10	1		
38	D	1	Total	C	O	P	0	0
			49	38	10	1		
38	D	1	Total	C	O	P	0	0
			49	38	10	1		
38	E	1	Total	C	O	P	0	0
			42	31	10	1		
38	L	1	Total	C	O	P	0	0
			49	38	10	1		
38	a	1	Total	C	O	P	0	0
			42	31	10	1		
38	d	1	Total	C	O	P	0	0
			49	38	10	1		
38	d	1	Total	C	O	P	0	0
			49	38	10	1		
38	d	1	Total	C	O	P	0	0
			49	38	10	1		
38	l	1	Total	C	O	P	0	0
			49	38	10	1		

- Molecule 39 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 40 | J | 1 | Total Mg
1 1 | 0 | 0 |
| 40 | j | 1 | Total Mg
1 1 | 0 | 0 |

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|--------------------|---------|---------|
| 41 | A | 161 | Total O
173 173 | 0 | 14 |
| 41 | B | 290 | Total O
294 294 | 0 | 4 |
| 41 | C | 228 | Total O
232 232 | 0 | 4 |



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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
41	D	146	Total 150	O 150	0	5
41	E	30	Total 30	O 30	0	0
41	F	9	Total 9	O 9	0	0
41	H	48	Total 49	O 49	0	1
41	I	5	Total 5	O 5	0	0
41	J	10	Total 10	O 10	0	0
41	K	9	Total 9	O 9	0	0
41	L	13	Total 14	O 14	0	1
41	M	23	Total 23	O 23	0	0
41	O	178	Total 180	O 180	0	2
41	T	17	Total 18	O 18	0	1
41	U	77	Total 77	O 77	0	0
41	V	117	Total 119	O 119	0	2
41	Y	4	Total 4	O 4	0	0
41	X	6	Total 6	O 6	0	0
41	Z	1	Total 1	O 1	0	0
41	a	153	Total 162	O 162	0	12
41	b	266	Total 269	O 269	0	3
41	c	200	Total 205	O 205	0	5
41	d	129	Total 132	O 132	0	3
41	e	19	Total 19	O 19	0	0

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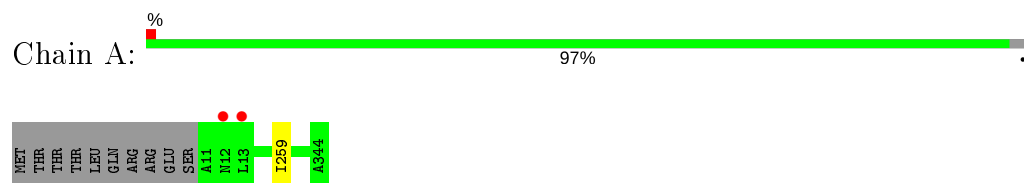
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
41	f	8	Total 8	O 8	0	0
41	h	44	Total 44	O 44	0	0
41	i	5	Total 5	O 5	0	0
41	j	6	Total 6	O 6	0	0
41	k	7	Total 7	O 7	0	0
41	l	9	Total 9	O 9	0	0
41	m	11	Total 11	O 11	0	0
41	o	155	Total 155	O 155	0	0
41	t	11	Total 11	O 11	0	0
41	u	93	Total 93	O 93	0	0
41	v	81	Total 82	O 82	0	1
41	y	2	Total 2	O 2	0	0
41	x	6	Total 6	O 6	0	0

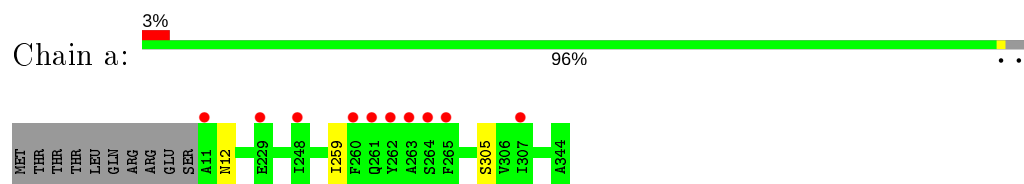
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

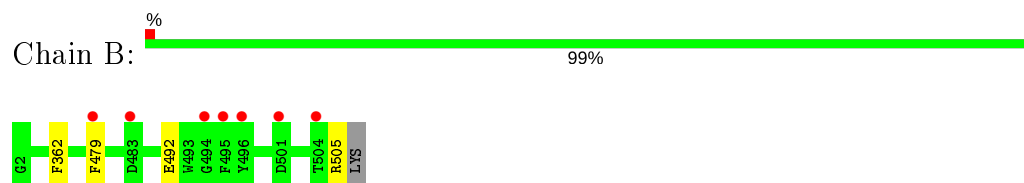
- Molecule 1: Photosystem II protein D1



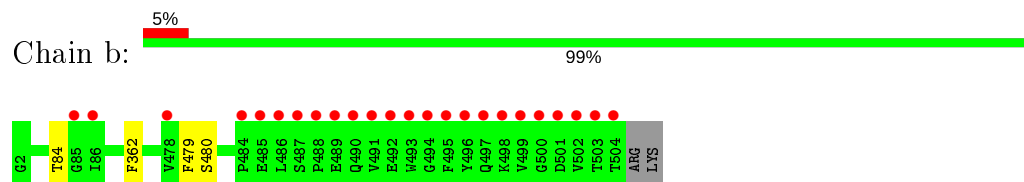
- Molecule 1: Photosystem II protein D1



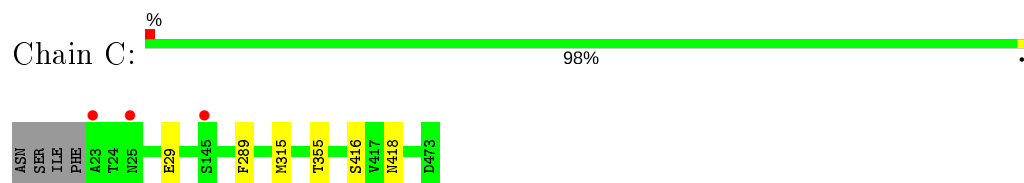
- Molecule 2: Photosystem II CP47 reaction center protein



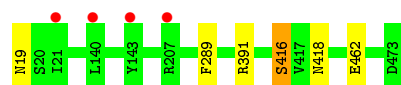
- Molecule 2: Photosystem II CP47 reaction center protein



- Molecule 3: Photosystem II CP43 reaction center protein



- Molecule 3: Photosystem II CP43 reaction center protein



- Molecule 4: Photosystem II D2 protein



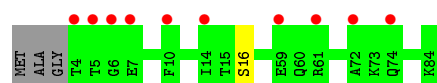
- Molecule 4: Photosystem II D2 protein



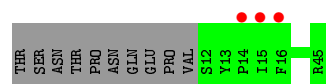
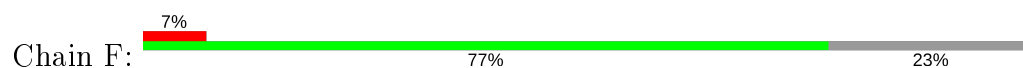
- Molecule 5: Cytochrome b559 subunit alpha



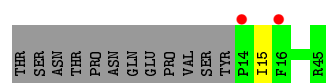
- Molecule 5: Cytochrome b559 subunit alpha



- Molecule 6: Cytochrome b559 subunit beta

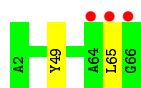


- Molecule 6: Cytochrome b559 subunit beta



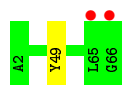
- Molecule 7: Photosystem II reaction center protein H

Chain H:  5% 97%



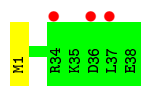
- Molecule 7: Photosystem II reaction center protein H

Chain h:  3% 98%

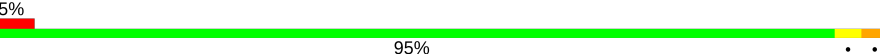


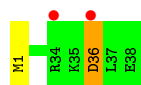
- Molecule 8: Photosystem II reaction center protein I

Chain I:  8% 97%



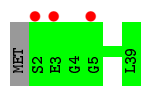
- Molecule 8: Photosystem II reaction center protein I

Chain i:  5% 95%



- Molecule 9: Photosystem II reaction center protein J

Chain J:  8% 97%



- Molecule 9: Photosystem II reaction center protein J

Chain j:  10% 97%



- Molecule 10: Photosystem II reaction center protein K

Chain K:  97%



- Molecule 10: Photosystem II reaction center protein K

Chain k: 95% 5%



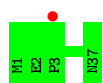
- Molecule 11: Photosystem II reaction center protein L

Chain L: 3% 97% .



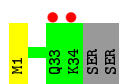
- Molecule 11: Photosystem II reaction center protein L

Chain l: 3% 100%



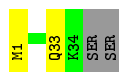
- Molecule 12: Photosystem II reaction center protein M

Chain M: 6% 92% . 6%



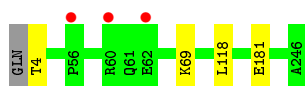
- Molecule 12: Photosystem II reaction center protein M

Chain m: 89% 6% 6%



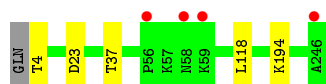
- Molecule 13: Photosystem II manganese-stabilizing polypeptide

Chain O: % 98% .

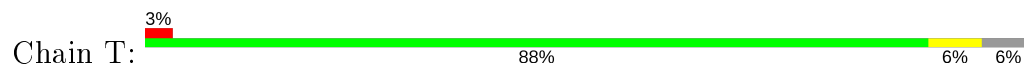


- Molecule 13: Photosystem II manganese-stabilizing polypeptide

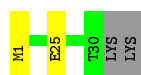
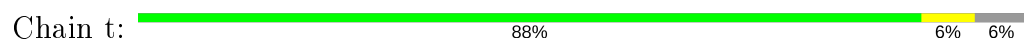
Chain o: 2% 98% .



- Molecule 14: Photosystem II reaction center protein T



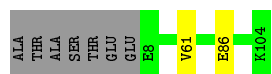
- Molecule 14: Photosystem II reaction center protein T



- Molecule 15: Photosystem II 12 kDa extrinsic protein



- Molecule 15: Photosystem II 12 kDa extrinsic protein

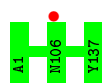


- Molecule 16: Cytochrome c-550



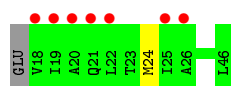
There are no outlier residues recorded for this chain.

- Molecule 16: Cytochrome c-550

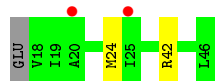
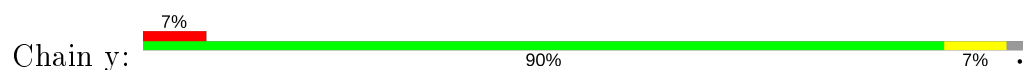


- Molecule 17: Photosystem II reaction center protein Ycf12

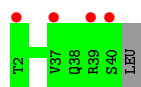




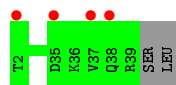
- Molecule 17: Photosystem II reaction center protein Ycf12



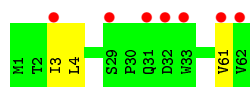
- Molecule 18: Photosystem II reaction center protein X



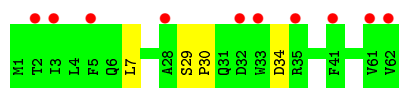
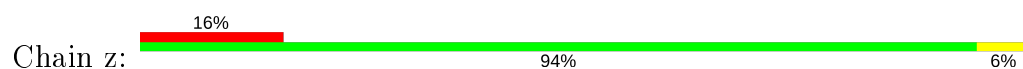
- Molecule 18: Photosystem II reaction center protein X



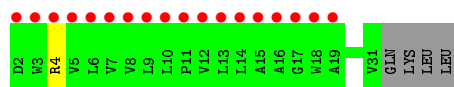
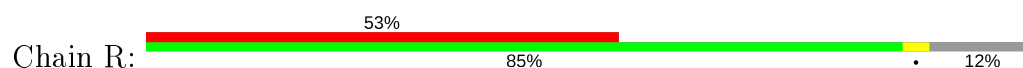
- Molecule 19: Photosystem II reaction center protein Z



- Molecule 19: Photosystem II reaction center protein Z



- Molecule 20: Photosystem II protein Y



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	121.97Å 228.72Å 286.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.15 178.86 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.99-2.15) 99.9 (178.86-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.156 , 0.203 0.159 , 0.205	Depositor DCC
R_{free} test set	26822 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.670	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 76.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	55675	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LHG, GOL, MG, OEX, PHO, DGD, CL, CA, LMT, CLA, PL9, OEY, LMG, FE2, BCT, HEM, FME, UNL, HTG, BCR, SQD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.44	0/3115	0.55	0/4242
1	a	0.44	0/3117	0.54	0/4245
2	B	0.44	0/4191	0.53	0/5709
2	b	0.42	0/4198	0.52	0/5720
3	C	0.39	0/3678	0.51	0/5007
3	c	0.38	0/3774	0.51	0/5135
4	D	0.48	0/2952	0.55	0/4021
4	d	0.45	0/2952	0.54	0/4021
5	E	0.34	0/693	0.49	0/944
5	e	0.33	0/695	0.49	0/948
6	F	0.41	0/284	0.51	0/387
6	f	0.40	0/265	0.52	0/360
7	H	0.36	0/535	0.55	0/728
7	h	0.35	0/524	0.51	0/713
8	I	0.35	0/311	0.49	0/419
8	i	0.34	0/311	0.45	0/419
9	J	0.33	0/278	0.41	0/376
9	j	0.35	0/286	0.45	0/386
10	K	0.34	0/303	0.50	0/416
10	k	0.34	0/303	0.50	0/416
11	L	0.44	0/319	0.48	0/433
11	l	0.43	0/319	0.46	0/433
12	M	0.48	0/270	0.57	0/368
12	m	0.43	0/262	0.54	0/357
13	O	0.38	0/1958	0.56	0/2654
13	o	0.37	0/1937	0.54	0/2625
14	T	0.49	0/266	0.54	0/362
14	t	0.49	0/266	0.52	0/362
15	U	0.38	0/785	0.53	0/1064
15	u	0.39	0/785	0.52	0/1064
16	V	0.39	0/1109	0.50	0/1502

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	v	0.35	0/1098	0.50	0/1488
17	Y	0.35	0/216	0.50	0/289
17	y	0.30	0/216	0.43	0/289
18	X	0.34	0/290	0.45	0/392
18	x	0.30	0/284	0.46	0/384
19	Z	0.31	0/490	0.43	0/669
19	z	0.28	0/490	0.44	0/669
20	R	0.23	0/245	0.37	0/338
All	All	0.41	0/44370	0.52	0/60354

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	384/344 (112%)	380 (99%)	3 (1%)	1 (0%)	41	37
1	a	384/344 (112%)	378 (98%)	5 (1%)	1 (0%)	41	37
2	B	512/505 (101%)	506 (99%)	6 (1%)	0	100	100
2	b	513/505 (102%)	503 (98%)	10 (2%)	0	100	100
3	C	461/455 (101%)	450 (98%)	9 (2%)	2 (0%)	34	29
3	c	473/455 (104%)	459 (97%)	12 (2%)	2 (0%)	34	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	355/342 (104%)	346 (98%)	9 (2%)	0	100	100
4	d	355/342 (104%)	345 (97%)	10 (3%)	0	100	100
5	E	81/84 (96%)	81 (100%)	0	0	100	100
5	e	81/84 (96%)	81 (100%)	0	0	100	100
6	F	32/44 (73%)	30 (94%)	2 (6%)	0	100	100
6	f	30/44 (68%)	30 (100%)	0	0	100	100
7	H	64/65 (98%)	61 (95%)	3 (5%)	0	100	100
7	h	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
8	I	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
8	i	36/38 (95%)	33 (92%)	2 (6%)	1 (3%)	5	1
9	J	36/39 (92%)	35 (97%)	1 (3%)	0	100	100
9	j	37/39 (95%)	36 (97%)	1 (3%)	0	100	100
10	K	35/37 (95%)	35 (100%)	0	0	100	100
10	k	35/37 (95%)	35 (100%)	0	0	100	100
11	L	36/37 (97%)	36 (100%)	0	0	100	100
11	l	36/37 (97%)	36 (100%)	0	0	100	100
12	M	33/36 (92%)	33 (100%)	0	0	100	100
12	m	32/36 (89%)	32 (100%)	0	0	100	100
13	O	249/244 (102%)	245 (98%)	4 (2%)	0	100	100
13	o	246/244 (101%)	240 (98%)	6 (2%)	0	100	100
14	T	29/32 (91%)	29 (100%)	0	0	100	100
14	t	29/32 (91%)	29 (100%)	0	0	100	100
15	U	95/104 (91%)	93 (98%)	2 (2%)	0	100	100
15	u	95/104 (91%)	93 (98%)	2 (2%)	0	100	100
16	V	136/137 (99%)	131 (96%)	5 (4%)	0	100	100
16	v	135/137 (98%)	129 (96%)	6 (4%)	0	100	100
17	Y	27/30 (90%)	26 (96%)	1 (4%)	0	100	100
17	y	27/30 (90%)	25 (93%)	2 (7%)	0	100	100
18	X	37/40 (92%)	37 (100%)	0	0	100	100
18	x	36/40 (90%)	35 (97%)	1 (3%)	0	100	100
19	Z	60/62 (97%)	58 (97%)	1 (2%)	1 (2%)	9	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	z	60/62 (97%)	58 (97%)	1 (2%)	1 (2%)	9	3
20	R	28/34 (82%)	27 (96%)	1 (4%)	0	100	100
All	All	5429/5384 (101%)	5309 (98%)	111 (2%)	9 (0%)	51	46

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	416[A]	SER
3	C	416[B]	SER
3	c	416[A]	SER
3	c	416[B]	SER
8	i	36	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	311/279 (112%)	311 (100%)	0	100	100
1	a	311/279 (112%)	309 (99%)	2 (1%)	86	90
2	B	412/403 (102%)	408 (99%)	4 (1%)	76	81
2	b	413/403 (102%)	409 (99%)	4 (1%)	76	81
3	C	361/356 (101%)	356 (99%)	5 (1%)	67	72
3	c	371/356 (104%)	363 (98%)	8 (2%)	52	55
4	D	290/277 (105%)	286 (99%)	4 (1%)	67	72
4	d	290/277 (105%)	287 (99%)	3 (1%)	76	81
5	E	74/73 (101%)	73 (99%)	1 (1%)	67	72
5	e	74/73 (101%)	73 (99%)	1 (1%)	67	72
6	F	28/38 (74%)	28 (100%)	0	100	100
6	f	26/38 (68%)	25 (96%)	1 (4%)	33	31
7	H	55/54 (102%)	53 (96%)	2 (4%)	35	33
7	h	54/54 (100%)	53 (98%)	1 (2%)	57	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	I	34/34 (100%)	34 (100%)	0	100	100
8	i	34/34 (100%)	33 (97%)	1 (3%)	42	42
9	J	26/27 (96%)	26 (100%)	0	100	100
9	j	27/27 (100%)	26 (96%)	1 (4%)	34	32
10	K	30/30 (100%)	29 (97%)	1 (3%)	38	37
10	k	30/30 (100%)	28 (93%)	2 (7%)	16	11
11	L	36/35 (103%)	35 (97%)	1 (3%)	43	44
11	l	36/35 (103%)	36 (100%)	0	100	100
12	M	31/32 (97%)	31 (100%)	0	100	100
12	m	30/32 (94%)	29 (97%)	1 (3%)	38	37
13	O	214/207 (103%)	209 (98%)	5 (2%)	50	53
13	o	211/207 (102%)	206 (98%)	5 (2%)	49	51
14	T	27/28 (96%)	25 (93%)	2 (7%)	13	9
14	t	27/28 (96%)	25 (93%)	2 (7%)	13	9
15	U	84/89 (94%)	82 (98%)	2 (2%)	49	51
15	u	84/89 (94%)	82 (98%)	2 (2%)	49	51
16	V	119/117 (102%)	119 (100%)	0	100	100
16	v	118/117 (101%)	118 (100%)	0	100	100
17	Y	22/23 (96%)	21 (96%)	1 (4%)	27	24
17	y	22/23 (96%)	20 (91%)	2 (9%)	9	5
18	X	32/33 (97%)	32 (100%)	0	100	100
18	x	31/33 (94%)	31 (100%)	0	100	100
19	Z	52/52 (100%)	50 (96%)	2 (4%)	33	31
19	z	52/52 (100%)	49 (94%)	3 (6%)	20	15
20	R	25/29 (86%)	24 (96%)	1 (4%)	31	29
All	All	4504/4403 (102%)	4434 (98%)	70 (2%)	65	67

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	12	ASN
3	c	391	ARG
15	u	86	GLU

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Mol	Chain	Res	Type
1	a	305	SER
2	b	479	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
13	O	124	ASN
1	a	12	ASN
13	o	130	GLN
13	O	147	ASN
19	Z	58	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
14	FME	T	1	14	8,9,10	0.70	0	7,9,11	1.30	1 (14%)
12	FME	M	1	12	8,9,10	0.67	0	7,9,11	1.39	2 (28%)
14	FME	t	1	14	8,9,10	0.79	0	7,9,11	2.41	4 (57%)
8	FME	i	1	8	8,9,10	0.60	0	7,9,11	1.21	1 (14%)
8	FME	I	1	8	8,9,10	0.63	0	7,9,11	1.26	1 (14%)
12	FME	m	1	12	8,9,10	0.66	0	7,9,11	1.33	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	FME	T	1	14	-	1/7/9/11	-
12	FME	M	1	12	-	2/7/9/11	-
14	FME	t	1	14	-	1/7/9/11	-
8	FME	i	1	8	-	0/7/9/11	-
8	FME	I	1	8	-	1/7/9/11	-
12	FME	m	1	12	-	0/7/9/11	-

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	t	1	FME	CA-N-CN	-3.87	116.87	122.82
14	t	1	FME	C-CA-N	2.86	114.89	109.73
14	T	1	FME	O-C-CA	-2.50	118.22	124.78
14	t	1	FME	O-C-CA	-2.43	118.40	124.78
14	t	1	FME	O1-CN-N	-2.33	119.13	125.27

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	T	1	FME	O1-CN-N-CA
8	I	1	FME	O1-CN-N-CA
12	M	1	FME	CA-CB-CG-SD
12	M	1	FME	CB-CA-N-CN
14	t	1	FME	CB-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 266 ligands modelled in this entry, 18 are unknown and 24 are monoatomic - leaving 224 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
28	GOL	B	626	-	5,5,5	0.43	0	5,5,5	0.33	0
24	CLA	B	602	41	59,73,73	2.03	12 (20%)	67,113,113	2.17	19 (28%)
24	CLA	A	407	41	59,73,73	1.96	13 (22%)	67,113,113	2.14	24 (35%)
24	CLA	b	622	-	59,73,73	2.05	14 (23%)	67,113,113	2.30	25 (37%)
29	LMT	C	521	-	36,36,36	0.48	0	47,47,47	1.13	3 (6%)
28	GOL	A	413	-	5,5,5	0.34	0	5,5,5	0.25	0
26	BCR	b	627	-	41,41,41	1.02	1 (2%)	56,56,56	1.35	5 (8%)
26	BCR	h	101	-	41,41,41	1.04	1 (2%)	56,56,56	1.39	8 (14%)
36	HTG	c	525	-	19,19,19	1.02	2 (10%)	23,24,24	1.47	2 (8%)
26	BCR	B	619	-	41,41,41	1.06	1 (2%)	56,56,56	1.47	9 (16%)
23	BCT	A	404[B]	21	0,3,3	0.00	-	0,3,3	0.00	-
24	CLA	B	603	-	59,73,73	2.06	13 (22%)	67,113,113	2.24	24 (35%)
24	CLA	C	513	-	59,73,73	2.01	13 (22%)	67,113,113	2.10	24 (35%)
24	CLA	B	613	-	59,73,73	2.04	13 (22%)	67,113,113	2.24	23 (34%)
24	CLA	b	616	-	59,73,73	2.01	13 (22%)	67,113,113	2.25	21 (31%)
24	CLA	C	507	41	59,73,73	1.97	13 (22%)	67,113,113	2.10	23 (34%)
23	BCT	a	419[A]	-	0,3,3	0.00	-	0,3,3	0.00	-
39	HEM	v	205	16	27,50,50	0.79	1 (3%)	17,82,82	1.26	1 (5%)
24	CLA	a	410	41	59,73,73	2.00	12 (20%)	67,113,113	2.11	23 (34%)
24	CLA	c	510	-	59,73,73	1.98	13 (22%)	67,113,113	2.13	23 (34%)
27	SQD	f	102	-	42,43,54	1.18	3 (7%)	51,54,65	1.41	7 (13%)
24	CLA	b	618	-	59,73,73	2.04	13 (22%)	67,113,113	2.14	23 (34%)
38	LHG	D	407	-	48,48,48	0.86	2 (4%)	51,54,54	1.09	5 (9%)
27	SQD	F	103	-	42,43,54	1.15	3 (7%)	51,54,65	1.64	11 (21%)
36	HTG	b	632	-	19,19,19	0.77	1 (5%)	23,24,24	1.29	2 (8%)
34	LMG	a	415	-	51,51,55	0.90	2 (3%)	59,59,63	1.17	4 (6%)
29	LMT	b	631	-	25,25,36	0.52	0	30,30,47	0.67	0
24	CLA	c	511	41	59,73,73	2.00	13 (22%)	67,113,113	2.27	20 (29%)
27	SQD	b	601	-	53,54,54	1.04	3 (5%)	62,65,65	1.55	9 (14%)
38	LHG	d	408	-	48,48,48	0.94	2 (4%)	51,54,54	0.98	2 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	BCR	t	101	-	41,41,41	0.99	1 (2%)	56,56,56	1.62	14 (25%)
24	CLA	C	509	-	59,73,73	2.10	13 (22%)	67,113,113	2.15	23 (34%)
24	CLA	d	403	-	59,73,73	2.01	13 (22%)	67,113,113	2.15	23 (34%)
24	CLA	b	611	41	59,73,73	2.04	12 (20%)	67,113,113	2.21	19 (28%)
28	GOL	O	301	-	5,5,5	0.37	0	5,5,5	0.41	0
24	CLA	c	515	3	59,73,73	1.99	13 (22%)	67,113,113	2.06	19 (28%)
32	PL9	d	405[B]	-	55,55,55	0.64	2 (3%)	68,69,69	1.61	16 (23%)
24	CLA	b	624	-	59,73,73	2.01	12 (20%)	67,113,113	2.30	24 (35%)
24	CLA	b	612	-	59,73,73	2.01	13 (22%)	67,113,113	2.24	21 (31%)
24	CLA	C	504	41	59,73,73	2.03	14 (23%)	67,113,113	2.25	23 (34%)
28	GOL	b	605	-	5,5,5	0.37	0	5,5,5	0.30	0
26	BCR	A	411	-	41,41,41	1.04	1 (2%)	56,56,56	1.21	5 (8%)
24	CLA	B	610	-	59,73,73	2.02	13 (22%)	67,113,113	2.14	22 (32%)
38	LHG	d	406	-	48,48,48	0.89	3 (6%)	51,54,54	1.05	4 (7%)
24	CLA	b	614	-	59,73,73	2.00	13 (22%)	67,113,113	2.29	21 (31%)
24	CLA	c	512	-	59,73,73	2.04	13 (22%)	67,113,113	2.23	25 (37%)
26	BCR	c	527	-	41,41,41	1.04	1 (2%)	56,56,56	1.56	9 (16%)
25	PHO	A	408	-	67,69,69	2.10	18 (26%)	85,99,99	1.98	23 (27%)
28	GOL	c	501	-	5,5,5	0.32	0	5,5,5	0.31	0
28	GOL	V	204	-	5,5,5	0.38	0	5,5,5	0.26	0
24	CLA	C	508	-	59,73,73	2.06	13 (22%)	67,113,113	2.26	23 (34%)
37	DGD	c	521	-	63,63,67	0.87	2 (3%)	77,77,81	1.08	6 (7%)
34	LMG	C	519	-	51,51,55	0.96	2 (3%)	59,59,63	0.98	3 (5%)
32	PL9	D	405[A]	-	55,55,55	0.63	2 (3%)	68,69,69	1.65	20 (29%)
24	CLA	B	608	41	59,73,73	1.97	13 (22%)	67,113,113	2.08	24 (35%)
26	BCR	D	404	-	41,41,41	1.02	1 (2%)	56,56,56	1.80	11 (19%)
28	GOL	v	202	-	5,5,5	0.35	0	5,5,5	0.25	0
25	PHO	a	420[B]	-	67,69,69	2.14	16 (23%)	85,99,99	1.96	21 (24%)
24	CLA	c	514	-	59,73,73	2.01	13 (22%)	67,113,113	2.15	23 (34%)
24	CLA	A	410	-	59,73,73	2.03	13 (22%)	67,113,113	2.17	27 (40%)
37	DGD	H	103	-	63,63,67	0.88	3 (4%)	77,77,81	1.05	7 (9%)
32	PL9	D	405[B]	-	55,55,55	0.64	2 (3%)	68,69,69	1.71	20 (29%)
26	BCR	c	518	-	41,41,41	1.03	1 (2%)	56,56,56	1.51	11 (19%)
24	CLA	B	614	-	59,73,73	2.03	13 (22%)	67,113,113	2.17	21 (31%)
29	LMT	f	103	-	36,36,36	0.46	0	47,47,47	0.83	1 (2%)
24	CLA	C	505	-	59,73,73	1.97	13 (22%)	67,113,113	2.18	18 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	BCR	k	101	-	41,41,41	1.00	1 (2%)	56,56,56	1.45	10 (17%)
27	SQD	A	412	-	53,54,54	0.97	3 (5%)	62,65,65	1.53	11 (17%)
26	BCR	a	413	-	41,41,41	1.04	1 (2%)	56,56,56	1.17	7 (12%)
28	GOL	B	629	-	5,5,5	0.36	0	5,5,5	0.33	0
37	DGD	C	517	-	63,63,67	0.88	2 (3%)	77,77,81	0.98	5 (6%)
28	GOL	T	102	-	5,5,5	0.39	0	5,5,5	0.26	0
26	BCR	C	515	-	41,41,41	0.99	1 (2%)	56,56,56	1.49	9 (16%)
24	CLA	B	604	-	59,73,73	2.06	14 (23%)	67,113,113	2.28	20 (29%)
24	CLA	C	503	-	59,73,73	1.99	13 (22%)	67,113,113	2.02	18 (26%)
32	PL9	a	416[A]	-	55,55,55	0.62	2 (3%)	68,69,69	1.91	20 (29%)
32	PL9	a	416[B]	-	55,55,55	0.63	2 (3%)	68,69,69	1.85	20 (29%)
36	HTG	b	633	-	19,19,19	1.16	2 (10%)	23,24,24	1.91	4 (17%)
24	CLA	D	403	-	59,73,73	1.99	13 (22%)	67,113,113	2.13	24 (35%)
28	GOL	o	301	-	5,5,5	0.37	0	5,5,5	0.27	0
26	BCR	K	101	-	41,41,41	1.01	1 (2%)	56,56,56	1.55	13 (23%)
25	PHO	A	409[A]	-	67,69,69	2.15	16 (23%)	85,99,99	1.94	20 (23%)
24	CLA	c	508	41	59,73,73	2.03	14 (23%)	67,113,113	2.29	26 (38%)
28	GOL	B	627	-	5,5,5	0.33	0	5,5,5	0.44	0
37	DGD	D	406	-	52,52,67	1.00	3 (5%)	60,60,81	1.16	4 (6%)
28	GOL	c	502	-	5,5,5	0.41	0	5,5,5	0.51	0
24	CLA	B	616	-	59,73,73	1.94	13 (22%)	67,113,113	2.10	23 (34%)
24	CLA	b	621	-	59,73,73	1.97	12 (20%)	67,113,113	2.14	22 (32%)
36	HTG	b	608	-	19,19,19	1.03	2 (10%)	23,24,24	1.48	2 (8%)
24	CLA	c	506	-	59,73,73	2.04	14 (23%)	67,113,113	2.19	21 (31%)
36	HTG	B	624	-	19,19,19	0.83	1 (5%)	23,24,24	1.48	3 (13%)
28	GOL	f	101	35	5,5,5	0.32	0	5,5,5	0.36	0
31	OYE	a	418[B]	1,3,41	0,16,16	0.00	-	-	-	-
36	HTG	d	411	-	16,16,19	1.13	2 (12%)	20,21,24	1.90	2 (10%)
27	SQD	A	416	-	53,54,54	1.03	3 (5%)	62,65,65	1.18	6 (9%)
26	BCR	B	620	-	41,41,41	1.06	1 (2%)	56,56,56	1.52	8 (14%)
38	LHG	d	407	-	48,48,48	0.90	2 (4%)	51,54,54	1.02	4 (7%)
38	LHG	E	101	-	41,41,48	1.03	2 (4%)	44,47,54	1.07	3 (6%)
24	CLA	B	615	-	59,73,73	1.98	13 (22%)	67,113,113	2.30	23 (34%)
24	CLA	A	406	41	59,73,73	1.97	13 (22%)	67,113,113	2.35	26 (38%)
34	LMG	j	101	40	51,51,55	0.92	2 (3%)	59,59,63	0.94	4 (6%)
29	LMT	A	417	-	36,36,36	0.61	1 (2%)	47,47,47	1.25	3 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
29	LMT	B	635	-	25,25,36	0.51	0	30,30,47	0.87	1 (3%)
32	PL9	d	405[A]	-	55,55,55	0.65	2 (3%)	68,69,69	1.55	13 (19%)
24	CLA	C	510	-	59,73,73	2.02	13 (22%)	67,113,113	2.17	23 (34%)
36	HTG	V	207	-	19,19,19	1.05	2 (10%)	23,24,24	1.25	3 (13%)
38	LHG	a	422	-	41,41,48	1.02	2 (4%)	44,47,54	0.95	3 (6%)
36	HTG	b	602	-	19,19,19	0.92	1 (5%)	23,24,24	1.18	2 (8%)
26	BCR	C	514	-	41,41,41	1.03	1 (2%)	56,56,56	1.55	10 (17%)
24	CLA	c	516	-	59,73,73	2.01	13 (22%)	67,113,113	2.30	22 (32%)
30	OEX	a	417[A]	1,3,41	0,15,15	0.00	-	-	-	-
24	CLA	b	619	-	59,73,73	1.97	12 (20%)	67,113,113	2.17	21 (31%)
26	BCR	T	103	-	41,41,41	1.06	1 (2%)	56,56,56	1.74	16 (28%)
24	CLA	b	613	-	59,73,73	1.99	13 (22%)	67,113,113	2.26	24 (35%)
28	GOL	t	102	-	5,5,5	0.47	0	5,5,5	0.16	0
24	CLA	b	623	-	59,73,73	2.01	13 (22%)	67,113,113	2.19	21 (31%)
28	GOL	A	415	-	5,5,5	0.41	0	5,5,5	0.21	0
24	CLA	b	626	-	59,73,73	2.02	13 (22%)	67,113,113	2.23	23 (34%)
28	GOL	V	201	35	5,5,5	0.36	0	5,5,5	0.24	0
36	HTG	B	633	-	19,19,19	1.01	2 (10%)	23,24,24	1.43	2 (8%)
29	LMT	T	104	-	25,25,36	0.50	0	30,30,47	0.93	1 (3%)
24	CLA	C	501	-	59,73,73	1.97	13 (22%)	67,113,113	2.17	20 (29%)
23	BCT	A	404[A]	21	0,3,3	0.00	-	0,3,3	0.00	-
24	CLA	d	402	-	59,73,73	2.01	13 (22%)	67,113,113	2.23	21 (31%)
29	LMT	F	101	-	36,36,36	0.48	0	47,47,47	0.92	1 (2%)
28	GOL	a	402	-	5,5,5	0.37	0	5,5,5	0.28	0
24	CLA	b	617	41	59,73,73	1.92	13 (22%)	67,113,113	2.16	20 (29%)
24	CLA	B	605	-	59,73,73	1.89	14 (23%)	67,113,113	2.24	20 (29%)
37	DGD	e	101	-	63,63,67	0.93	2 (3%)	77,77,81	1.24	7 (9%)
28	GOL	C	525	-	5,5,5	0.39	0	5,5,5	0.67	0
38	LHG	D	408	-	48,48,48	0.90	2 (4%)	51,54,54	0.84	3 (5%)
36	HTG	b	609	-	19,19,19	1.06	2 (10%)	23,24,24	1.23	3 (13%)
28	GOL	b	607	-	5,5,5	0.37	0	5,5,5	0.31	0
23	BCT	a	419[B]	21	0,3,3	0.00	-	0,3,3	0.00	-
38	LHG	D	409	-	48,48,48	0.95	2 (4%)	51,54,54	1.07	3 (5%)
24	CLA	c	505	-	59,73,73	1.99	13 (22%)	67,113,113	2.18	21 (31%)
36	HTG	B	625	-	19,19,19	1.07	2 (10%)	23,24,24	1.87	4 (17%)
37	DGD	C	518	-	63,63,67	0.85	2 (3%)	77,77,81	0.92	4 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
29	LMT	M	101	-	36,36,36	0.41	0	47,47,47	0.94	1 (2%)
24	CLA	b	620	41	59,73,73	2.05	13 (22%)	67,113,113	2.10	21 (31%)
39	HEM	V	206	16	27,50,50	0.85	1 (3%)	17,82,82	1.56	2 (11%)
39	HEM	e	102	5,6	27,50,50	0.80	1 (3%)	17,82,82	1.90	2 (11%)
29	LMT	a	421	-	36,36,36	0.46	0	47,47,47	0.83	1 (2%)
37	DGD	C	516	-	63,63,67	0.86	2 (3%)	77,77,81	1.09	6 (7%)
36	HTG	B	623	-	19,19,19	1.03	1 (5%)	23,24,24	1.24	1 (4%)
24	CLA	C	512	-	59,73,73	2.00	13 (22%)	67,113,113	2.20	21 (31%)
29	LMT	a	404	-	36,36,36	0.48	1 (2%)	47,47,47	1.20	3 (6%)
34	LMG	z	101	-	39,39,55	1.07	2 (5%)	47,47,63	1.13	4 (8%)
28	GOL	v	203	-	5,5,5	0.40	0	5,5,5	0.26	0
34	LMG	Z	101	-	37,37,55	0.95	2 (5%)	45,45,63	1.38	6 (13%)
24	CLA	B	606	-	59,73,73	1.97	12 (20%)	67,113,113	2.26	22 (32%)
24	CLA	c	517	-	59,73,73	1.97	13 (22%)	67,113,113	2.15	23 (34%)
27	SQD	a	414	-	53,54,54	0.98	3 (5%)	62,65,65	1.53	12 (19%)
24	CLA	C	511	3	59,73,73	2.05	12 (20%)	67,113,113	2.14	23 (34%)
28	GOL	B	636	-	5,5,5	0.40	0	5,5,5	0.53	0
29	LMT	D	401	-	36,36,36	0.43	0	47,47,47	0.99	1 (2%)
24	CLA	c	509	-	59,73,73	1.95	13 (22%)	67,113,113	2.17	20 (29%)
27	SQD	a	405	-	53,54,54	1.06	3 (5%)	62,65,65	1.22	4 (6%)
34	LMG	A	422	-	51,51,55	0.94	2 (3%)	59,59,63	1.13	5 (8%)
27	SQD	B	621	-	53,54,54	1.03	3 (5%)	62,65,65	1.45	10 (16%)
37	DGD	h	102	-	63,63,67	0.91	3 (4%)	77,77,81	0.97	4 (5%)
24	CLA	a	409	-	59,73,73	1.98	13 (22%)	67,113,113	2.18	26 (38%)
24	CLA	B	612	-	59,73,73	1.97	13 (22%)	67,113,113	2.26	22 (32%)
24	CLA	D	402	-	59,73,73	1.94	14 (23%)	67,113,113	2.26	22 (32%)
25	PHO	a	420[A]	-	67,69,69	2.13	16 (23%)	85,99,99	2.01	22 (25%)
28	GOL	T	101	-	5,5,5	0.50	0	5,5,5	0.19	0
24	CLA	B	609	-	59,73,73	1.99	14 (23%)	67,113,113	2.18	23 (34%)
28	GOL	B	628	-	5,5,5	0.35	0	5,5,5	0.55	0
34	LMG	D	412	40	51,51,55	0.89	2 (3%)	59,59,63	1.00	3 (5%)
24	CLA	c	513	-	59,73,73	2.05	13 (22%)	67,113,113	2.17	23 (34%)
34	LMG	B	622	-	51,51,55	0.93	2 (3%)	59,59,63	1.08	4 (6%)
28	GOL	b	603	-	5,5,5	0.43	0	5,5,5	0.47	0
28	GOL	b	604	-	5,5,5	0.36	0	5,5,5	0.25	0
24	CLA	A	405	-	59,73,73	2.01	12 (20%)	67,113,113	2.18	21 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
28	GOL	V	205	-	5,5,5	0.34	0	5,5,5	0.37	0
24	CLA	B	607	-	59,73,73	1.99	14 (23%)	67,113,113	2.28	24 (35%)
28	GOL	B	631	-	5,5,5	0.37	0	5,5,5	0.30	0
36	HTG	C	523	-	19,19,19	1.03	2 (10%)	23,24,24	1.81	4 (17%)
28	GOL	a	401	-	5,5,5	0.48	0	5,5,5	0.50	0
28	GOL	v	201	-	5,5,5	0.34	0	5,5,5	0.25	0
36	HTG	B	632	-	19,19,19	1.09	2 (10%)	23,24,24	1.36	3 (13%)
32	PL9	A	420[B]	-	55,55,55	0.63	2 (3%)	68,69,69	1.76	22 (32%)
26	BCR	Y	101	-	41,41,41	1.01	1 (2%)	56,56,56	1.61	8 (14%)
26	BCR	d	404	-	41,41,41	1.12	1 (2%)	56,56,56	1.56	10 (17%)
28	GOL	V	202	-	5,5,5	0.37	0	5,5,5	0.28	0
24	CLA	C	506	-	59,73,73	1.98	13 (22%)	67,113,113	2.18	23 (34%)
24	CLA	C	502	-	59,73,73	1.96	13 (22%)	67,113,113	2.18	23 (34%)
36	HTG	C	522	-	19,19,19	1.00	2 (10%)	23,24,24	1.57	2 (8%)
25	PHO	A	409[B]	-	67,69,69	2.16	16 (23%)	85,99,99	1.89	22 (25%)
34	LMG	c	523	-	51,51,55	0.96	2 (3%)	59,59,63	1.22	8 (13%)
28	GOL	A	414	-	5,5,5	0.46	0	5,5,5	0.53	0
26	BCR	b	629	-	41,41,41	1.08	1 (2%)	56,56,56	1.22	6 (10%)
34	LMG	c	522	-	51,51,55	0.91	2 (3%)	59,59,63	1.13	5 (8%)
24	CLA	b	615	-	59,73,73	1.99	12 (20%)	67,113,113	2.20	19 (28%)
36	HTG	H	101	-	16,16,19	1.12	2 (12%)	20,21,24	1.22	1 (5%)
28	GOL	B	630	-	5,5,5	0.40	0	5,5,5	0.14	0
34	LMG	b	630	-	51,51,55	0.91	2 (3%)	59,59,63	1.03	4 (6%)
24	CLA	B	617	-	59,73,73	1.98	13 (22%)	67,113,113	2.25	22 (32%)
24	CLA	c	507	-	59,73,73	2.02	13 (22%)	67,113,113	2.08	19 (28%)
34	LMG	C	520	-	51,51,55	0.96	2 (3%)	59,59,63	1.10	2 (3%)
29	LMT	M	104	-	36,36,36	0.46	0	47,47,47	0.87	1 (2%)
29	LMT	M	103	-	36,36,36	0.52	1 (2%)	47,47,47	0.99	3 (6%)
26	BCR	b	628	-	41,41,41	0.96	1 (2%)	56,56,56	1.34	9 (16%)
31	OEY	A	419[B]	1,3,41	0,16,16	0.00	-	-	-	-
26	BCR	H	102	-	41,41,41	1.10	1 (2%)	56,56,56	1.44	9 (16%)
38	LHG	l	101	-	48,48,48	0.92	2 (4%)	51,54,54	1.10	4 (7%)
36	HTG	c	524	-	19,19,19	1.04	2 (10%)	23,24,24	1.53	2 (8%)
24	CLA	a	412	-	59,73,73	2.01	13 (22%)	67,113,113	2.19	25 (37%)
37	DGD	c	520	-	63,63,67	0.87	2 (3%)	77,77,81	0.96	2 (2%)
24	CLA	B	611	41	59,73,73	2.06	13 (22%)	67,113,113	2.20	24 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	b	625	-	59,73,73	1.98	13 (22%)	67,113,113	2.18	22 (32%)
39	HEM	F	102	5,6	27,50,50	0.85	1 (3%)	17,82,82	2.29	3 (17%)
26	BCR	B	618	-	41,41,41	0.99	1 (2%)	56,56,56	1.39	8 (14%)
37	DGD	c	519	-	63,63,67	0.83	2 (3%)	77,77,81	1.09	5 (6%)
24	CLA	d	401	41	59,73,73	2.04	14 (23%)	67,113,113	2.20	25 (37%)
30	OEX	A	418[A]	1,3,41	0,15,15	0.00	-	-	-	-
26	BCR	y	101	-	41,41,41	1.04	1 (2%)	56,56,56	1.56	11 (19%)
32	PL9	A	420[A]	-	55,55,55	0.62	1 (1%)	68,69,69	1.76	21 (30%)
38	LHG	L	101	-	48,48,48	0.92	2 (4%)	51,54,54	1.05	4 (7%)
25	PHO	a	411	-	67,69,69	2.13	16 (23%)	85,99,99	1.87	22 (25%)
28	GOL	C	524	-	5,5,5	0.38	0	5,5,5	0.77	0
29	LMT	m	102	-	36,36,36	0.45	0	47,47,47	1.01	3 (6%)
28	GOL	b	606	-	5,5,5	0.38	0	5,5,5	0.26	0
28	GOL	V	203	-	5,5,5	0.35	0	5,5,5	0.43	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	GOL	B	626	-	-	1/4/4/4	-
24	CLA	B	602	41	3/3/20/25	12/37/135/135	-
24	CLA	A	407	41	2/2/20/25	2/37/135/135	-
24	CLA	b	622	-	3/3/20/25	1/37/135/135	-
29	LMT	C	521	-	-	11/21/61/61	0/2/2/2
28	GOL	O	301	-	-	2/4/4/4	-
26	BCR	b	627	-	-	2/29/63/63	0/2/2/2
26	BCR	h	101	-	-	1/29/63/63	0/2/2/2
36	HTG	c	525	-	-	0/10/30/30	0/1/1/1
26	BCR	B	619	-	-	0/29/63/63	0/2/2/2
26	BCR	k	101	-	-	2/29/63/63	0/2/2/2
24	CLA	B	603	-	2/2/20/25	5/37/135/135	-
24	CLA	C	513	-	3/3/20/25	7/37/135/135	-
24	CLA	B	613	-	3/3/20/25	3/37/135/135	-
24	CLA	b	616	-	2/2/20/25	9/37/135/135	-
24	CLA	C	507	41	3/3/20/25	7/37/135/135	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	HEM	v	205	16	-	0/6/54/54	-
24	CLA	a	410	41	2/2/20/25	6/37/135/135	-
24	CLA	b	623	-	3/3/20/25	2/37/135/135	-
27	SQD	f	102	-	-	14/38/58/69	0/1/1/1
24	CLA	b	618	-	2/2/20/25	2/37/135/135	-
38	LHG	D	407	-	-	13/53/53/53	-
27	SQD	F	103	-	-	16/38/58/69	0/1/1/1
36	HTG	b	632	-	-	3/10/30/30	0/1/1/1
34	LMG	a	415	-	-	16/46/66/70	0/1/1/1
29	LMT	b	631	-	-	4/17/37/61	0/1/1/2
24	CLA	c	511	41	3/3/20/25	4/37/135/135	-
27	SQD	b	601	-	-	22/49/69/69	0/1/1/1
38	LHG	d	408	-	-	11/53/53/53	-
26	BCR	t	101	-	-	2/29/63/63	0/2/2/2
24	CLA	C	509	-	3/3/20/25	11/37/135/135	-
24	CLA	d	403	-	3/3/20/25	3/37/135/135	-
26	BCR	K	101	-	-	1/29/63/63	0/2/2/2
28	GOL	A	413	-	-	1/4/4/4	-
24	CLA	b	626	-	3/3/20/25	9/37/135/135	-
24	CLA	c	517	-	2/2/20/25	4/37/135/135	-
24	CLA	b	612	-	2/2/20/25	3/37/135/135	-
24	CLA	C	504	41	3/3/20/25	5/37/135/135	-
28	GOL	b	605	-	-	1/4/4/4	-
26	BCR	A	411	-	-	0/29/63/63	0/2/2/2
24	CLA	B	610	-	2/2/20/25	3/37/135/135	-
38	LHG	d	406	-	-	10/53/53/53	-
24	CLA	b	614	-	3/3/20/25	6/37/135/135	-
24	CLA	c	512	-	3/3/20/25	4/37/135/135	-
26	BCR	c	527	-	-	0/29/63/63	0/2/2/2
38	LHG	a	422	-	-	19/46/46/53	-
28	GOL	c	501	-	-	0/4/4/4	-
28	GOL	V	204	-	-	1/4/4/4	-
37	DGD	c	521	-	-	15/51/91/95	0/2/2/2
34	LMG	C	519	-	-	13/46/66/70	0/1/1/1
32	PL9	D	405[A]	-	-	8/53/73/73	0/1/1/1
24	CLA	B	608	41	3/3/20/25	6/37/135/135	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	BCR	D	404	-	-	8/29/63/63	0/2/2/2
28	GOL	v	202	-	-	2/4/4/4	-
25	PHO	a	420[B]	-	-	3/53/103/103	0/5/6/6
24	CLA	c	514	-	3/3/20/25	9/37/135/135	-
24	CLA	A	410	-	3/3/20/25	7/37/135/135	-
37	DGD	H	103	-	-	13/51/91/95	0/2/2/2
32	PL9	D	405[B]	-	-	7/53/73/73	0/1/1/1
26	BCR	c	518	-	-	2/29/63/63	0/2/2/2
24	CLA	B	614	-	3/3/20/25	3/37/135/135	-
29	LMT	f	103	-	-	10/21/61/61	0/2/2/2
24	CLA	C	505	-	1/1/20/25	5/37/135/135	-
27	SQD	A	412	-	-	8/49/69/69	0/1/1/1
26	BCR	a	413	-	-	0/29/63/63	0/2/2/2
24	CLA	C	508	-	3/3/20/25	5/37/135/135	-
37	DGD	C	517	-	-	17/51/91/95	0/2/2/2
28	GOL	T	102	-	-	2/4/4/4	-
26	BCR	C	515	-	-	2/29/63/63	0/2/2/2
24	CLA	B	604	-	2/2/20/25	6/37/135/135	-
24	CLA	C	503	-	3/3/20/25	2/37/135/135	-
32	PL9	a	416[A]	-	-	14/53/73/73	0/1/1/1
32	PL9	a	416[B]	-	-	14/53/73/73	0/1/1/1
36	HTG	b	633	-	-	5/10/30/30	0/1/1/1
24	CLA	D	403	-	3/3/20/25	7/37/135/135	-
28	GOL	o	301	-	-	0/4/4/4	-
24	CLA	b	611	41	3/3/20/25	17/37/135/135	-
25	PHO	A	409[A]	-	-	2/53/103/103	0/5/6/6
24	CLA	c	508	41	3/3/20/25	5/37/135/135	-
28	GOL	B	627	-	-	2/4/4/4	-
37	DGD	D	406	-	-	21/47/67/95	0/1/1/2
28	GOL	c	502	-	-	1/4/4/4	-
24	CLA	B	616	-	3/3/20/25	10/37/135/135	-
24	CLA	b	621	-	2/2/20/25	3/37/135/135	-
36	HTG	b	608	-	-	1/10/30/30	0/1/1/1
24	CLA	c	506	-	1/1/20/25	4/37/135/135	-
36	HTG	B	624	-	-	2/10/30/30	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	GOL	f	101	35	-	3/4/4/4	-
36	HTG	d	411	-	-	1/7/27/30	0/1/1/1
27	SQD	A	416	-	-	15/49/69/69	0/1/1/1
26	BCR	B	620	-	-	0/29/63/63	0/2/2/2
38	LHG	d	407	-	-	10/53/53/53	-
38	LHG	E	101	-	-	20/46/46/53	-
24	CLA	B	615	-	2/2/20/25	15/37/135/135	-
24	CLA	A	406	41	3/3/20/25	6/37/135/135	-
34	LMG	j	101	40	-	11/46/66/70	0/1/1/1
29	LMT	A	417	-	-	5/21/61/61	0/2/2/2
29	LMT	B	635	-	-	7/17/37/61	0/1/1/2
32	PL9	d	405[A]	-	-	8/53/73/73	0/1/1/1
24	CLA	C	510	-	3/3/20/25	8/37/135/135	-
36	HTG	V	207	-	-	3/10/30/30	0/1/1/1
25	PHO	A	408	-	-	4/53/103/103	0/5/6/6
36	HTG	b	602	-	-	3/10/30/30	0/1/1/1
28	GOL	B	629	-	-	1/4/4/4	-
26	BCR	C	514	-	-	2/29/63/63	0/2/2/2
24	CLA	c	516	-	3/3/20/25	9/37/135/135	-
24	CLA	b	619	-	2/2/20/25	4/37/135/135	-
26	BCR	T	103	-	-	3/29/63/63	0/2/2/2
24	CLA	b	613	-	2/2/20/25	5/37/135/135	-
28	GOL	t	102	-	-	0/4/4/4	-
24	CLA	c	510	-	3/3/20/25	15/37/135/135	-
28	GOL	A	415	-	-	2/4/4/4	-
24	CLA	c	515	3	3/3/20/25	6/37/135/135	-
28	GOL	V	201	35	-	2/4/4/4	-
36	HTG	B	633	-	-	0/10/30/30	0/1/1/1
29	LMT	T	104	-	-	7/17/37/61	0/1/1/2
24	CLA	C	501	-	3/3/20/25	5/37/135/135	-
24	CLA	d	402	-	1/1/20/25	3/37/135/135	-
29	LMT	F	101	-	-	3/21/61/61	0/2/2/2
28	GOL	a	402	-	-	2/4/4/4	-
24	CLA	b	617	41	3/3/20/25	0/37/135/135	-
24	CLA	B	605	-	3/3/20/25	6/37/135/135	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
37	DGD	e	101	-	-	27/51/91/95	0/2/2/2
28	GOL	C	525	-	-	0/4/4/4	-
38	LHG	D	408	-	-	12/53/53/53	-
36	HTG	b	609	-	-	0/10/30/30	0/1/1/1
28	GOL	b	607	-	-	3/4/4/4	-
38	LHG	D	409	-	-	12/53/53/53	-
24	CLA	c	505	-	3/3/20/25	2/37/135/135	-
36	HTG	B	625	-	-	4/10/30/30	0/1/1/1
37	DGD	C	518	-	-	11/51/91/95	0/2/2/2
29	LMT	M	101	-	-	4/21/61/61	0/2/2/2
24	CLA	b	620	41	3/3/20/25	6/37/135/135	-
39	HEM	V	206	16	-	0/6/54/54	-
39	HEM	e	102	5,6	-	0/6/54/54	-
29	LMT	a	421	-	-	4/21/61/61	0/2/2/2
37	DGD	C	516	-	-	15/51/91/95	0/2/2/2
36	HTG	B	623	-	-	4/10/30/30	0/1/1/1
24	CLA	C	512	-	3/3/20/25	8/37/135/135	-
29	LMT	a	404	-	-	9/21/61/61	0/2/2/2
34	LMG	z	101	-	-	14/34/54/70	0/1/1/1
28	GOL	v	203	-	-	2/4/4/4	-
34	LMG	Z	101	-	-	14/31/51/70	0/1/1/1
24	CLA	B	606	-	3/3/20/25	5/37/135/135	-
24	CLA	b	624	-	2/2/20/25	19/37/135/135	-
27	SQD	a	414	-	-	14/49/69/69	0/1/1/1
24	CLA	C	511	3	3/3/20/25	3/37/135/135	-
28	GOL	B	636	-	-	0/4/4/4	-
29	LMT	D	401	-	-	8/21/61/61	0/2/2/2
24	CLA	c	509	-	2/2/20/25	2/37/135/135	-
27	SQD	a	405	-	-	17/49/69/69	0/1/1/1
34	LMG	A	422	-	-	20/46/66/70	0/1/1/1
27	SQD	B	621	-	-	20/49/69/69	0/1/1/1
37	DGD	h	102	-	-	10/51/91/95	0/2/2/2
24	CLA	a	409	-	3/3/20/25	4/37/135/135	-
24	CLA	B	612	-	2/2/20/25	0/37/135/135	-
24	CLA	D	402	-	1/1/20/25	1/37/135/135	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	PHO	a	420[A]	-	-	3/53/103/103	0/5/6/6
28	GOL	T	101	-	-	2/4/4/4	-
24	CLA	B	609	-	2/2/20/25	1/37/135/135	-
28	GOL	B	628	-	-	2/4/4/4	-
34	LMG	D	412	40	-	7/46/66/70	0/1/1/1
24	CLA	c	513	-	3/3/20/25	11/37/135/135	-
34	LMG	B	622	-	-	9/46/66/70	0/1/1/1
28	GOL	b	603	-	-	0/4/4/4	-
28	GOL	b	604	-	-	0/4/4/4	-
24	CLA	A	405	-	3/3/20/25	7/37/135/135	-
28	GOL	V	205	-	-	2/4/4/4	-
24	CLA	B	607	-	2/2/20/25	4/37/135/135	-
28	GOL	B	631	-	-	1/4/4/4	-
36	HTG	C	523	-	-	3/10/30/30	0/1/1/1
28	GOL	a	401	-	-	0/4/4/4	-
28	GOL	v	201	-	-	2/4/4/4	-
36	HTG	B	632	-	-	3/10/30/30	0/1/1/1
32	PL9	A	420[B]	-	-	10/53/73/73	0/1/1/1
26	BCR	Y	101	-	-	4/29/63/63	0/2/2/2
26	BCR	d	404	-	-	4/29/63/63	0/2/2/2
28	GOL	V	202	-	-	2/4/4/4	-
24	CLA	C	506	-	3/3/20/25	8/37/135/135	-
24	CLA	C	502	-	3/3/20/25	8/37/135/135	-
36	HTG	C	522	-	-	0/10/30/30	0/1/1/1
25	PHO	A	409[B]	-	-	2/53/103/103	0/5/6/6
34	LMG	c	523	-	-	3/46/66/70	0/1/1/1
28	GOL	A	414	-	-	2/4/4/4	-
26	BCR	b	629	-	-	0/29/63/63	0/2/2/2
34	LMG	c	522	-	-	15/46/66/70	0/1/1/1
24	CLA	b	615	-	2/2/20/25	4/37/135/135	-
36	HTG	H	101	-	-	0/7/27/30	0/1/1/1
28	GOL	B	630	-	-	4/4/4/4	-
34	LMG	b	630	-	-	10/46/66/70	0/1/1/1
24	CLA	B	617	-	3/3/20/25	6/37/135/135	-
24	CLA	c	507	-	2/2/20/25	4/37/135/135	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	LMG	C	520	-	-	12/46/66/70	0/1/1/1
29	LMT	M	104	-	-	7/21/61/61	0/2/2/2
29	LMT	M	103	-	-	9/21/61/61	0/2/2/2
26	BCR	b	628	-	-	1/29/63/63	0/2/2/2
32	PL9	d	405[B]	-	-	5/53/73/73	0/1/1/1
26	BCR	H	102	-	-	1/29/63/63	0/2/2/2
38	LHG	l	101	-	-	15/53/53/53	-
36	HTG	c	524	-	-	3/10/30/30	0/1/1/1
24	CLA	a	412	-	3/3/20/25	9/37/135/135	-
37	DGD	c	520	-	-	18/51/91/95	0/2/2/2
24	CLA	B	611	41	3/3/20/25	4/37/135/135	-
24	CLA	b	625	-	3/3/20/25	4/37/135/135	-
39	HEM	F	102	5,6	-	0/6/54/54	-
26	BCR	B	618	-	-	2/29/63/63	0/2/2/2
37	DGD	c	519	-	-	14/51/91/95	0/2/2/2
24	CLA	d	401	41	3/3/20/25	6/37/135/135	-
26	BCR	y	101	-	-	4/29/63/63	0/2/2/2
32	PL9	A	420[A]	-	-	10/53/73/73	0/1/1/1
38	LHG	L	101	-	-	17/53/53/53	-
25	PHO	a	411	-	-	6/53/103/103	0/5/6/6
28	GOL	C	524	-	-	2/4/4/4	-
29	LMT	m	102	-	-	7/21/61/61	0/2/2/2
28	GOL	b	606	-	-	2/4/4/4	-
28	GOL	V	203	-	-	2/4/4/4	-

The worst 5 of 1174 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	b	622	CLA	C3B-C2B	6.68	1.49	1.40
24	B	613	CLA	C3B-C2B	6.54	1.49	1.40
24	C	509	CLA	C3B-C2B	6.51	1.49	1.40
24	B	603	CLA	C3B-C2B	6.46	1.49	1.40
24	C	504	CLA	C3B-C2B	6.40	1.49	1.40

The worst 5 of 2328 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	B	606	CLA	CHD-C4C-C3C	-7.30	114.11	124.84
24	b	615	CLA	CHD-C4C-C3C	-7.17	114.29	124.84
24	b	612	CLA	C4A-NA-C1A	-7.13	103.50	106.71
25	A	408	PHO	CMD-C2D-C1D	7.05	135.93	125.06
39	F	102	HEM	CAD-CBD-CGD	7.03	124.46	112.67

5 of 182 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
24	B	602	CLA	NC
24	B	602	CLA	ND
24	B	602	CLA	NA
24	A	407	CLA	NC
24	A	407	CLA	NA

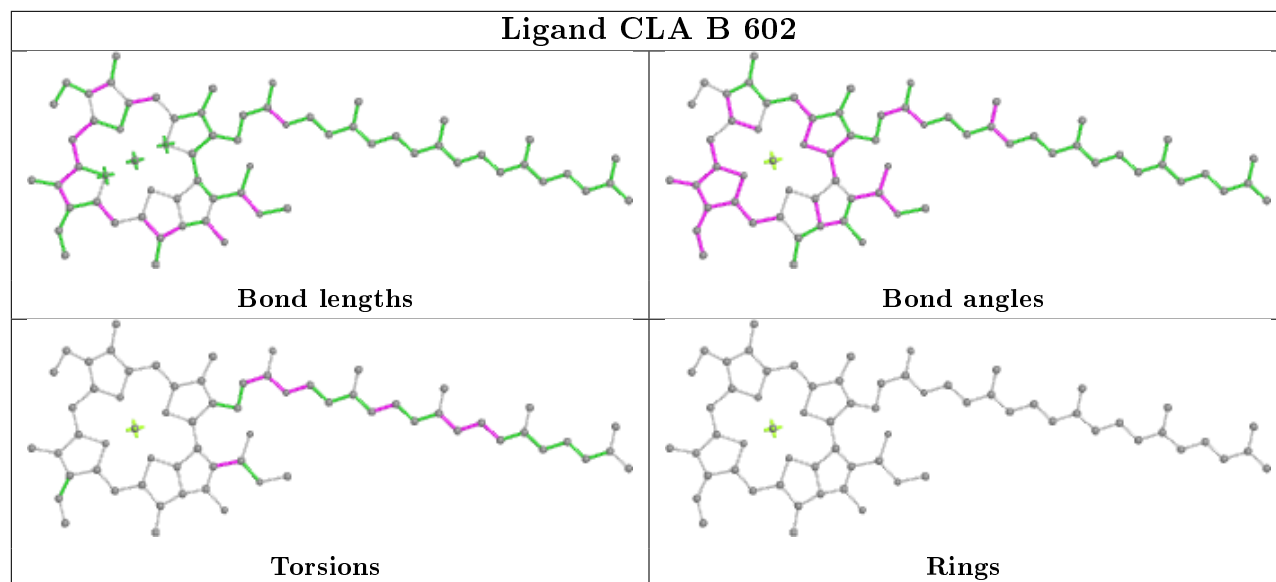
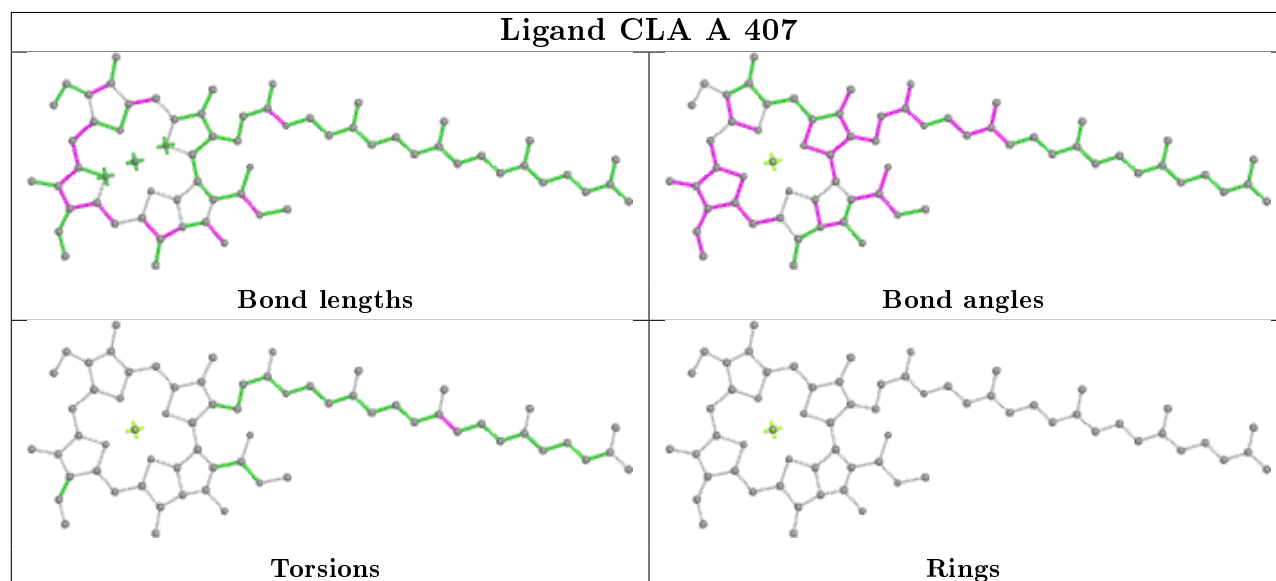
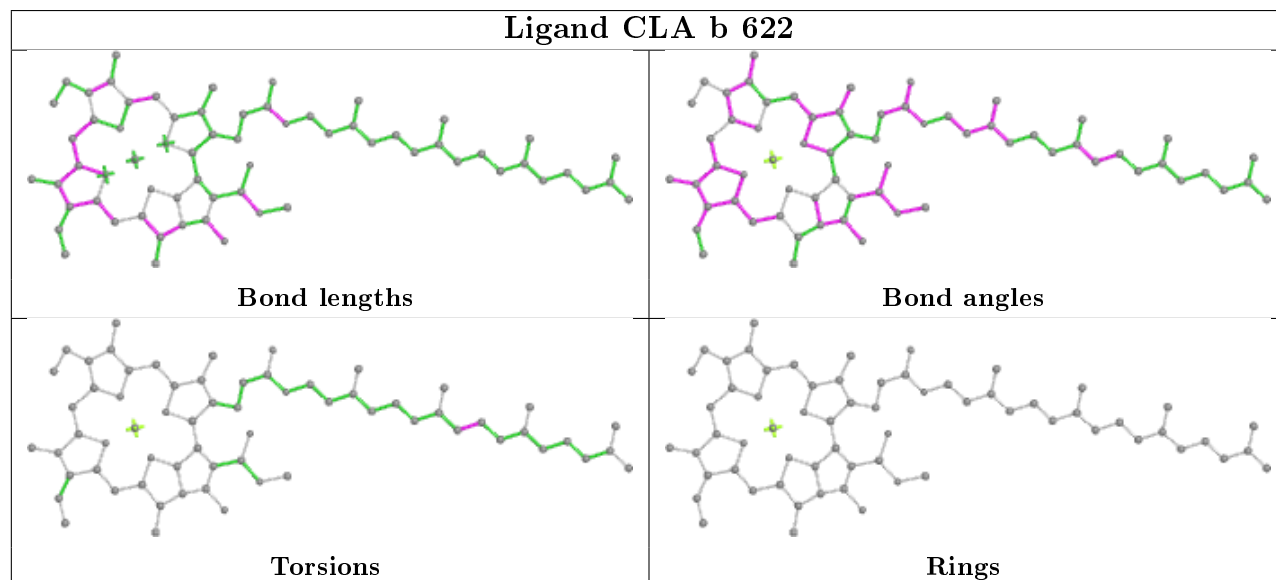
5 of 1293 torsion outliers are listed below:

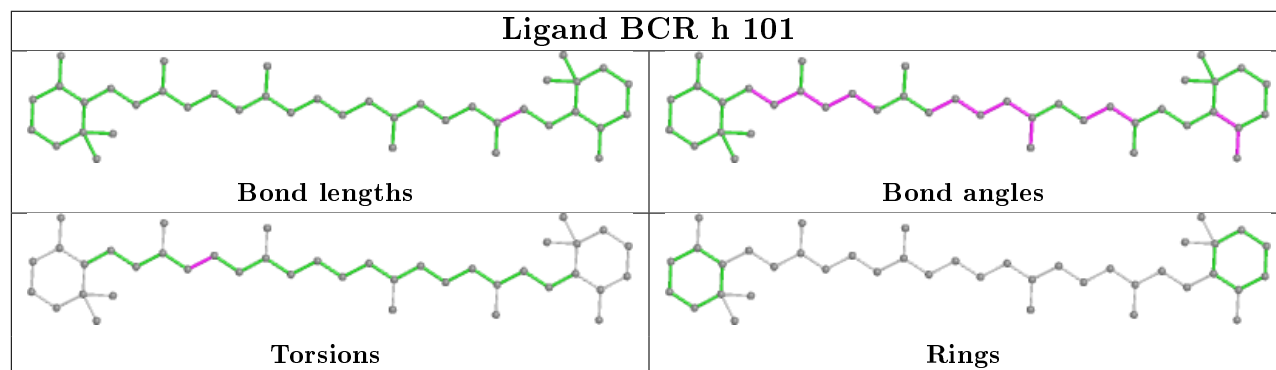
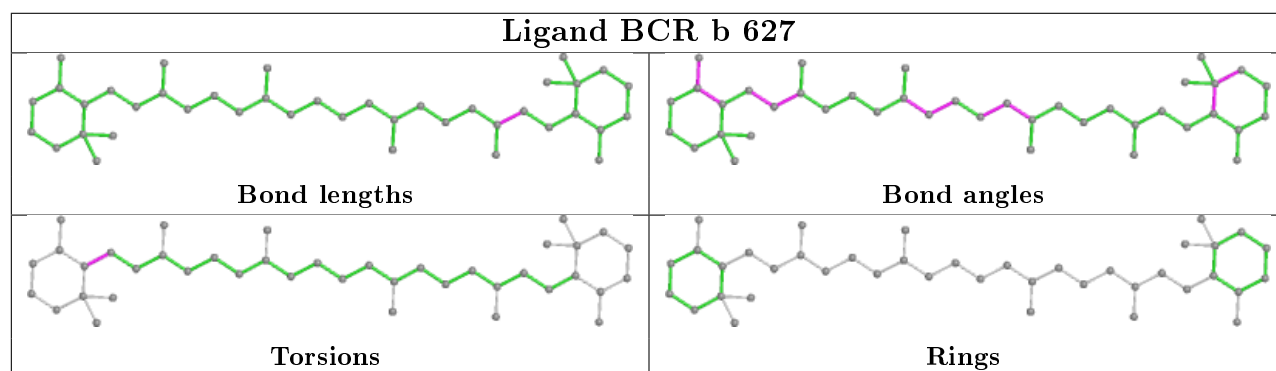
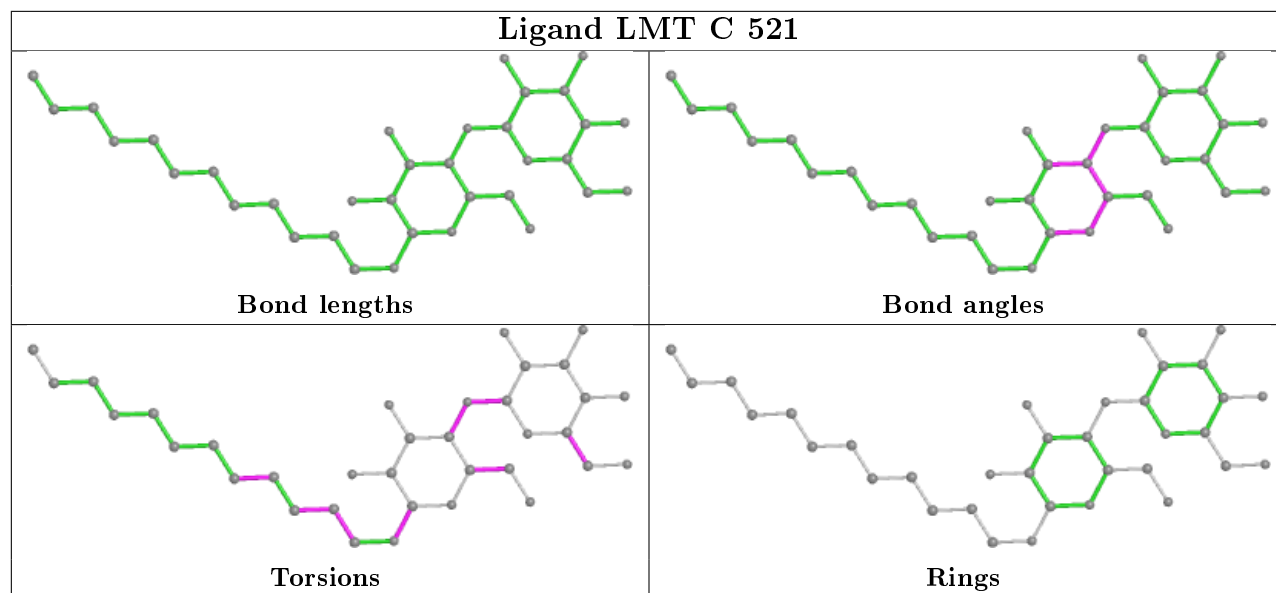
Mol	Chain	Res	Type	Atoms
29	C	521	LMT	C2'-C1'-O1'-C1
29	C	521	LMT	O5'-C1'-O1'-C1
27	F	103	SQD	O49-C7-O47-C45
27	F	103	SQD	C8-C7-O47-C45
27	F	103	SQD	C5-C6-S-O7

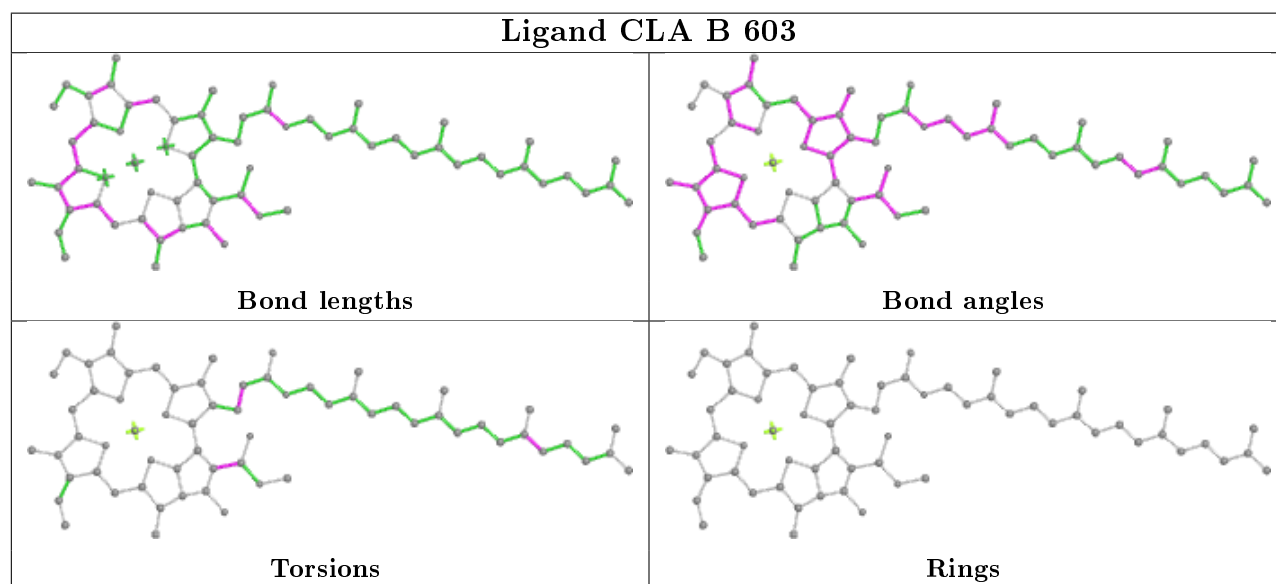
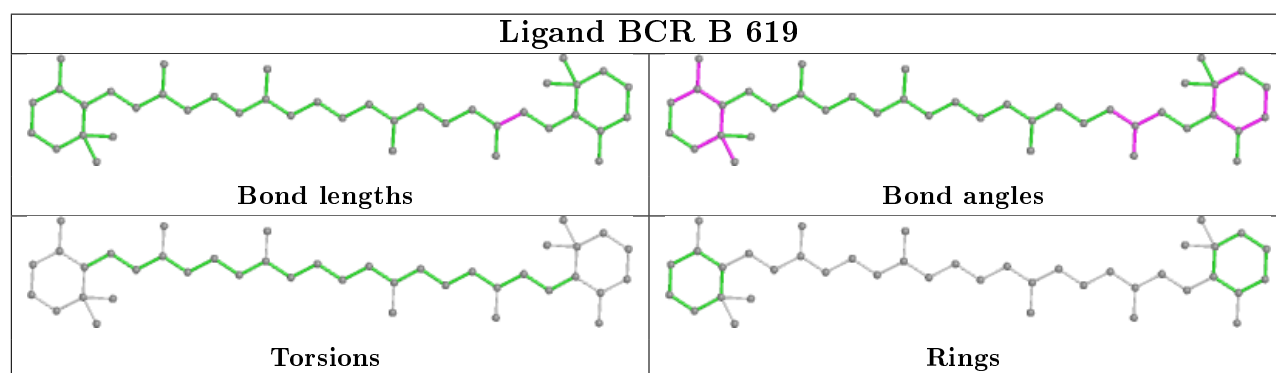
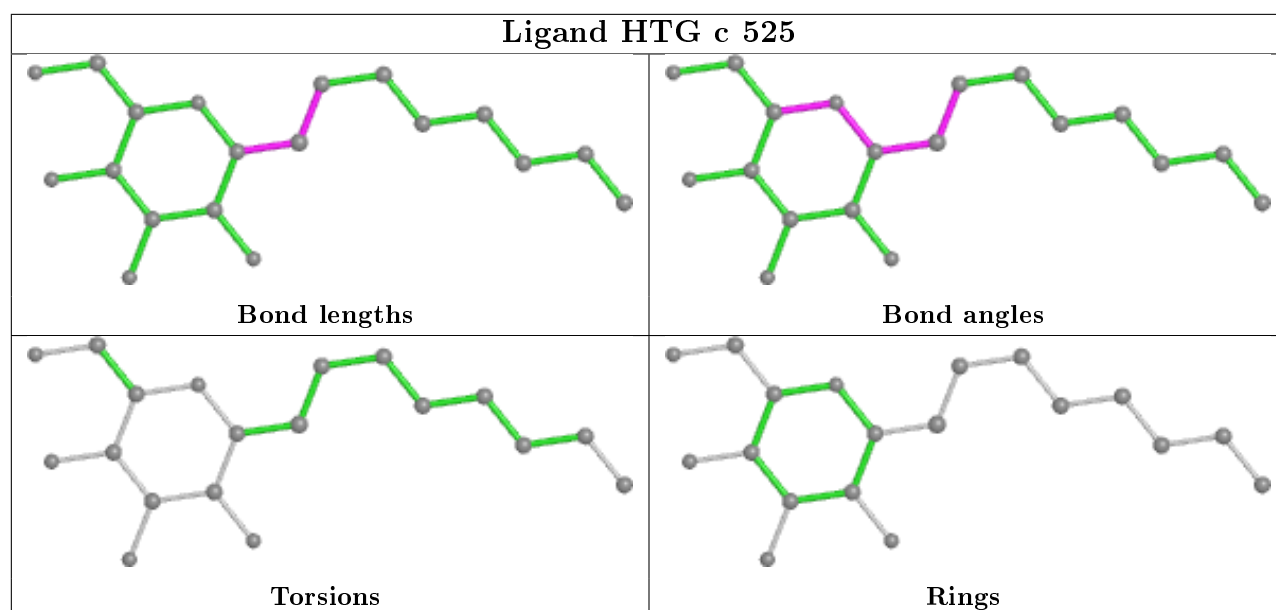
There are no ring outliers.

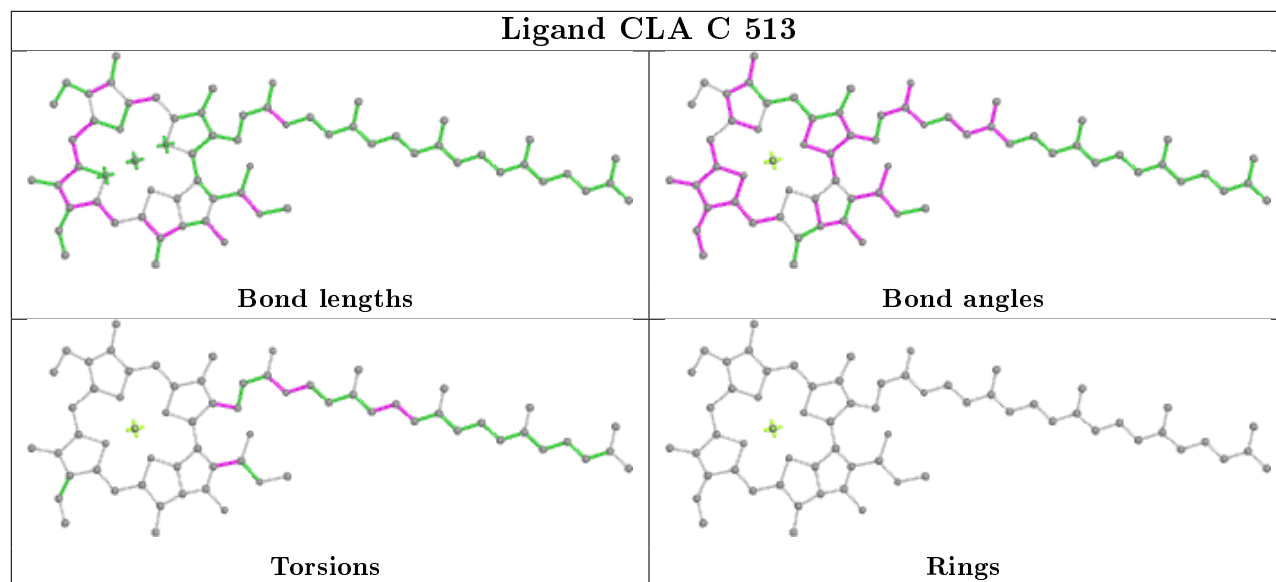
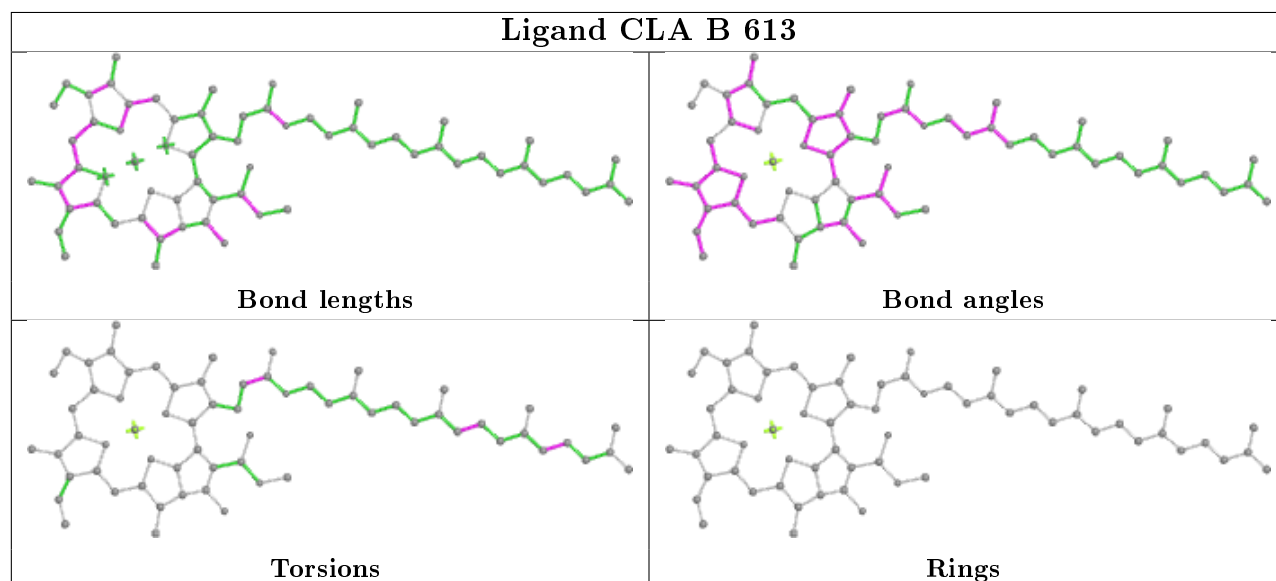
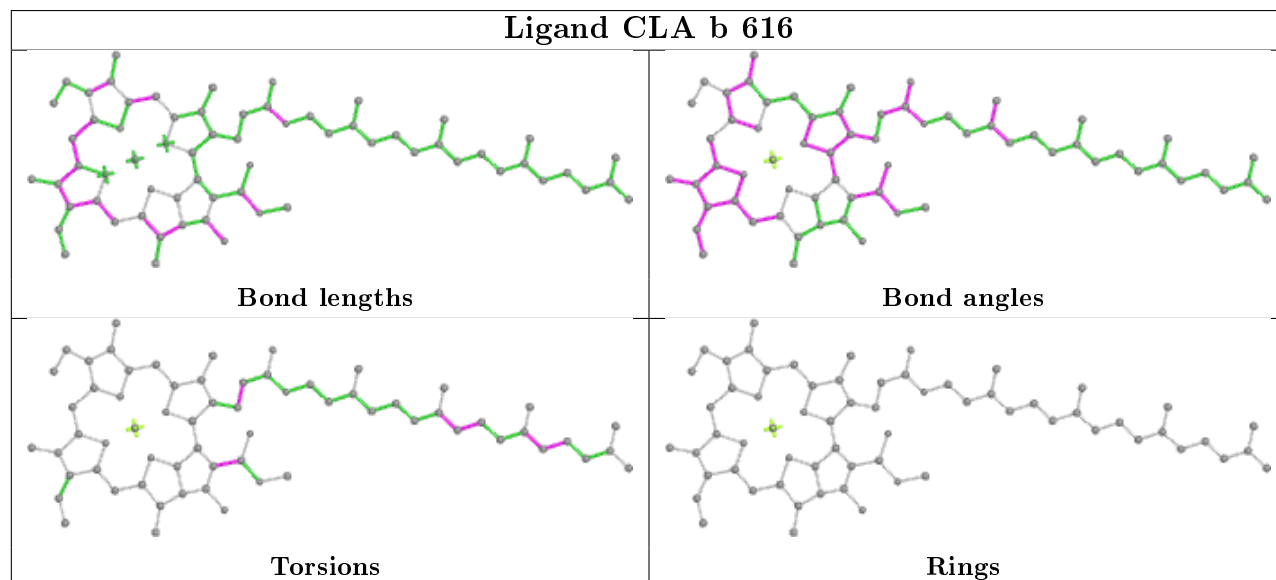
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

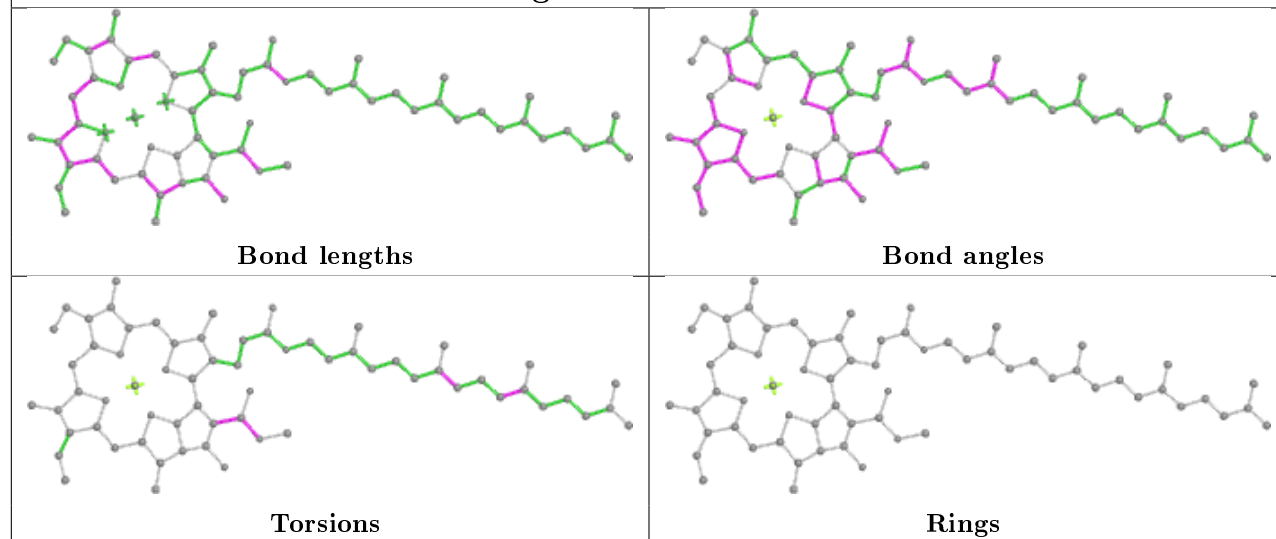
Ligand CLA B 602**Ligand CLA A 407****Ligand CLA b 622**



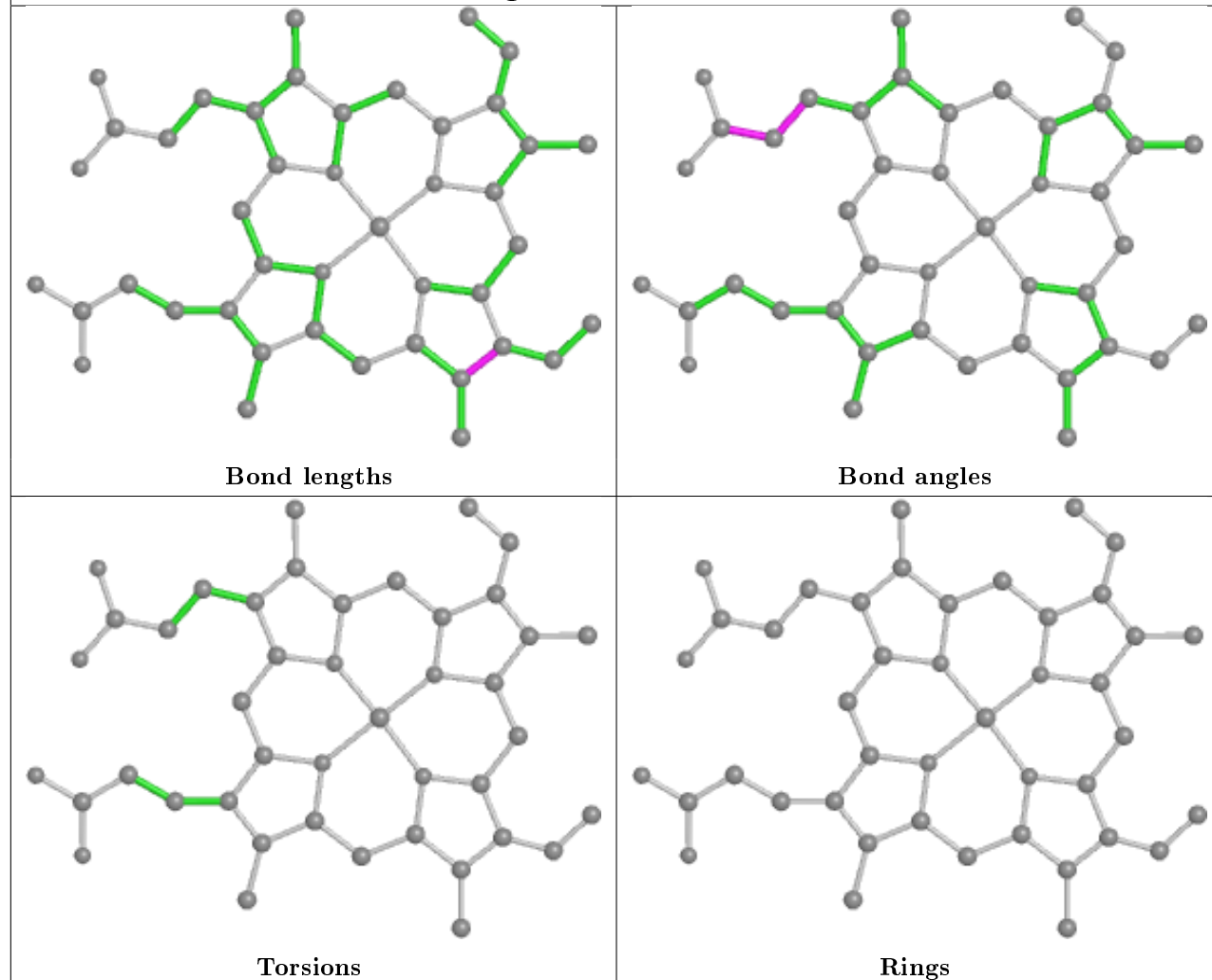


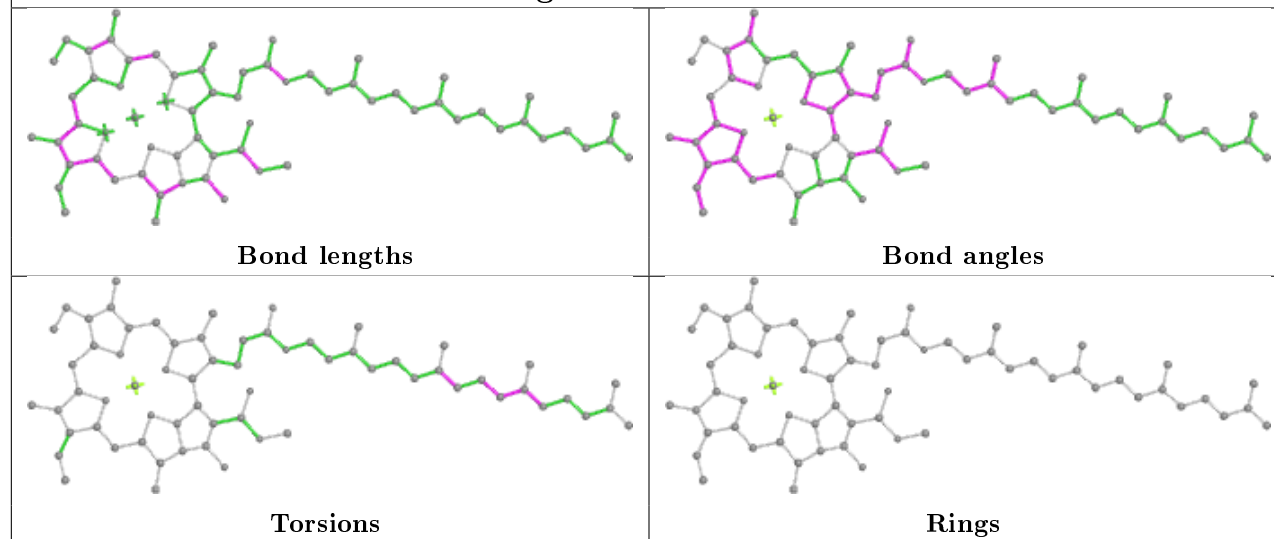
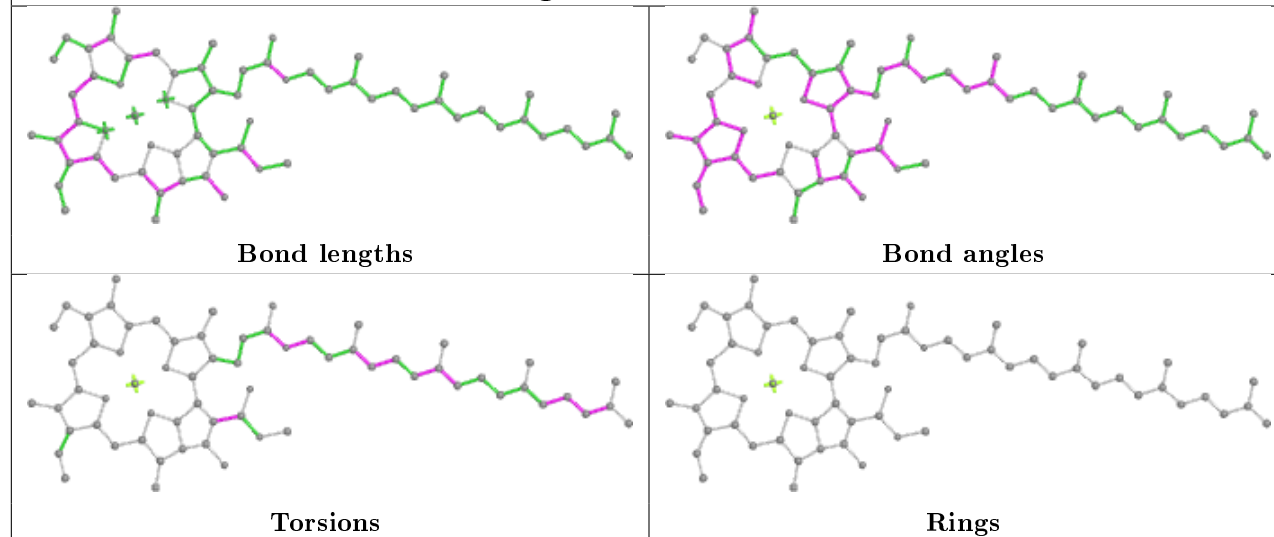
Ligand CLA C 513**Ligand CLA B 613****Ligand CLA b 616**

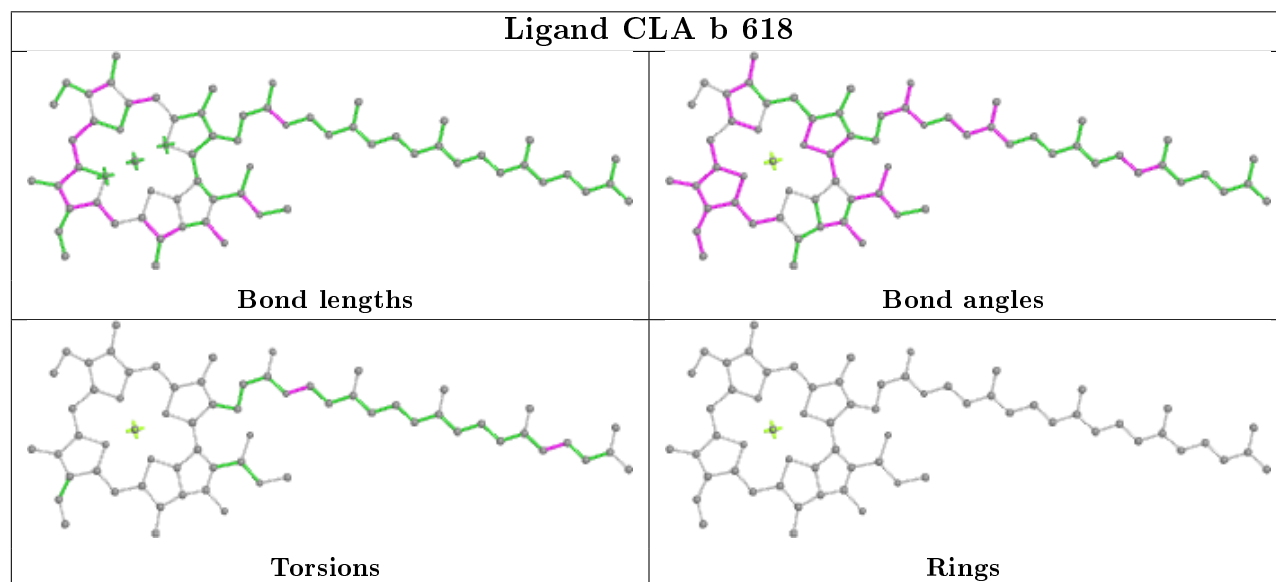
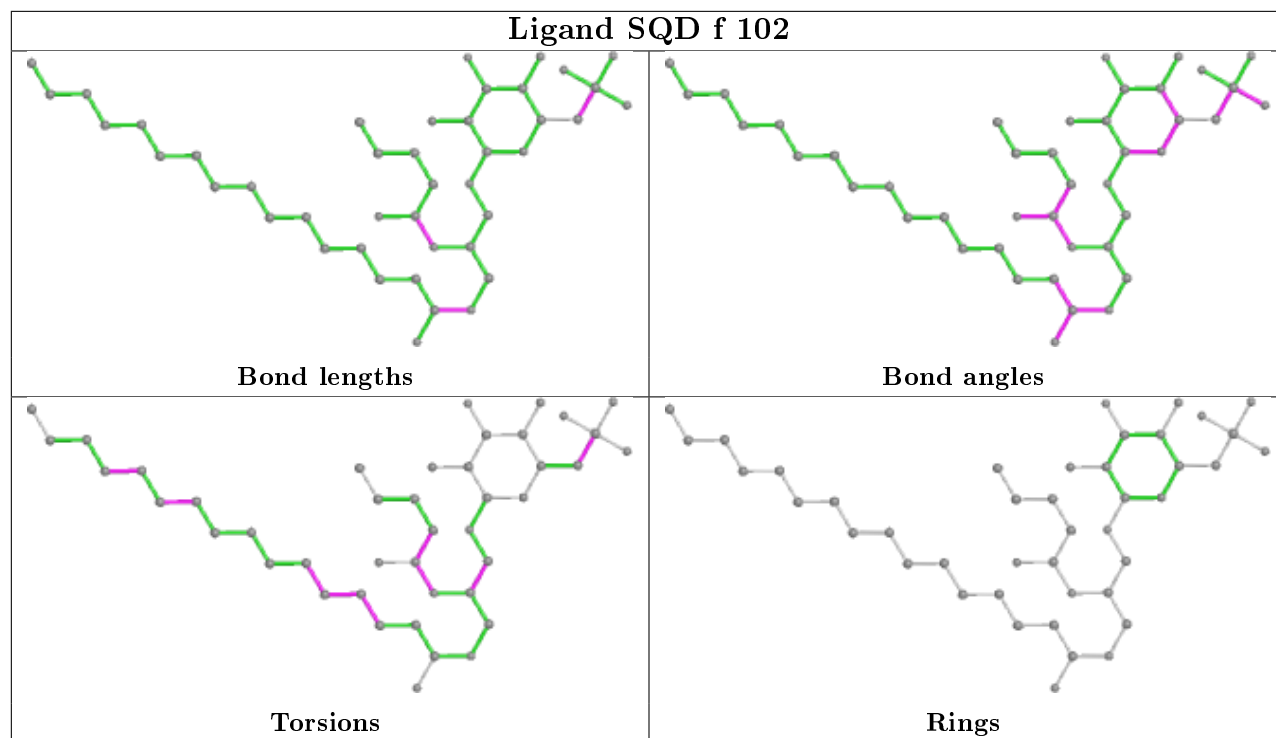
Ligand CLA C 507

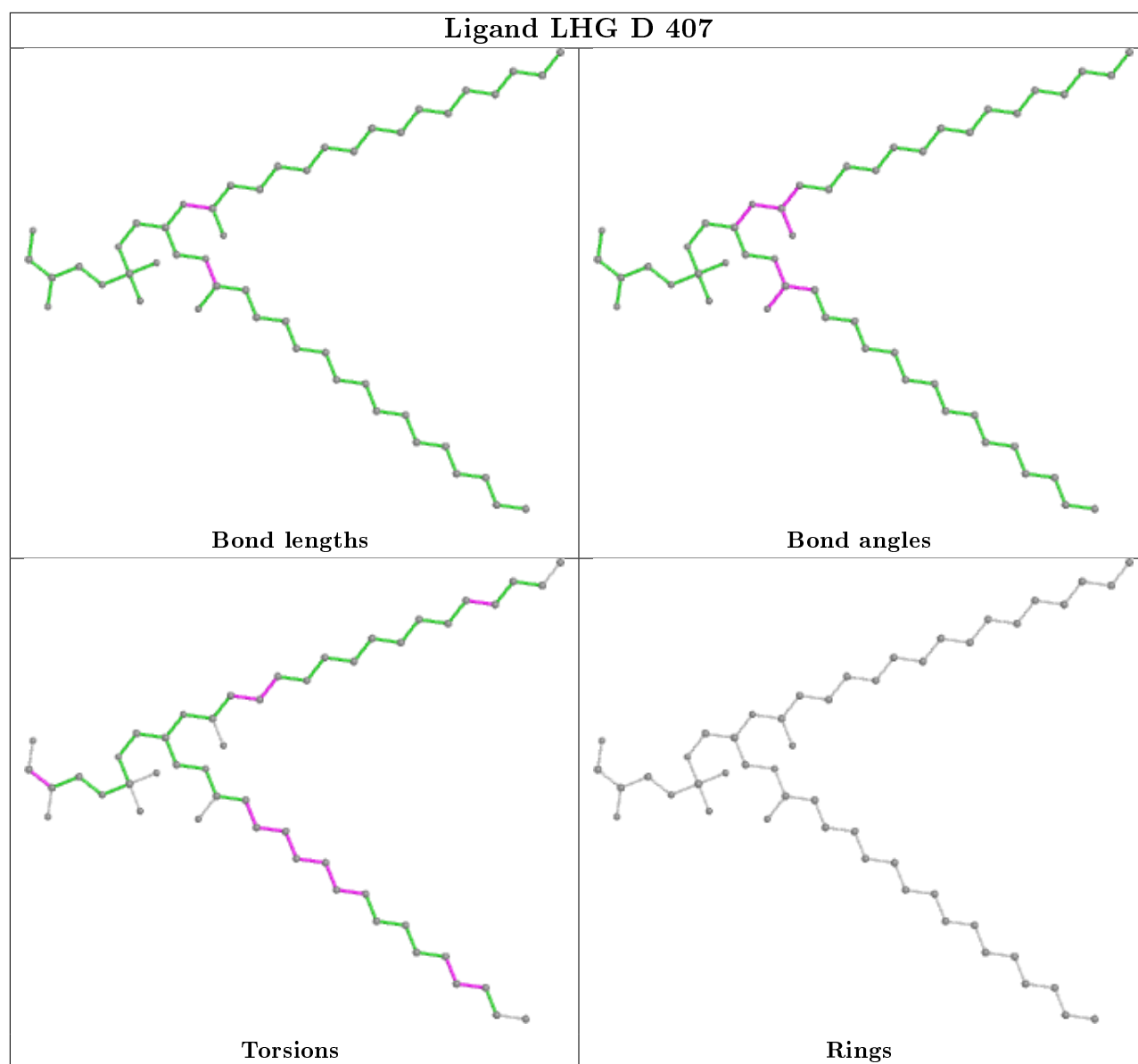


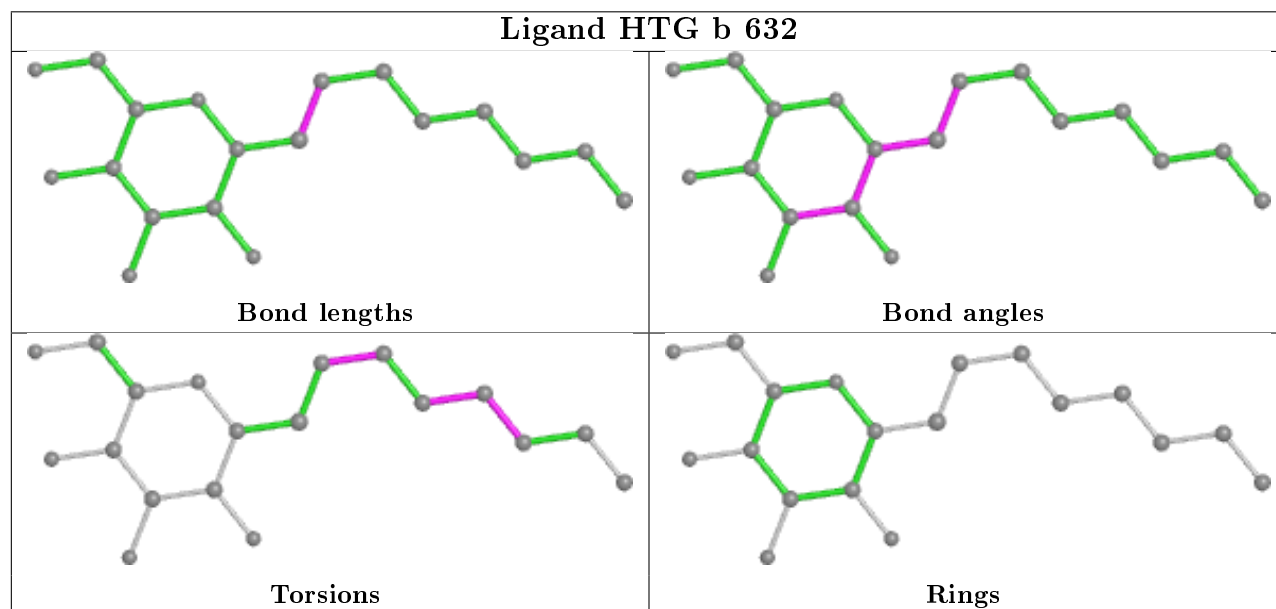
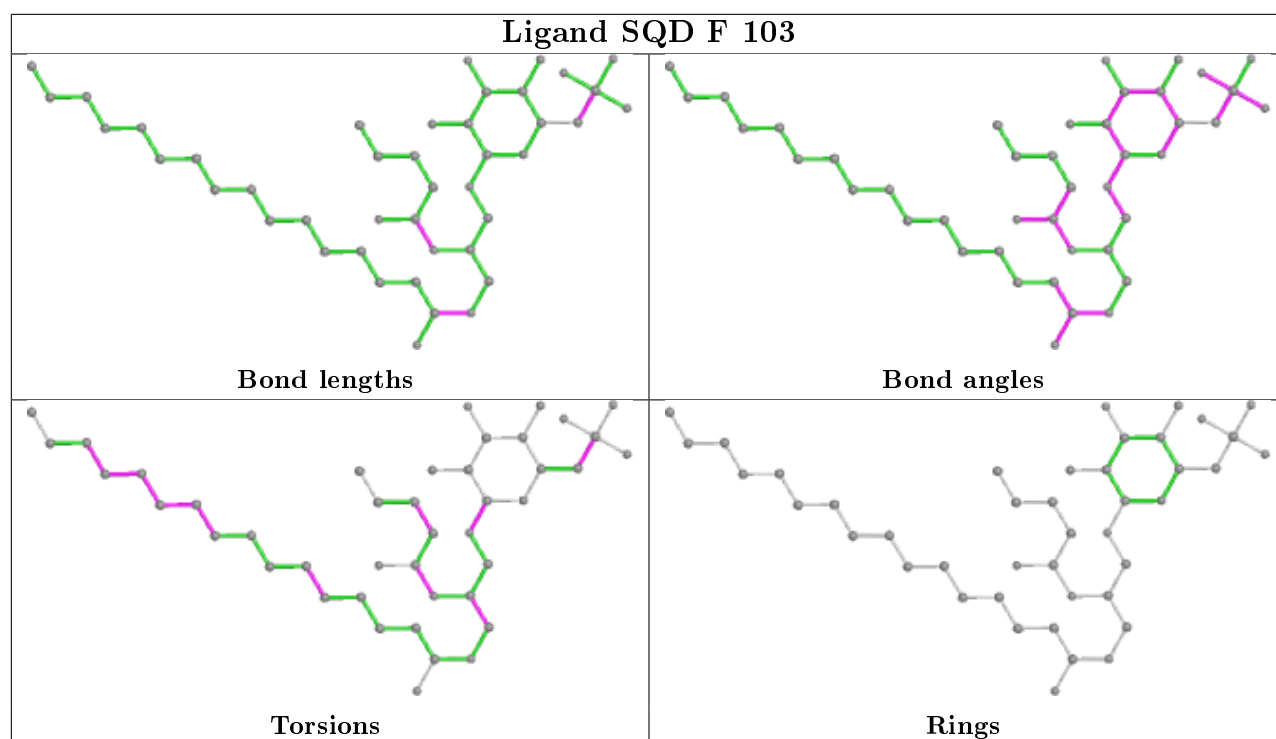
Ligand HEM v 205

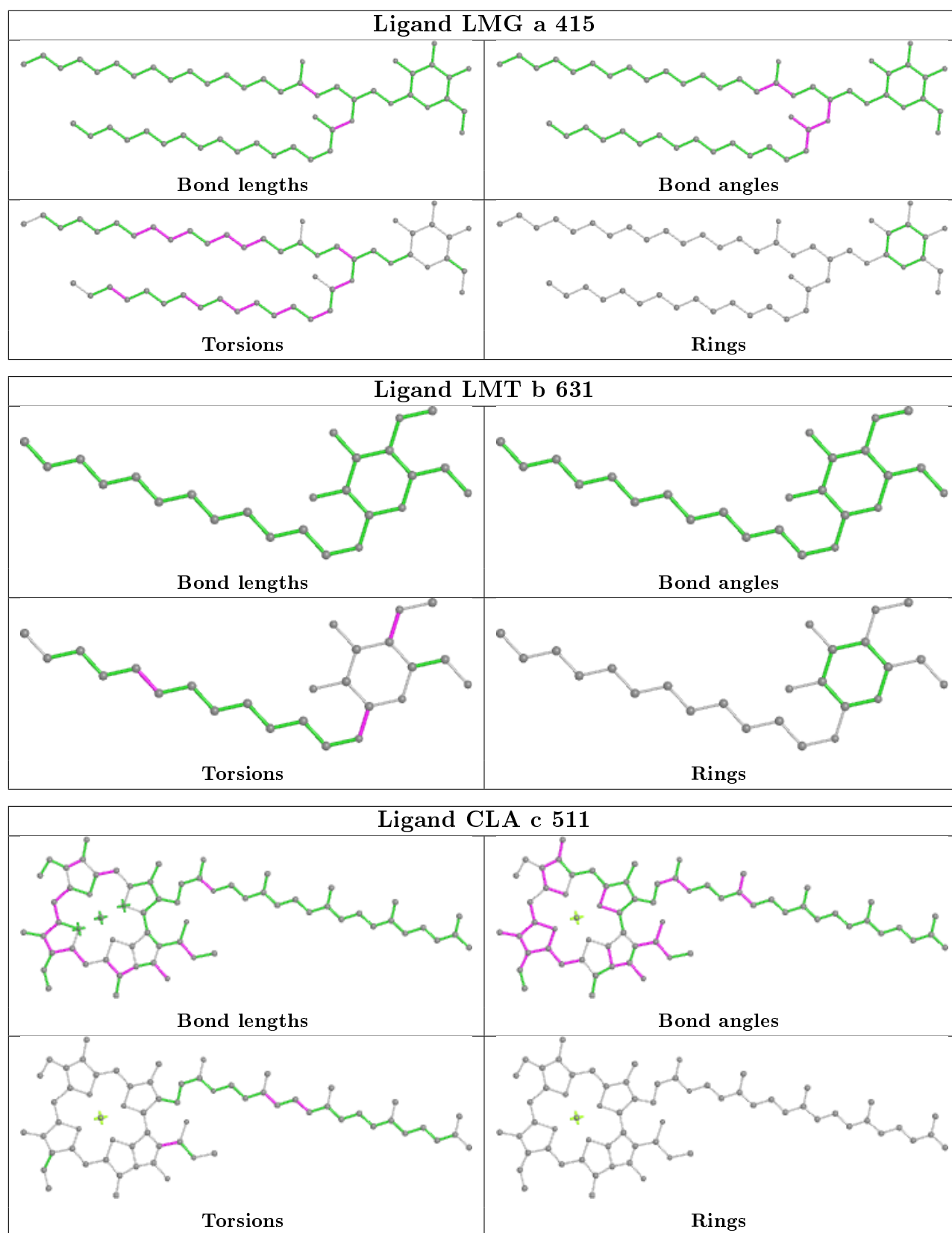


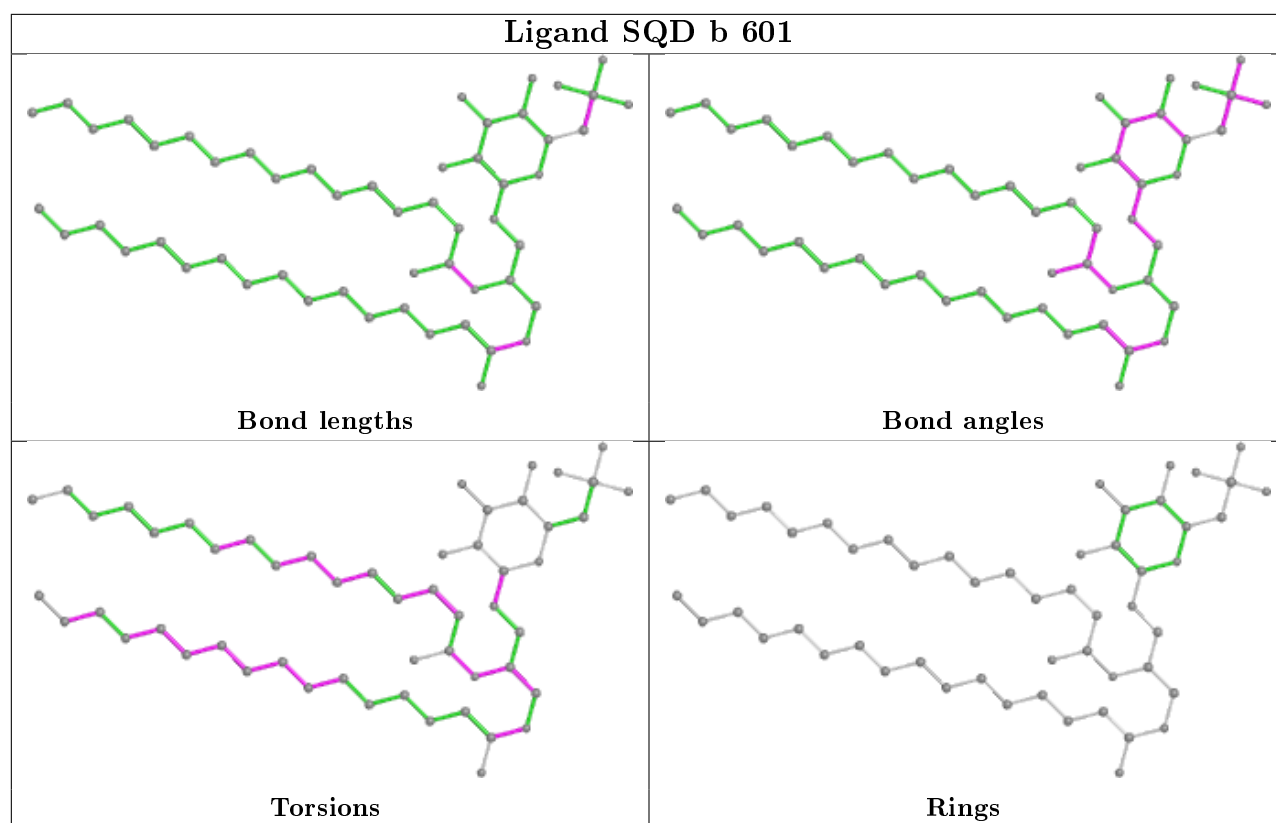
Ligand CLA a 410**Ligand CLA c 510**



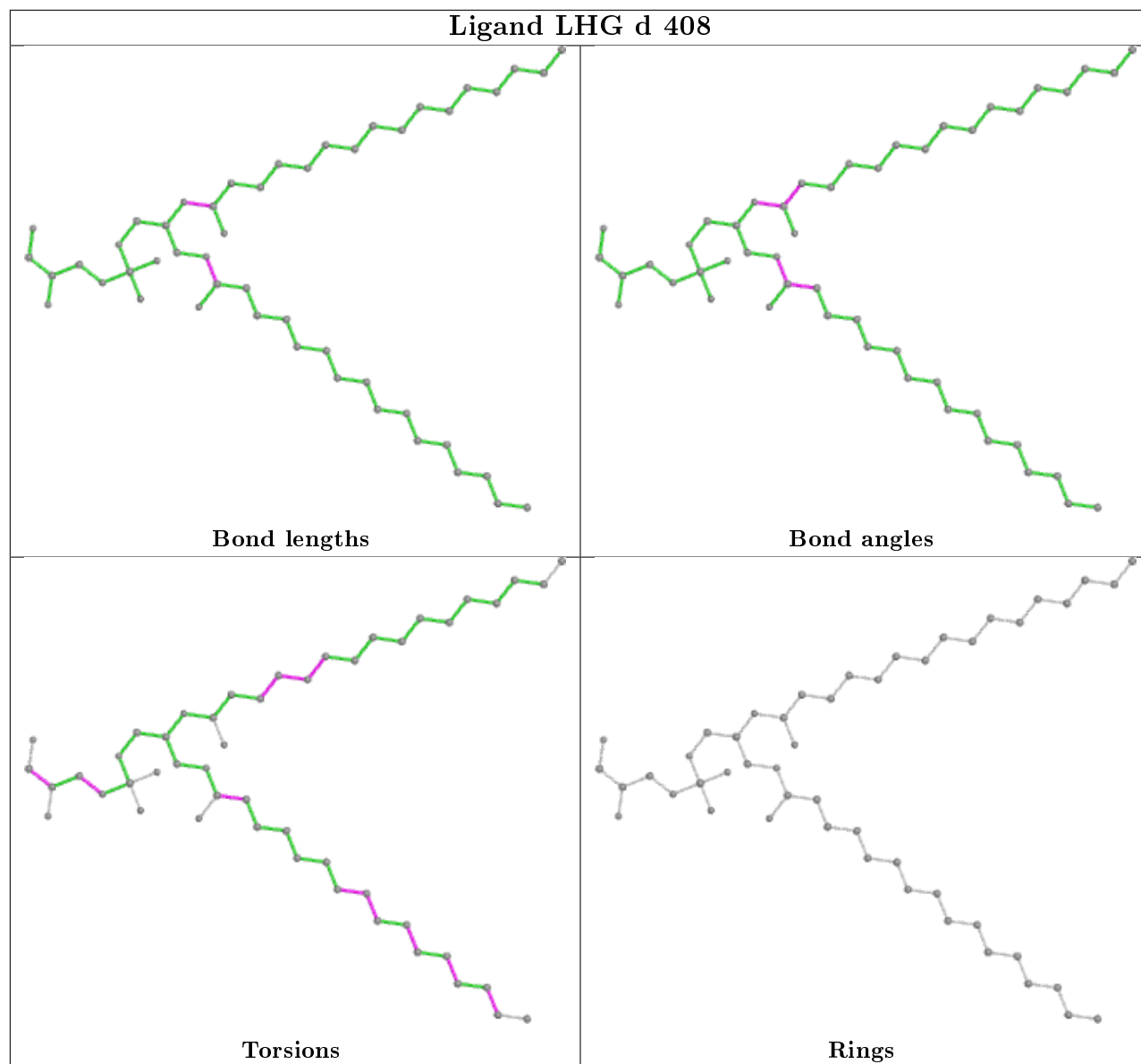




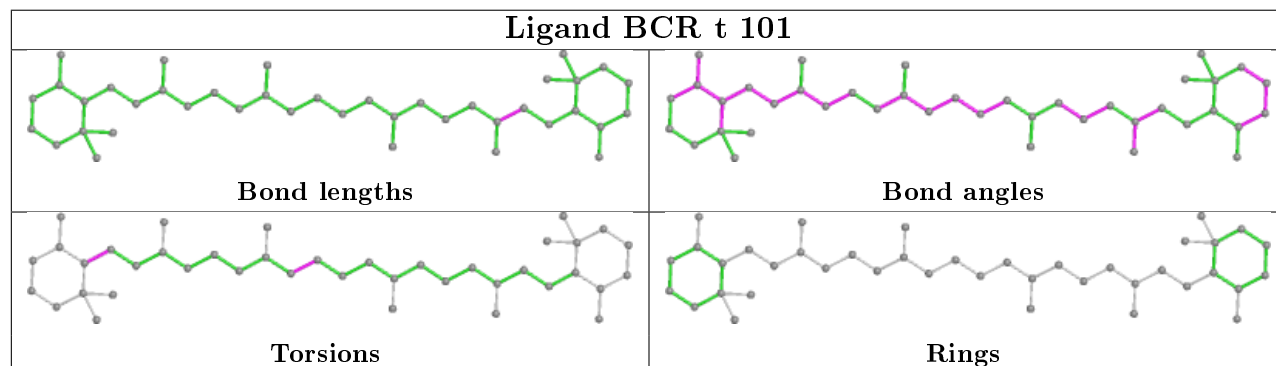


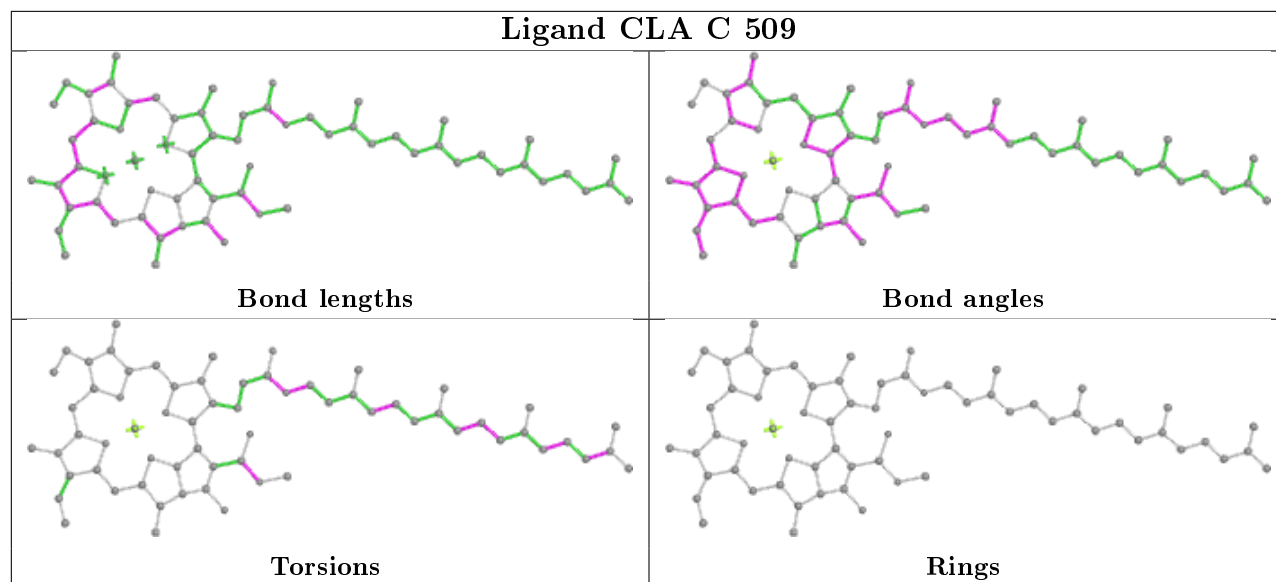
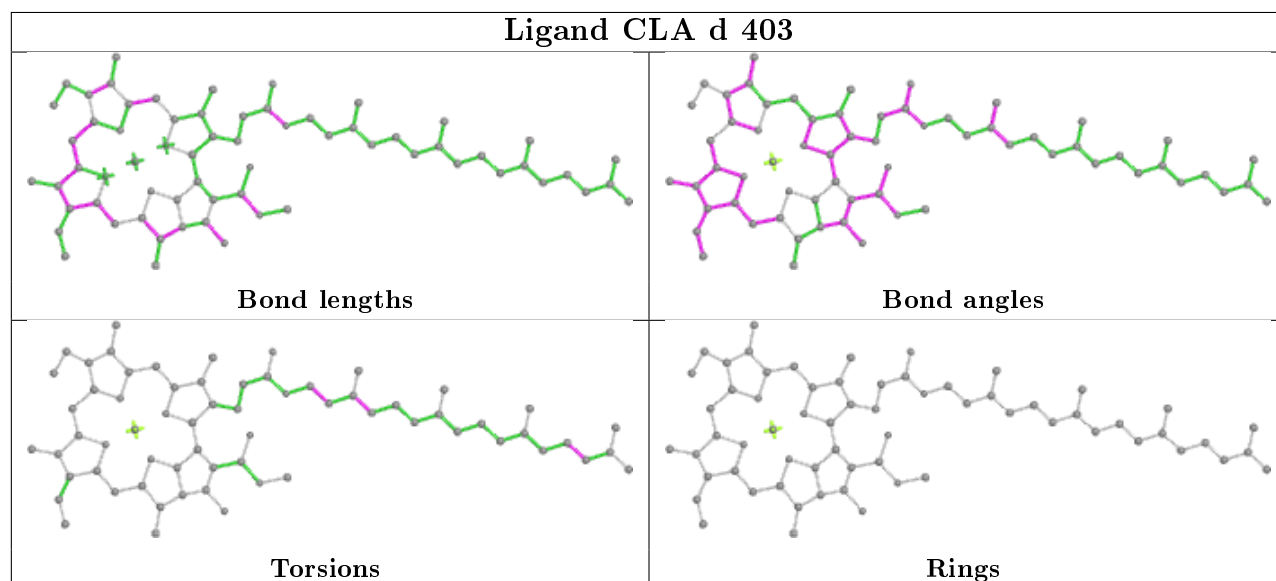
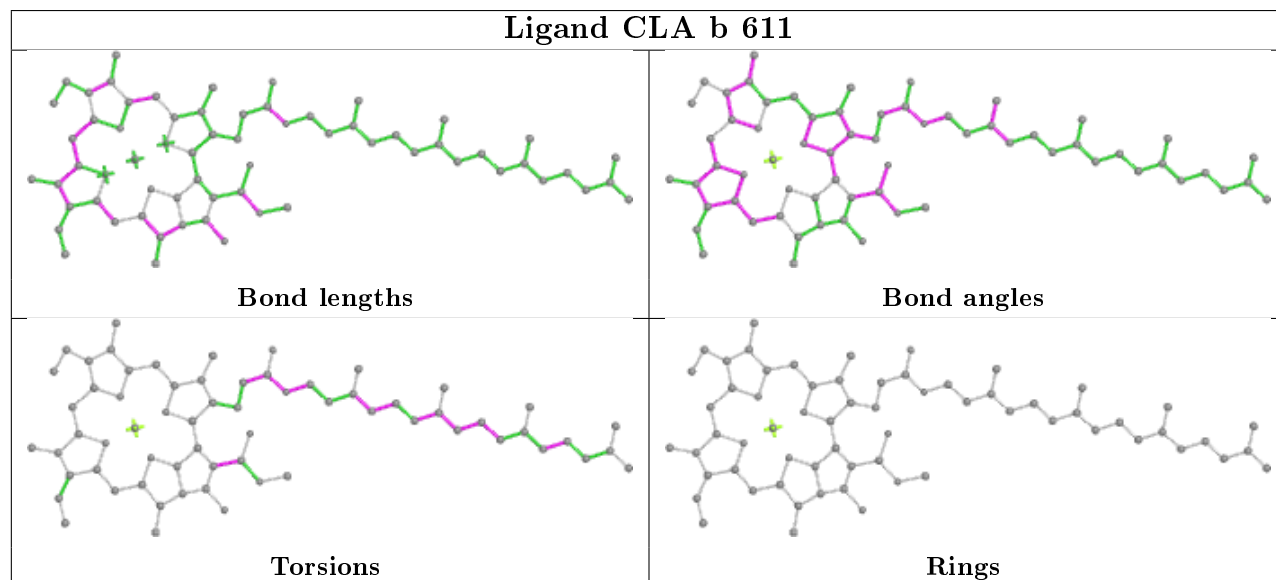


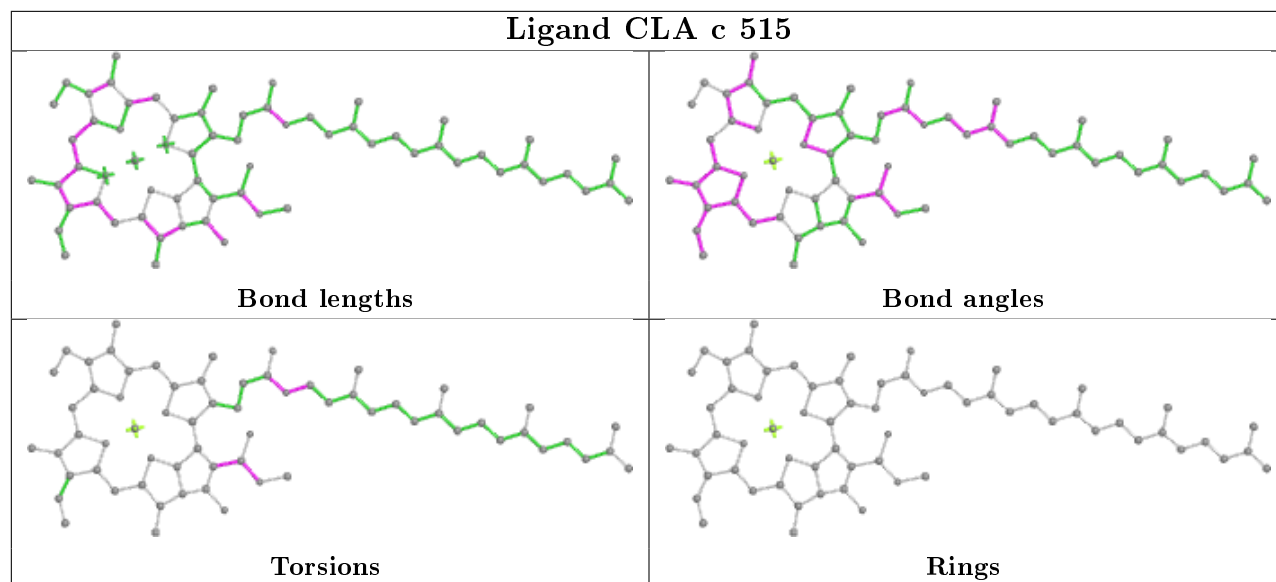
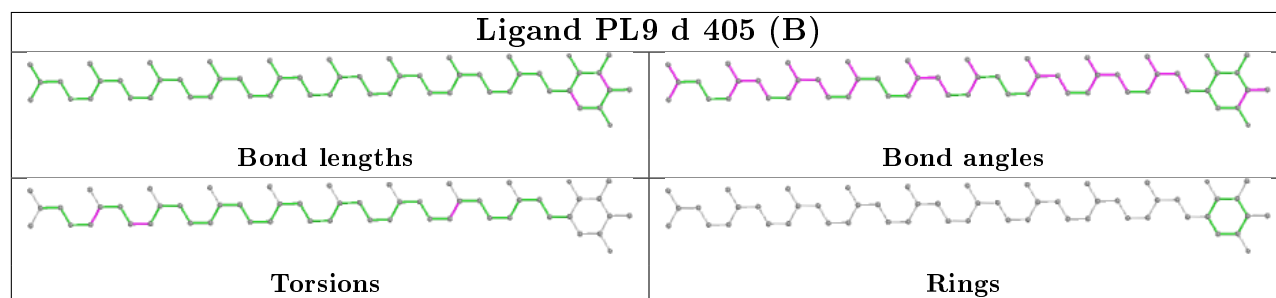
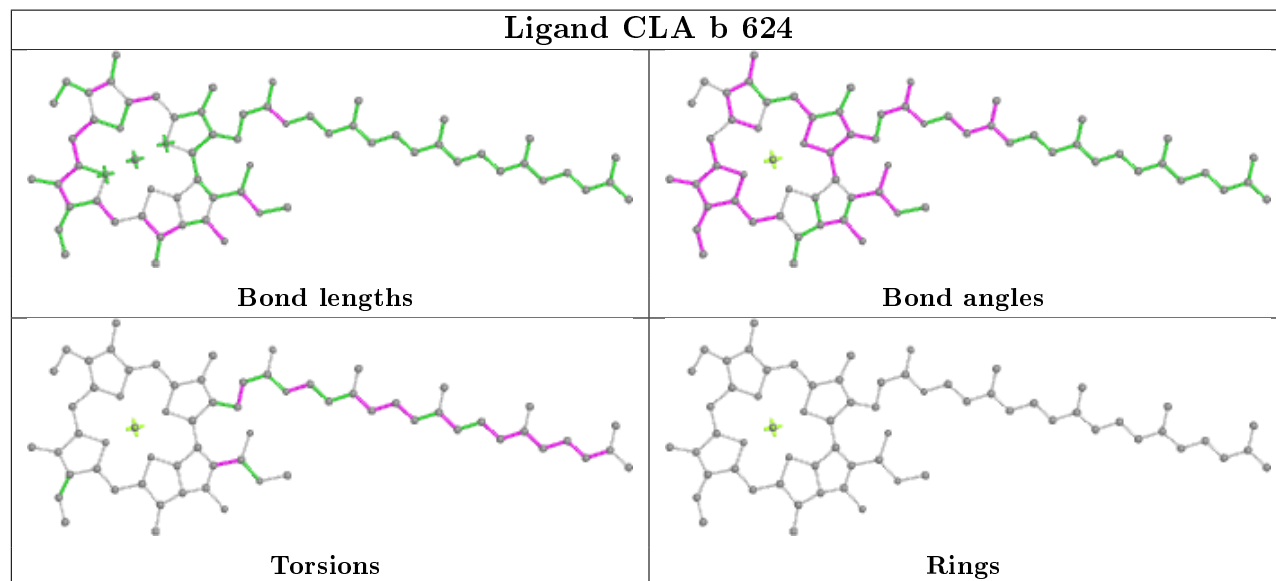
Ligand LHG d 408

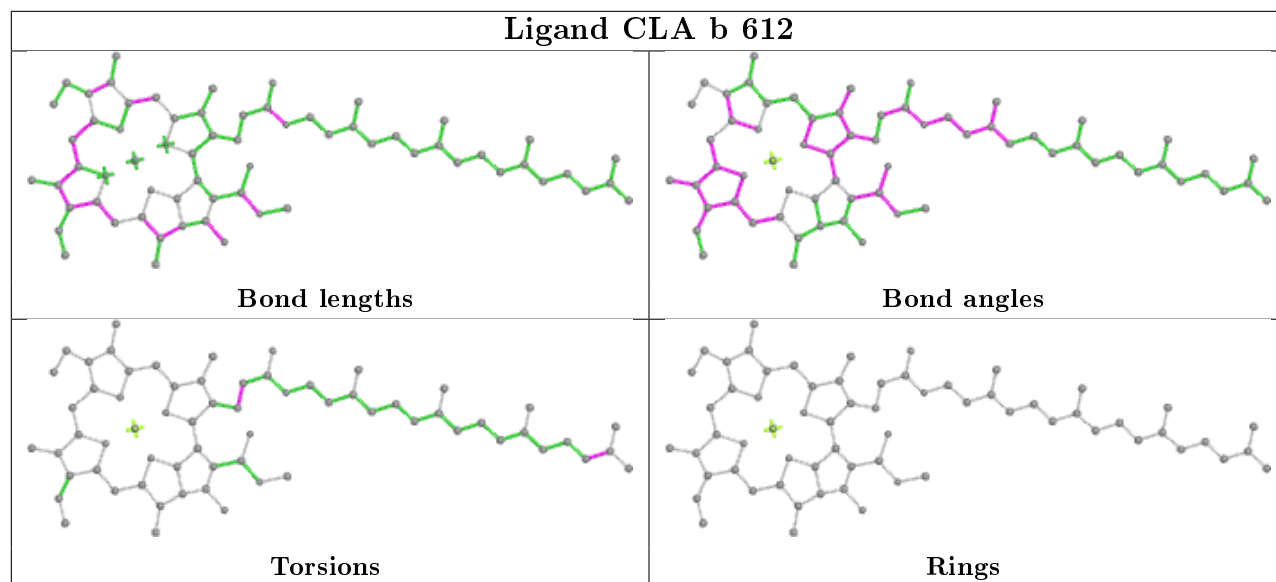
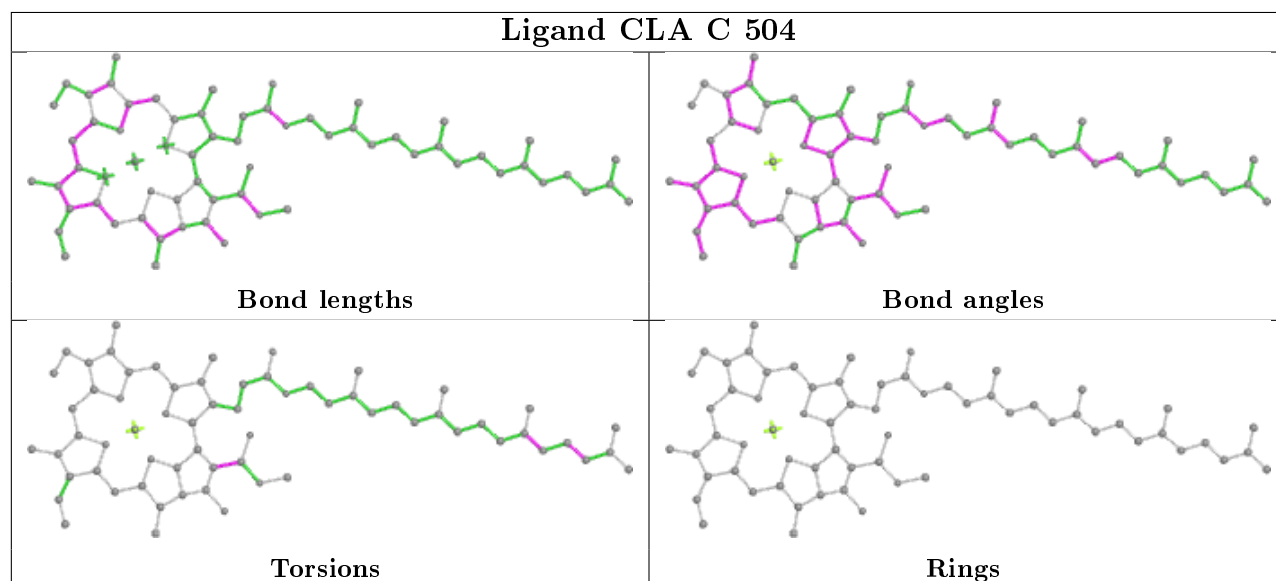
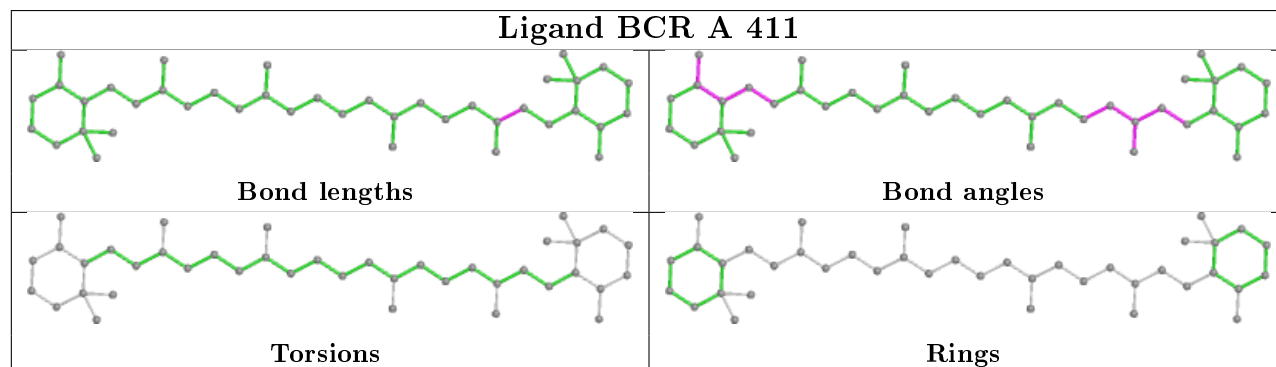


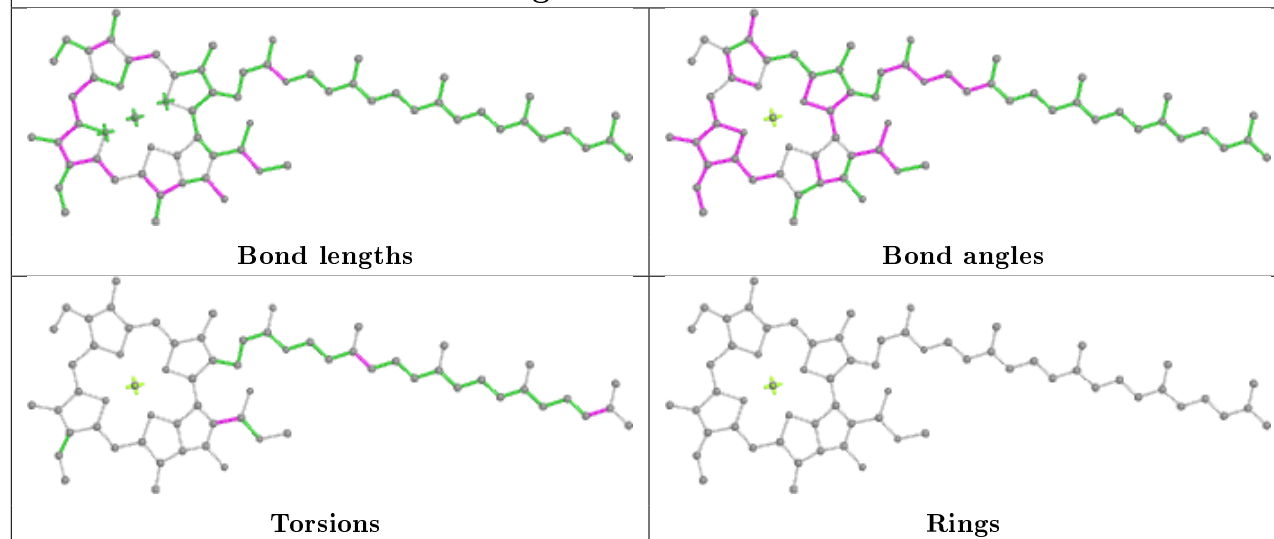
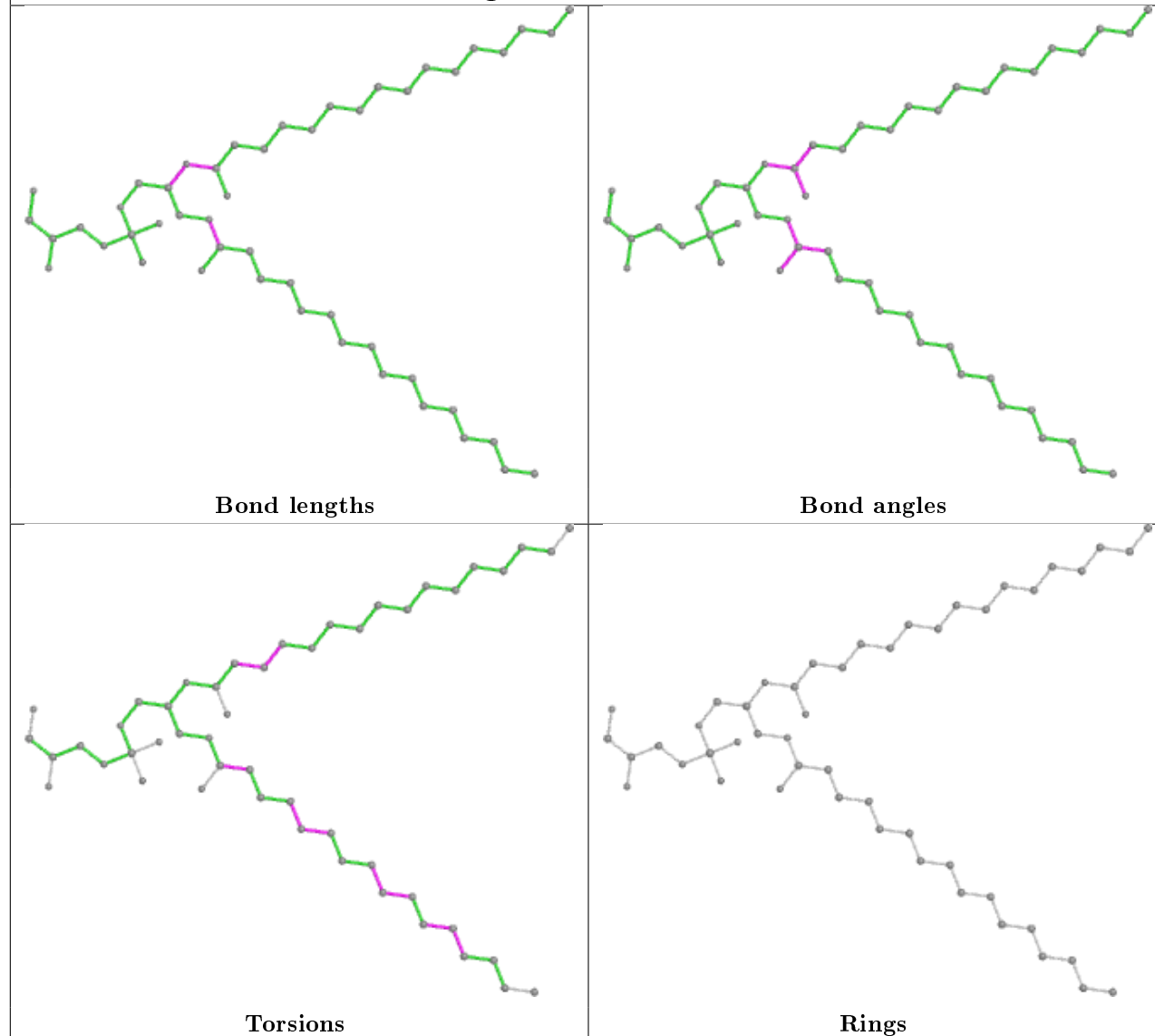
Ligand BCR t 101

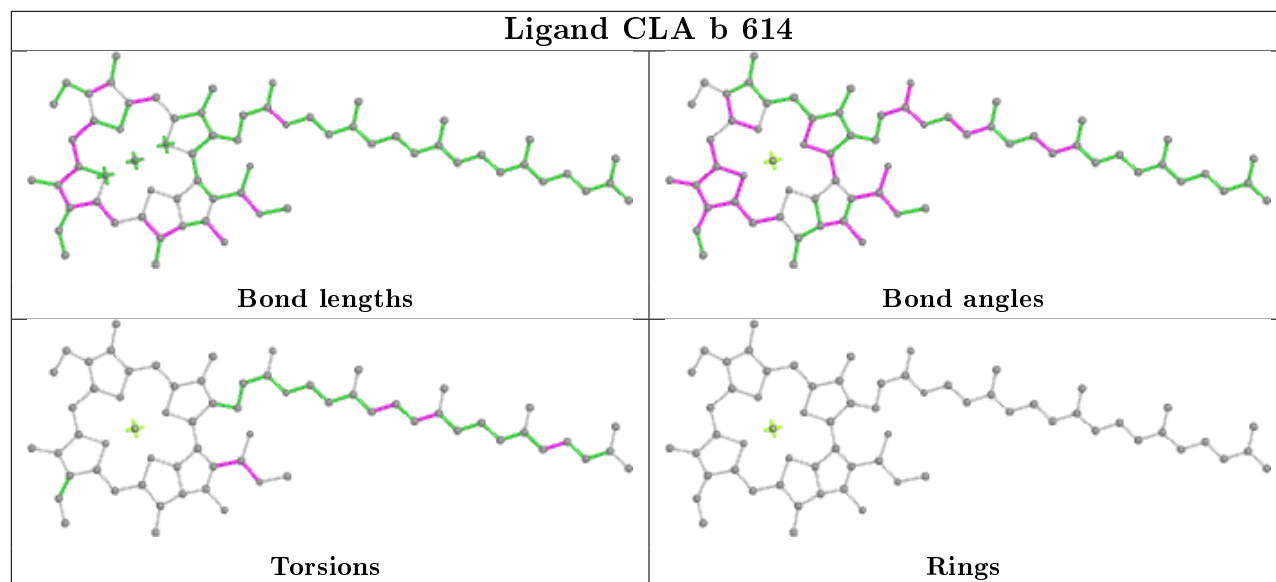
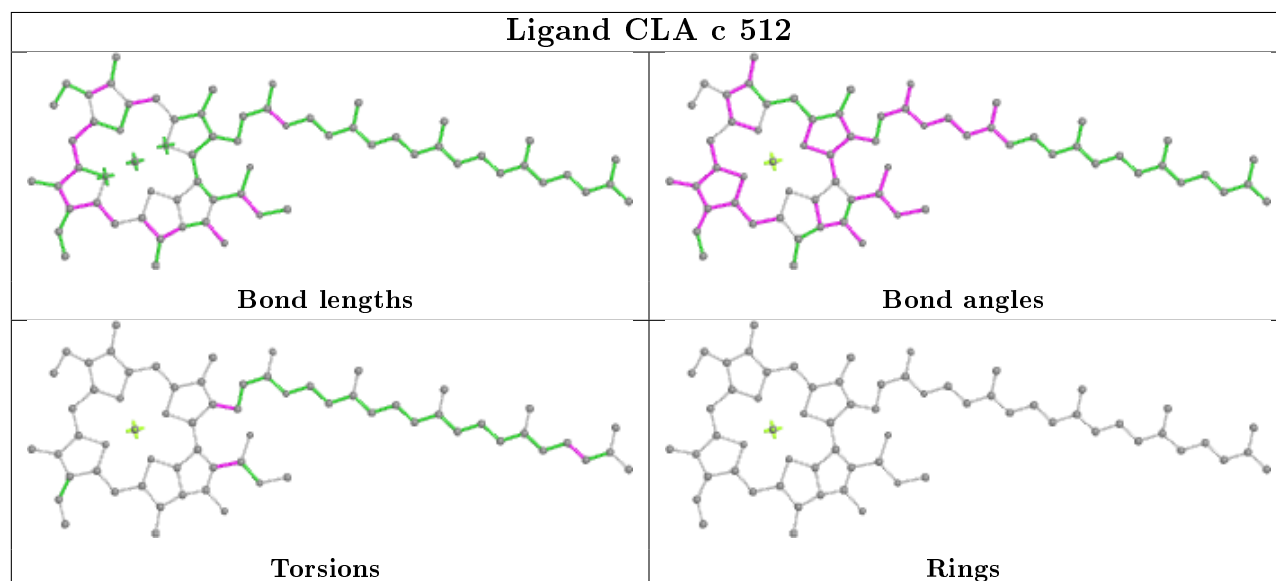
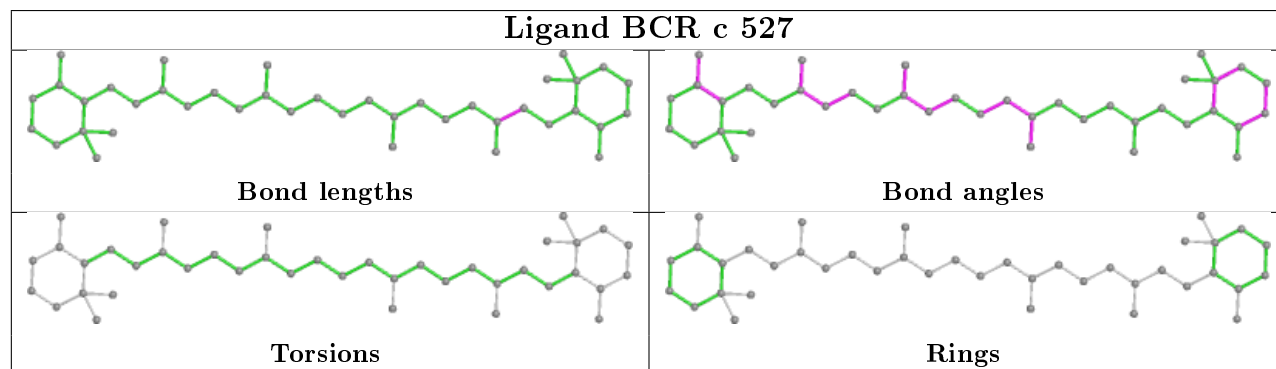


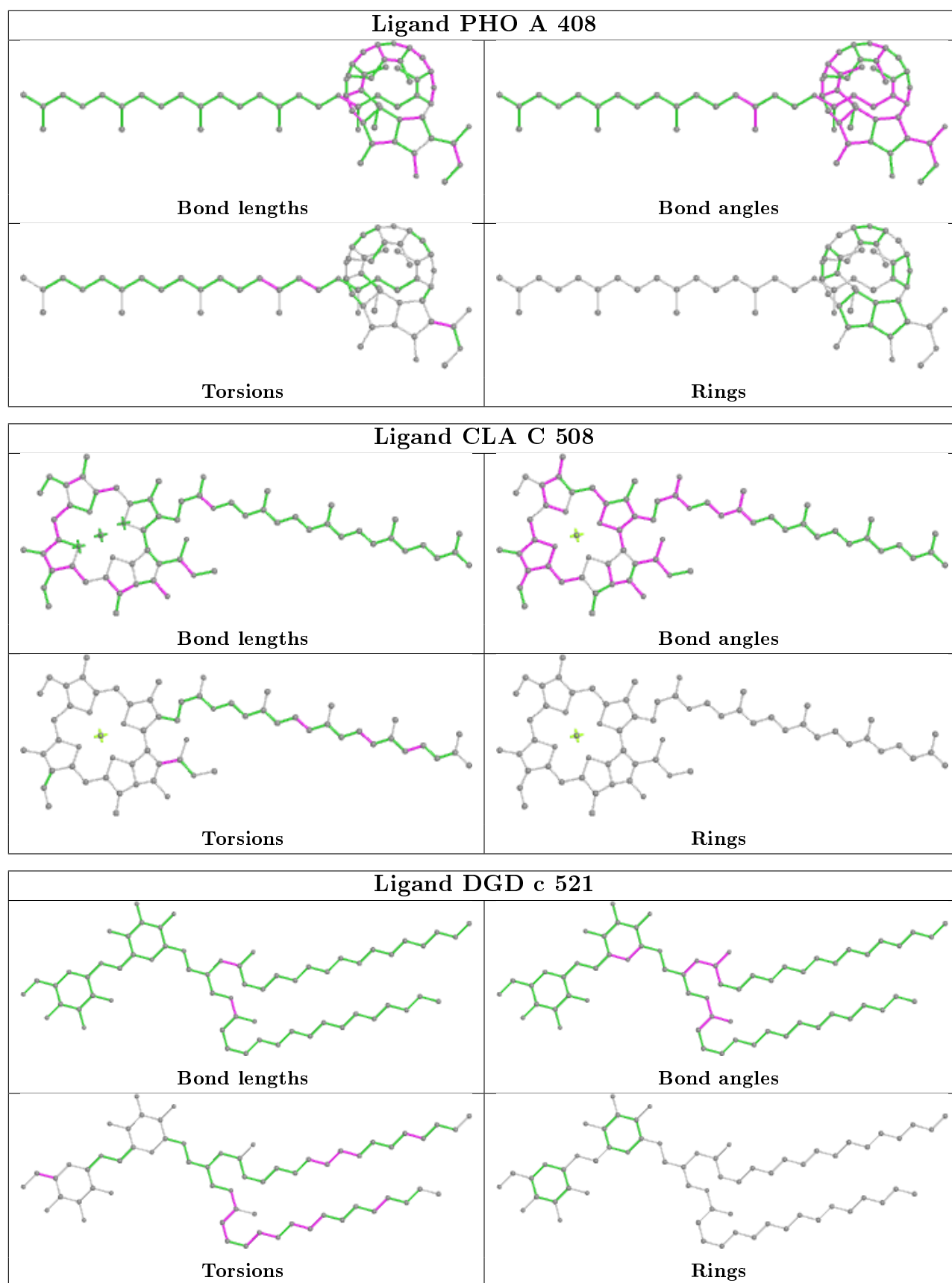
Ligand CLA C 509**Ligand CLA d 403****Ligand CLA b 611**

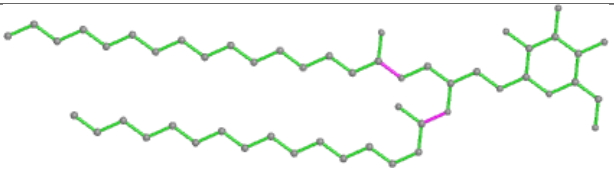
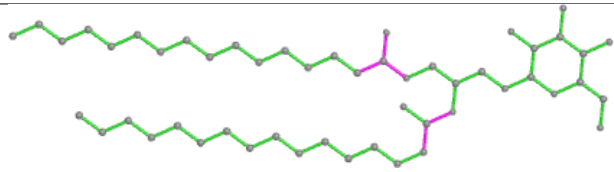
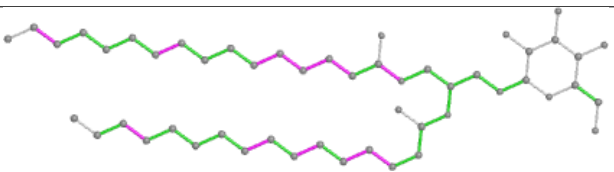
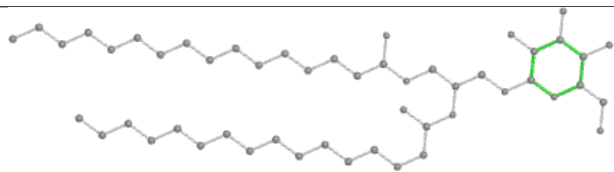
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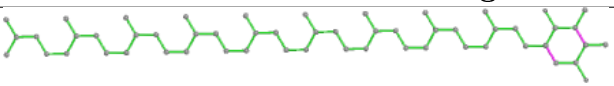
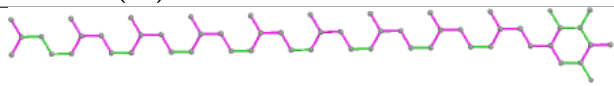
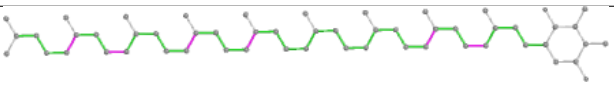
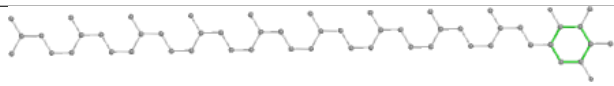
Ligand CLA b 612**Ligand CLA C 504****Ligand BCR A 411**

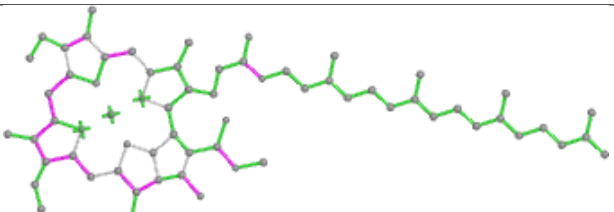
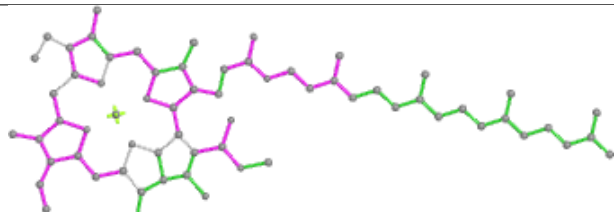
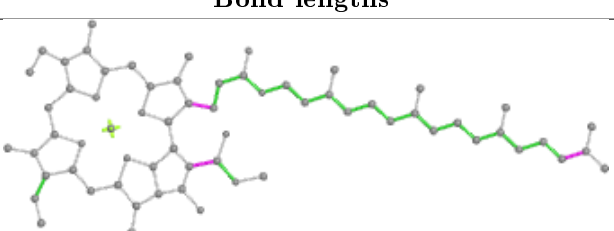
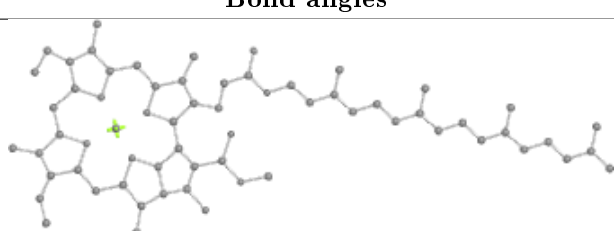
Ligand CLA B 610**Ligand LHG d 406**

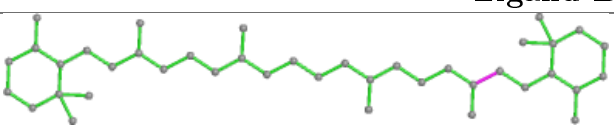
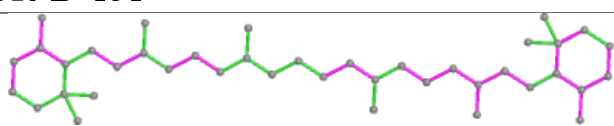
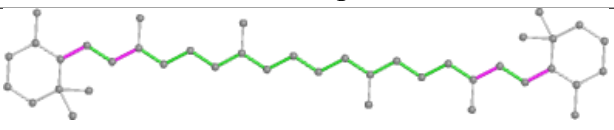
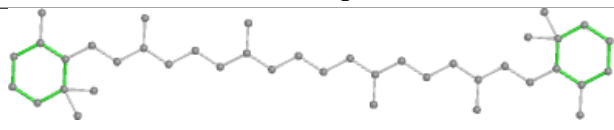
Ligand CLA b 614**Ligand CLA c 512****Ligand BCR c 527**

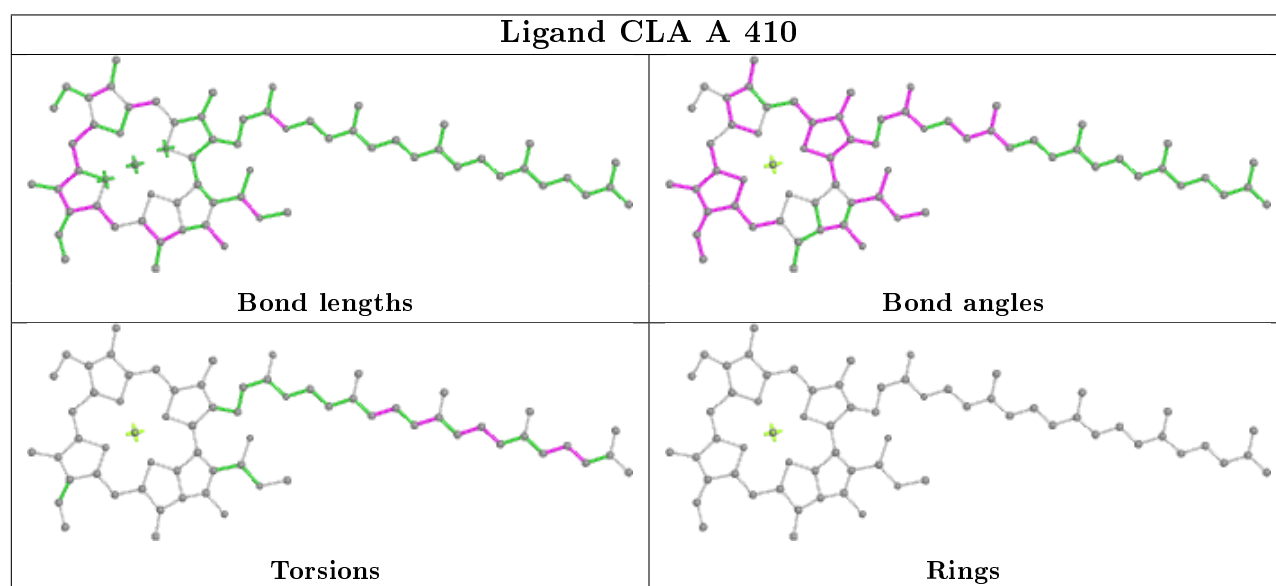
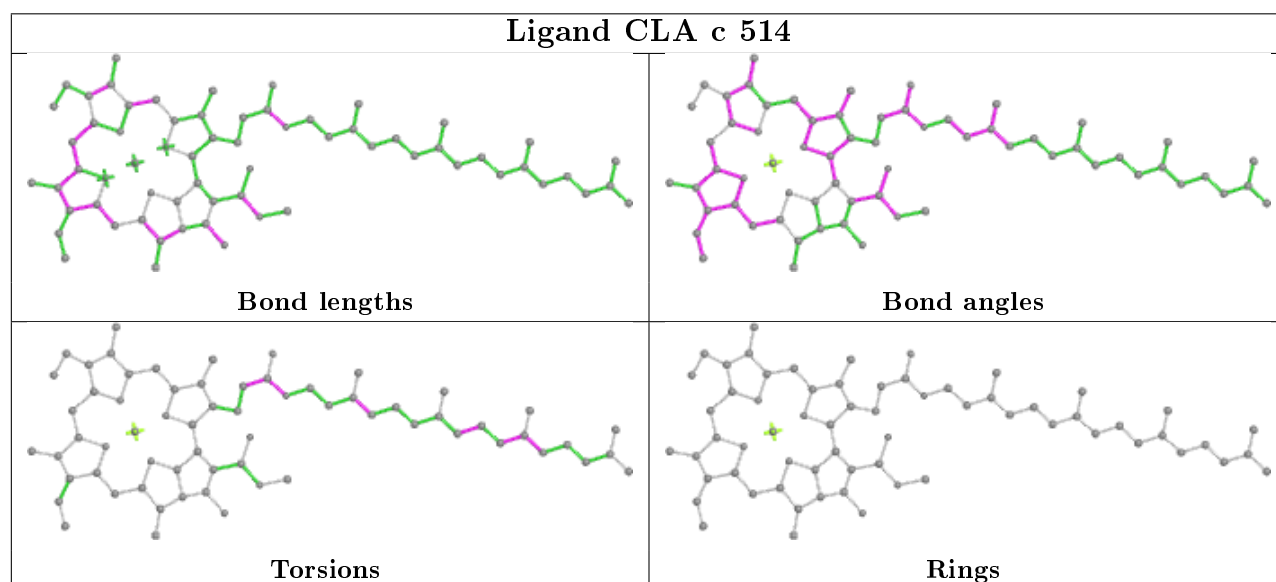
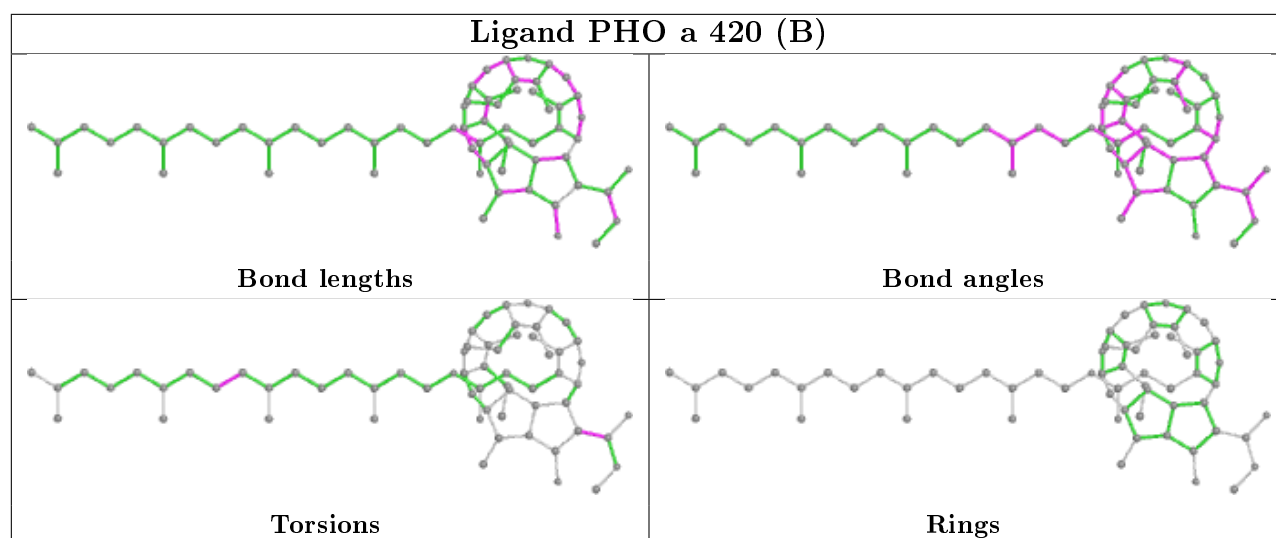


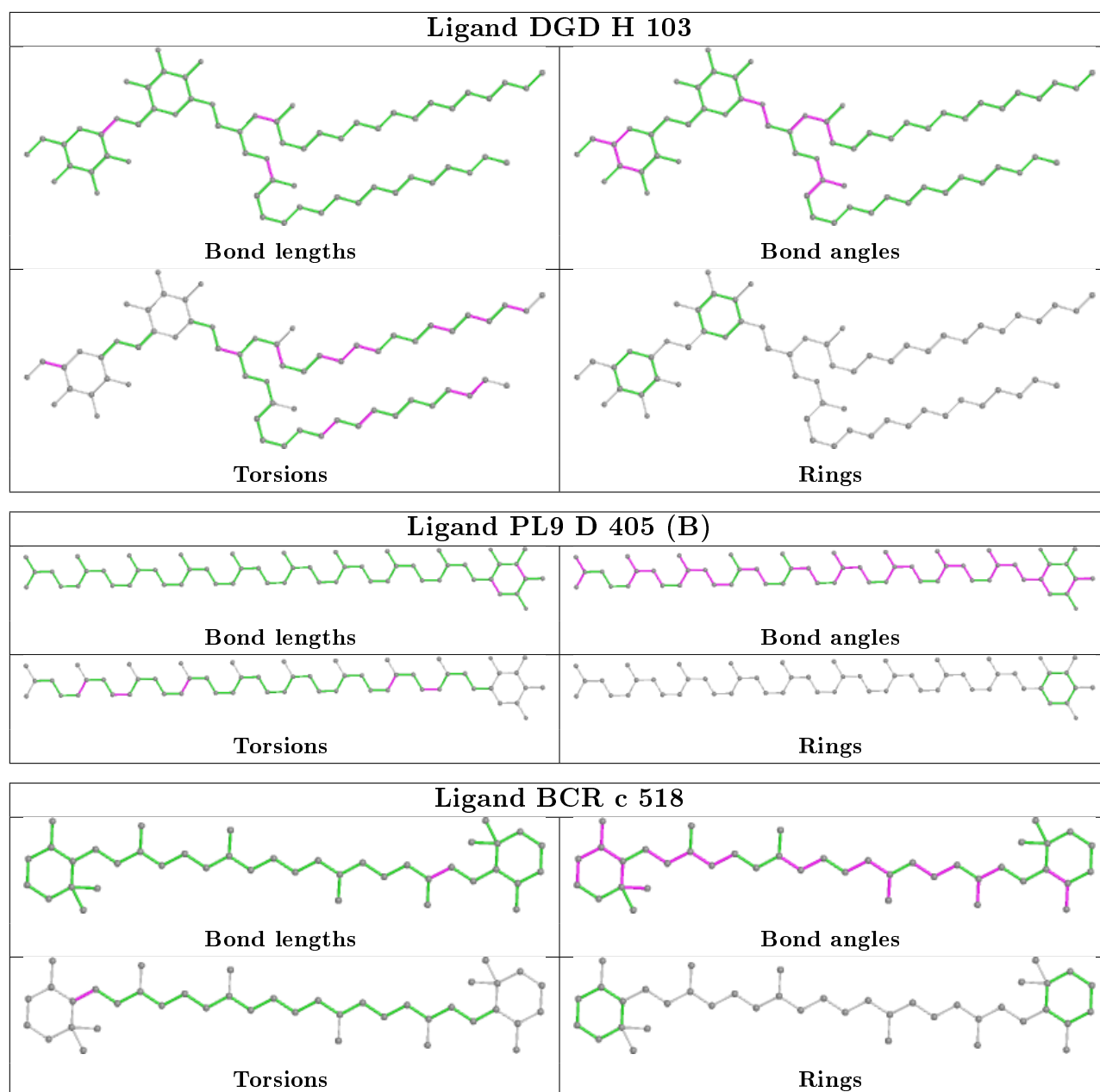
Ligand LMG C 519	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PL9 D 405 (A)	
	
Bond lengths	Bond angles
	
Torsions	Rings

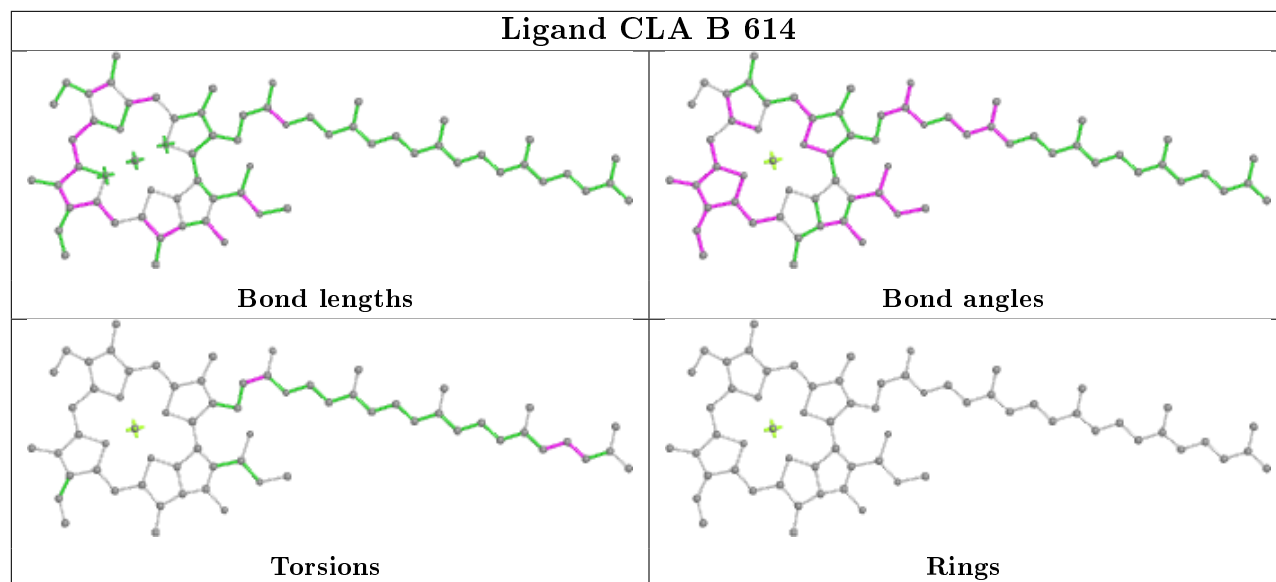
Ligand CLA B 608	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand BCR D 404	
	
Bond lengths	Bond angles
	
Torsions	Rings

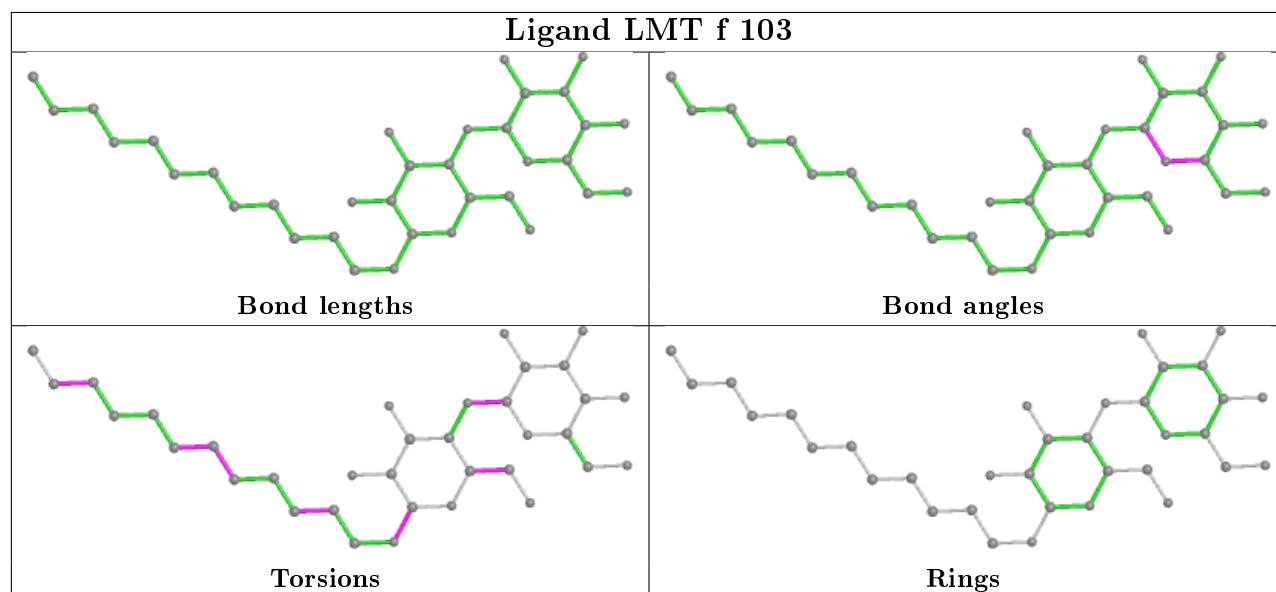




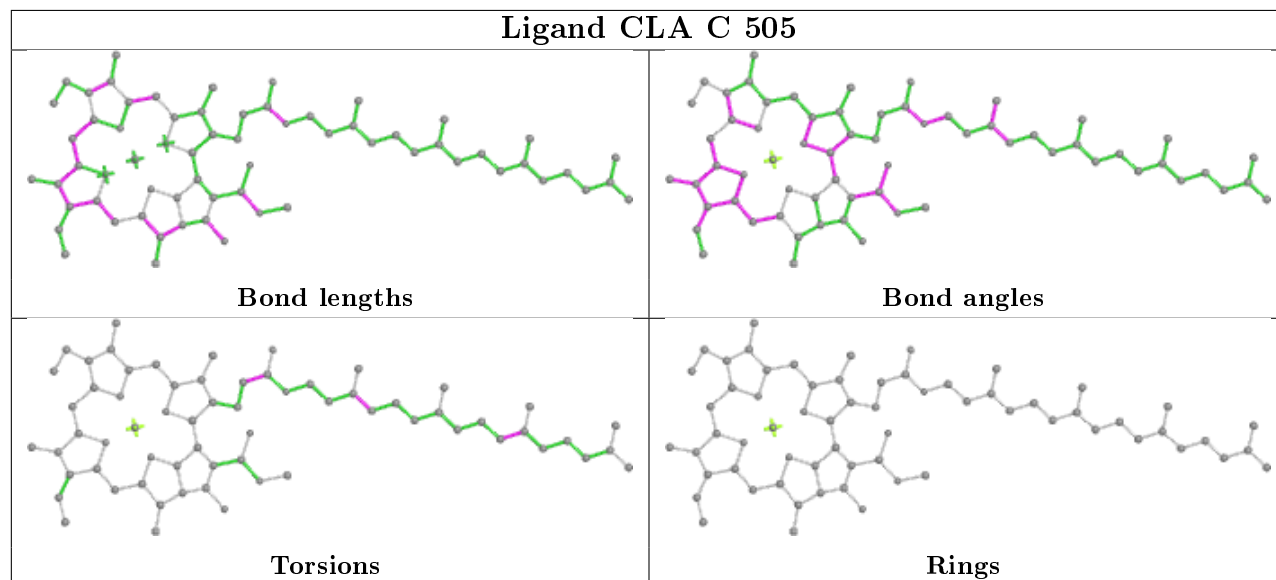
Ligand CLA B 614

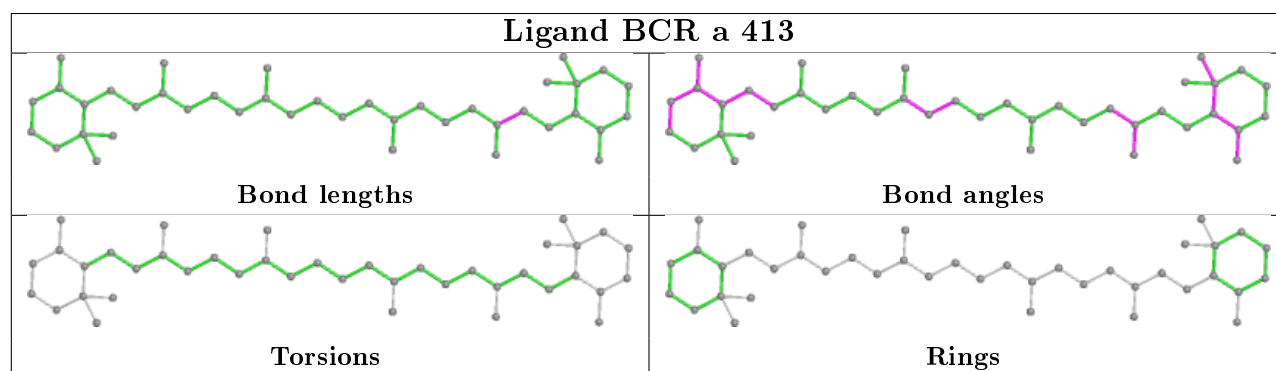
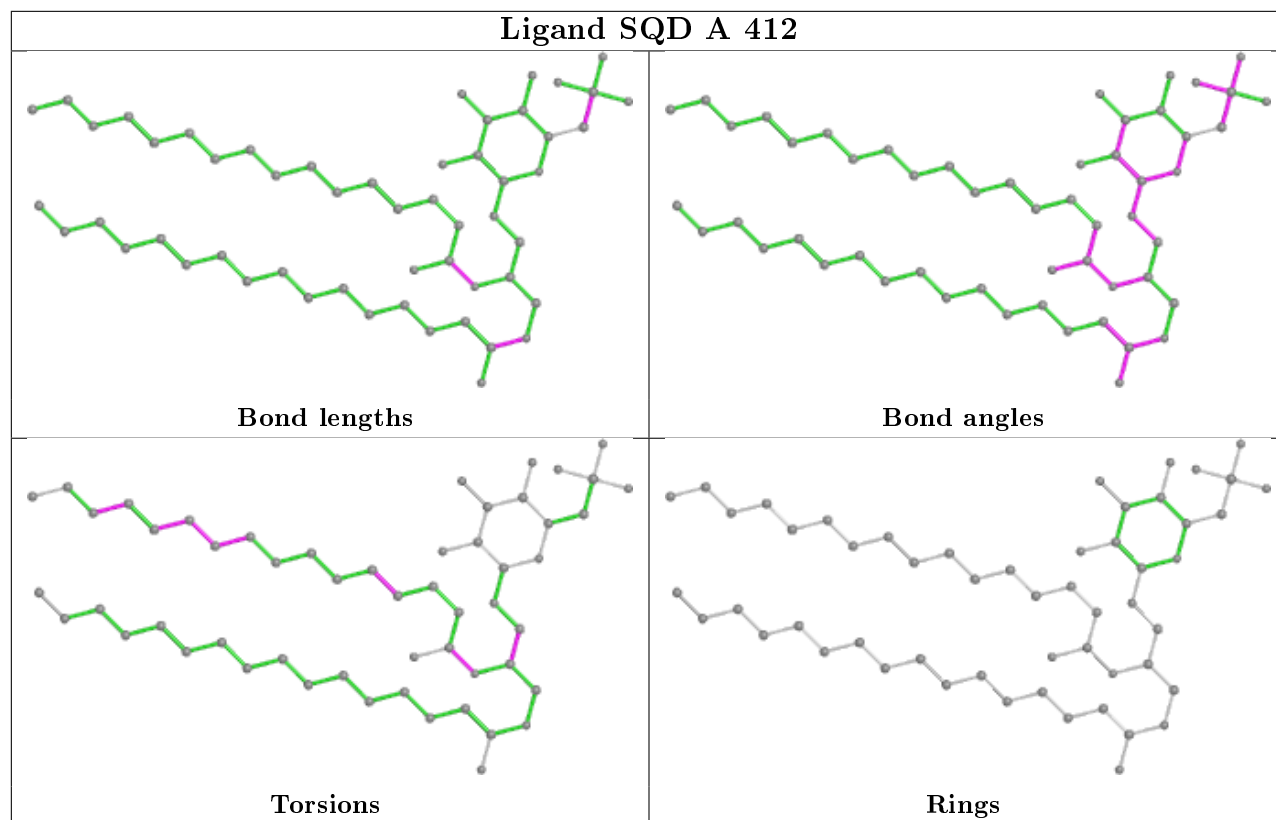
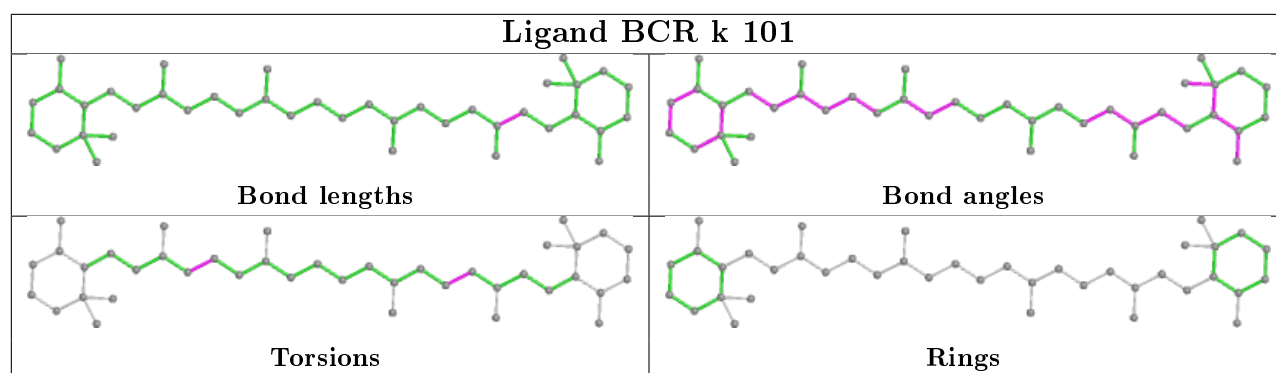


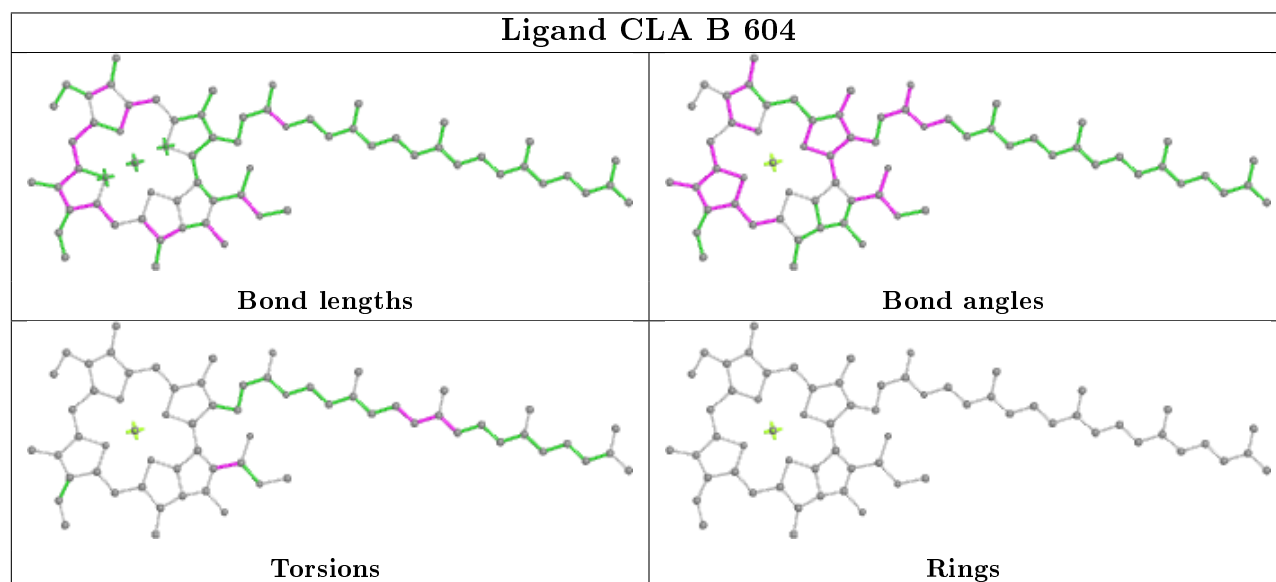
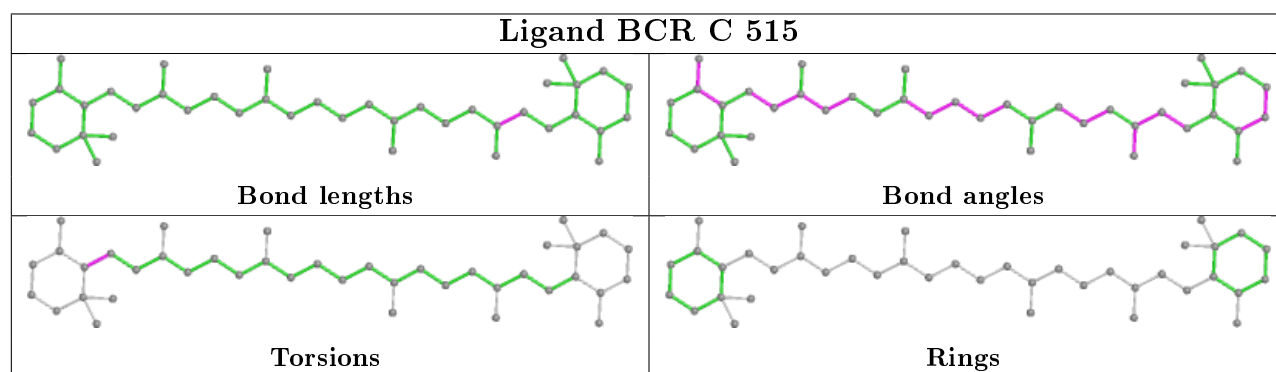
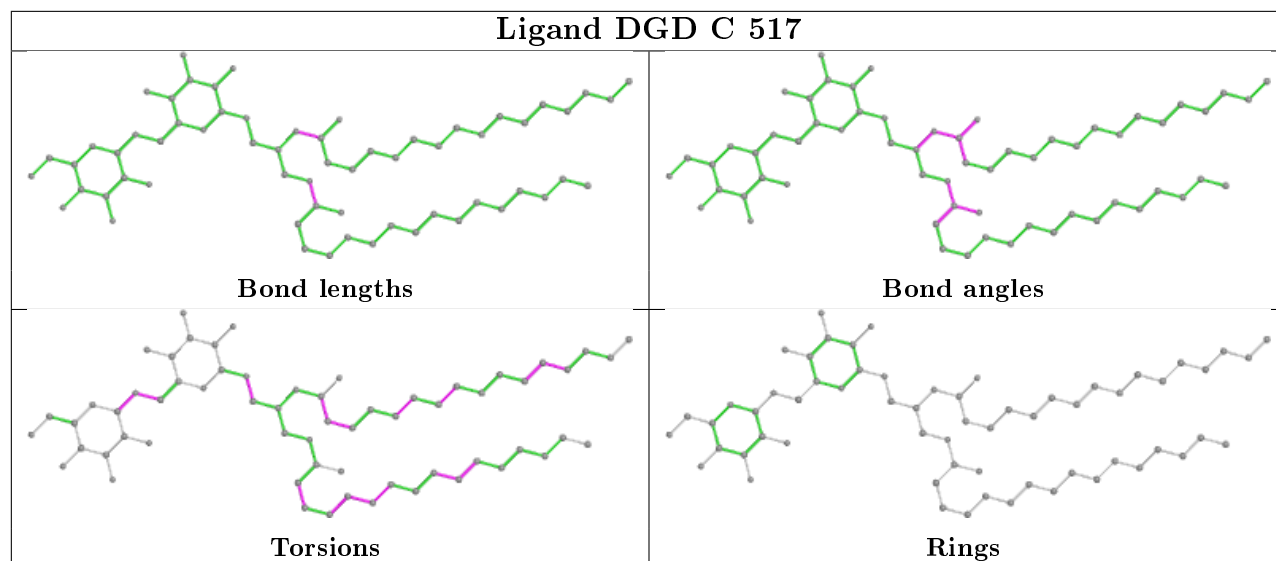
Ligand LMT f 103

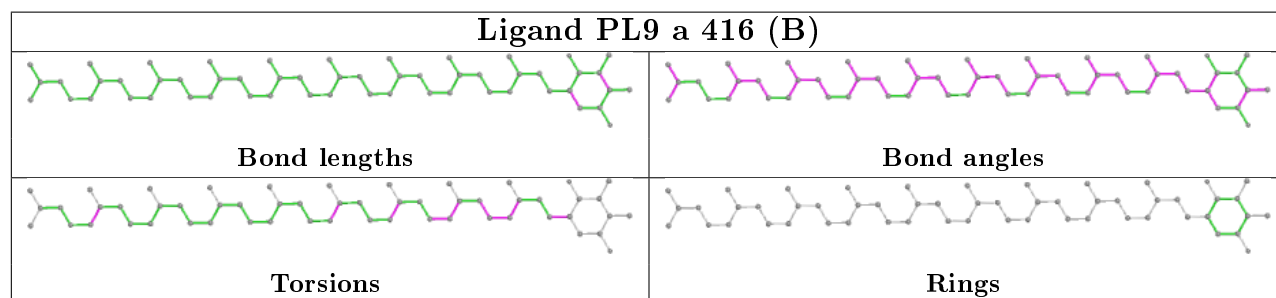
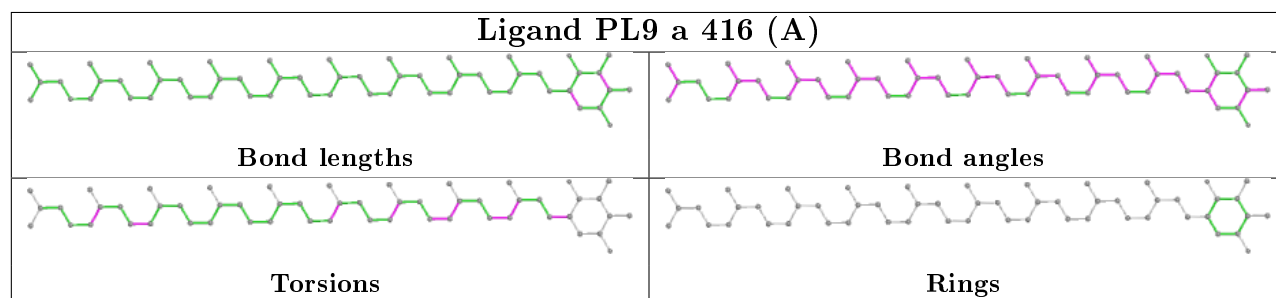
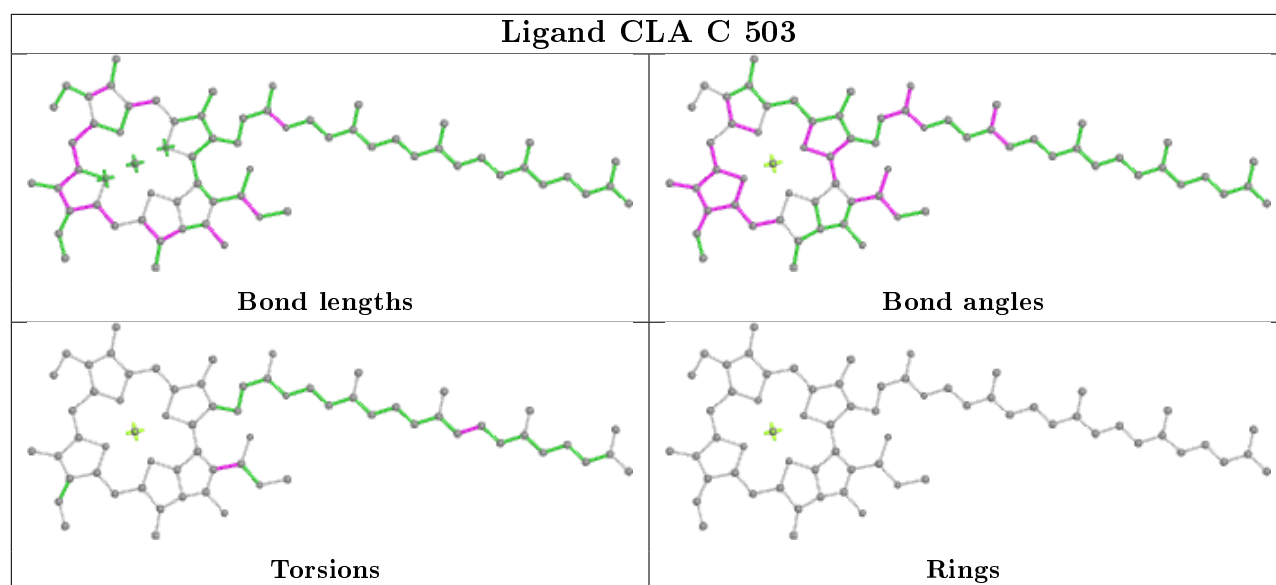


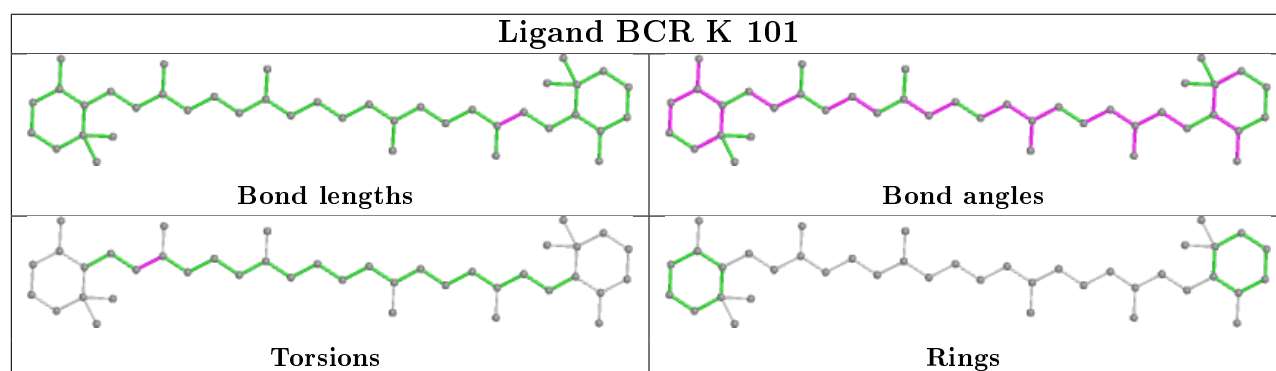
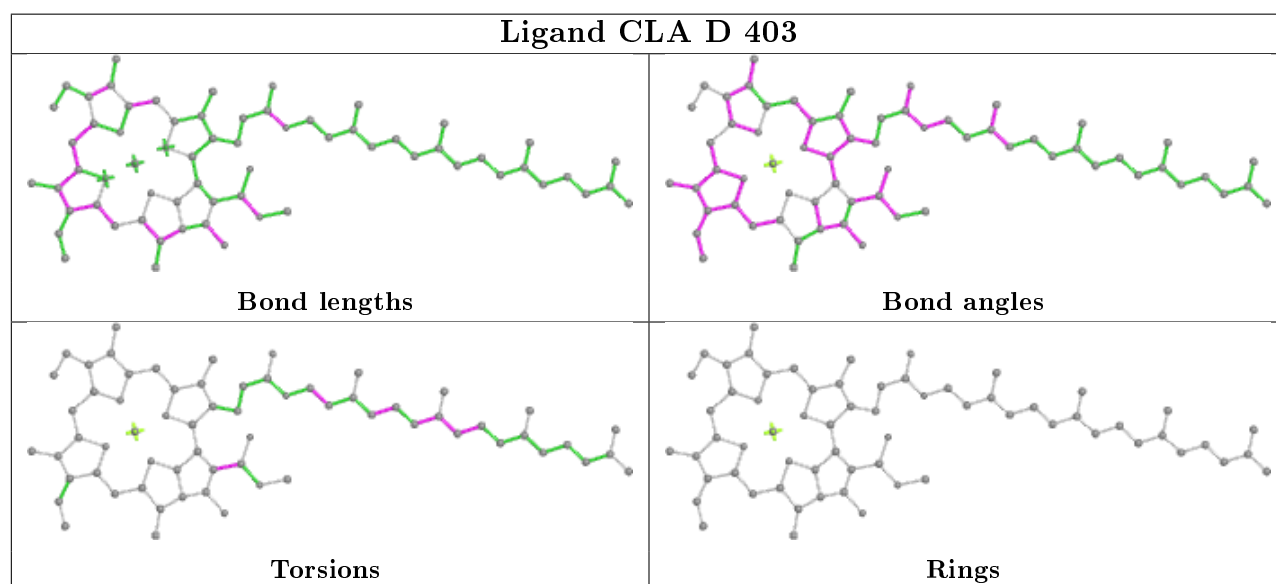
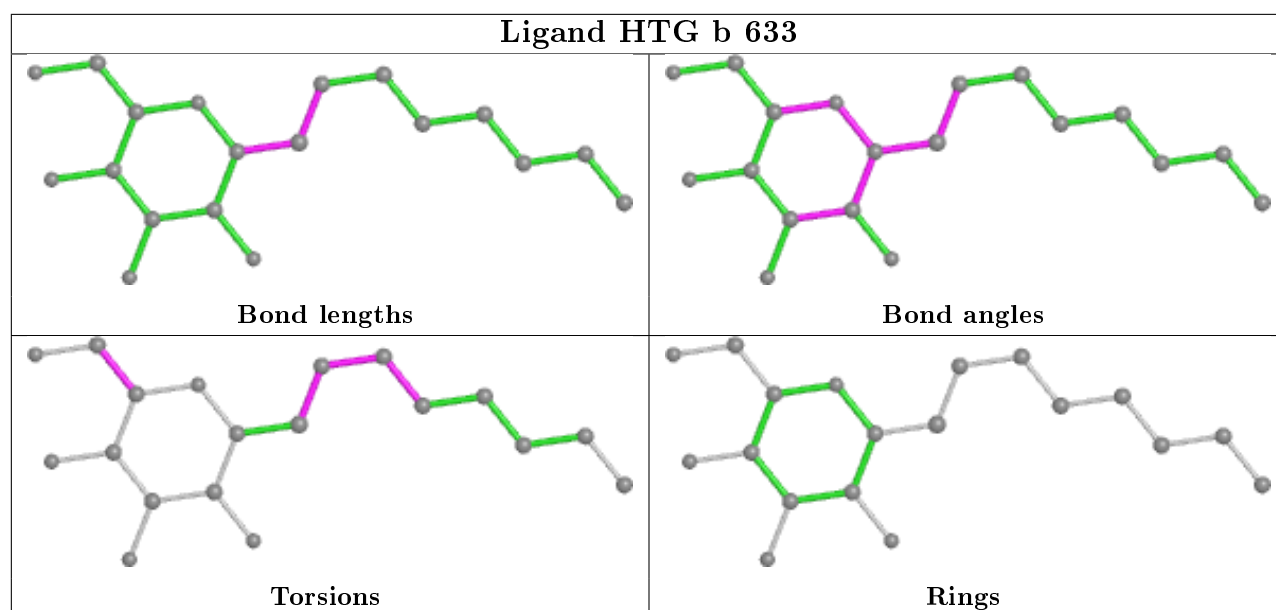
Ligand CLA C 505

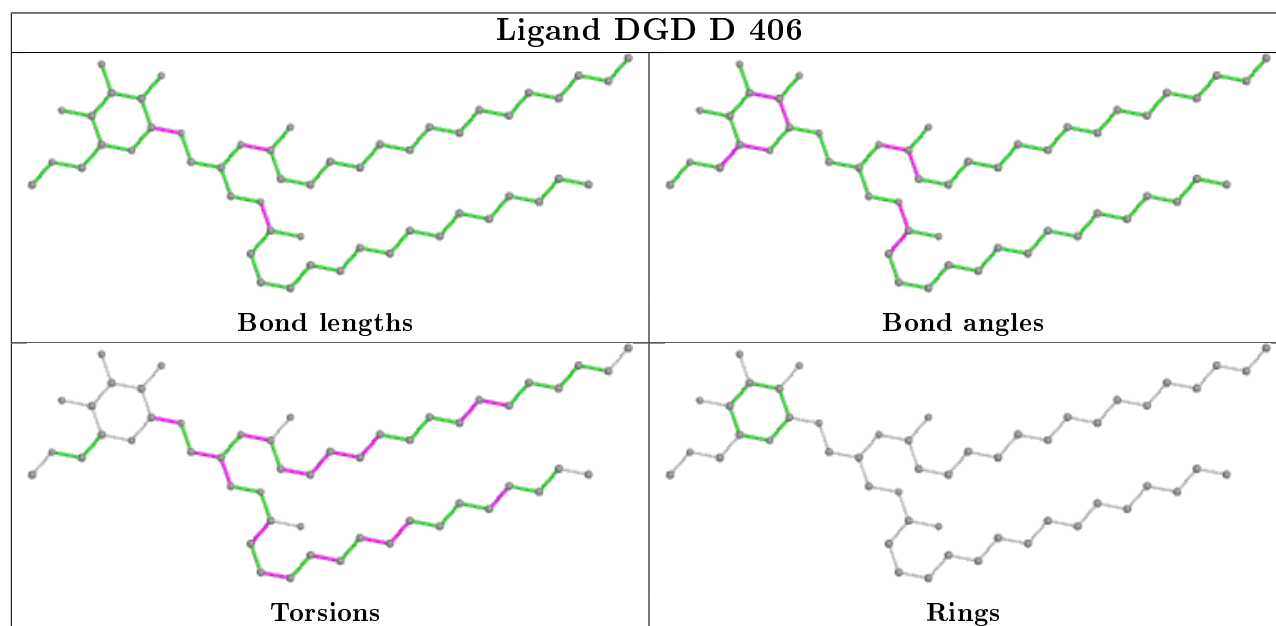
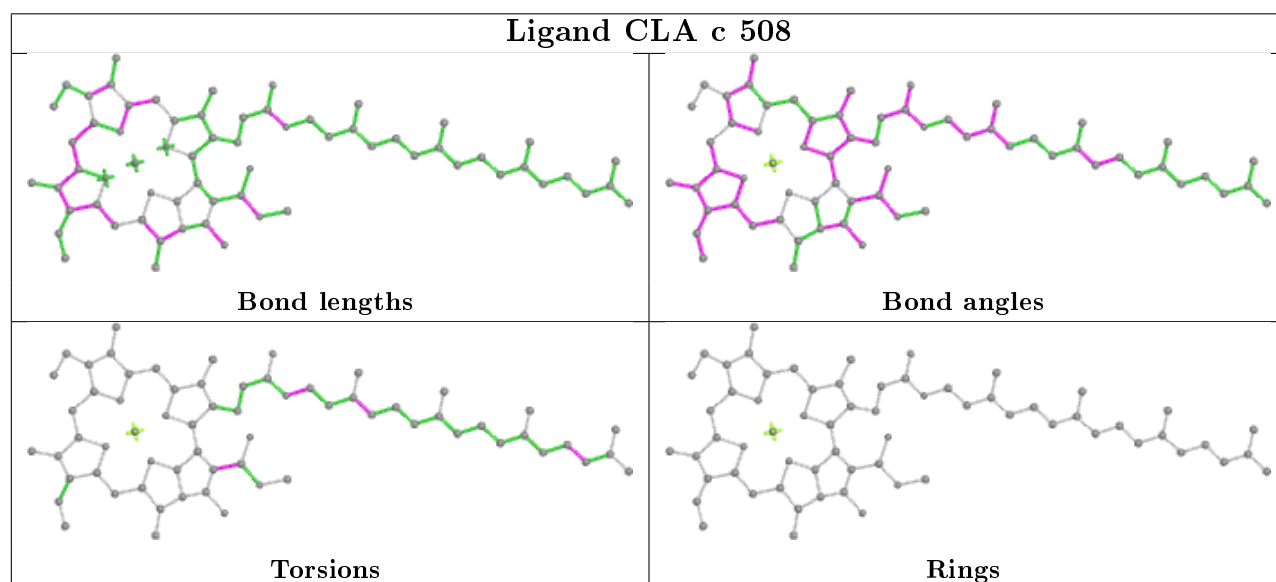
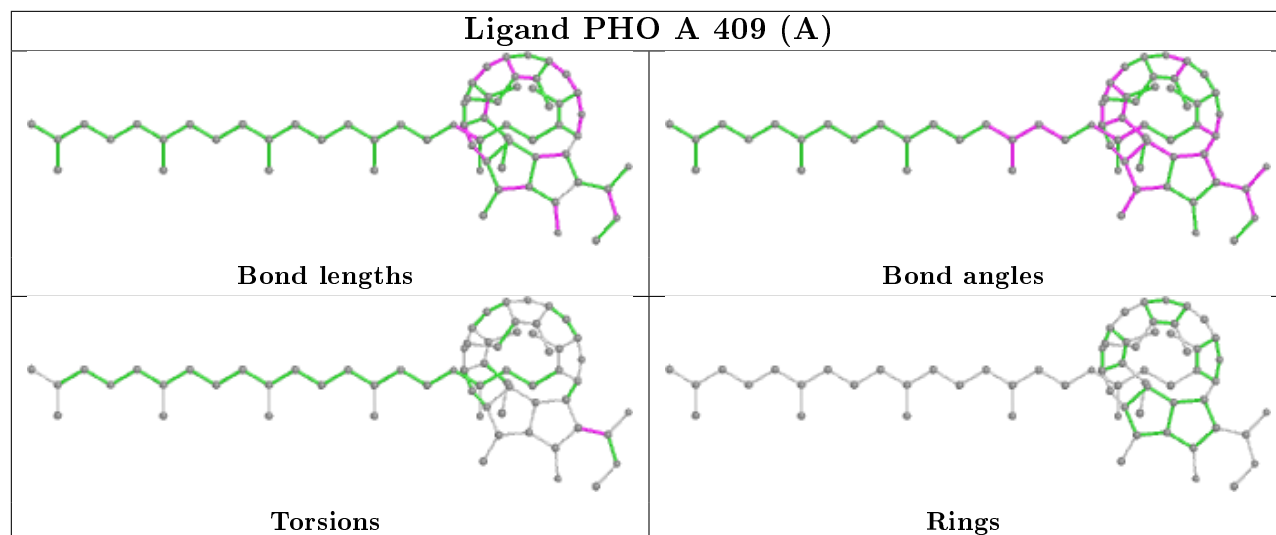




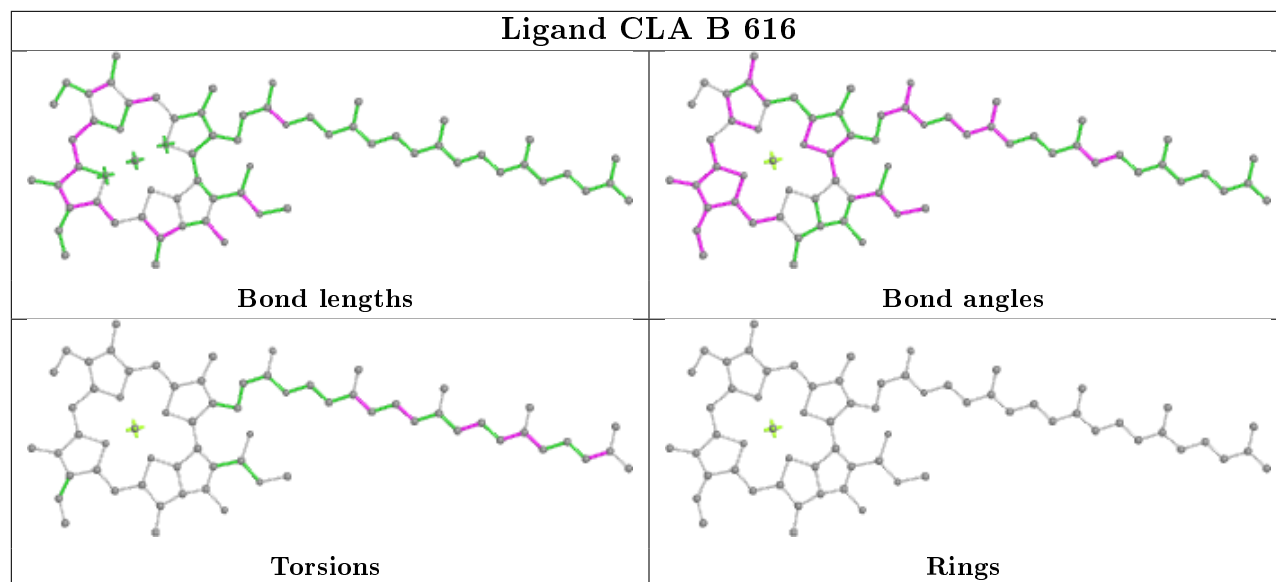




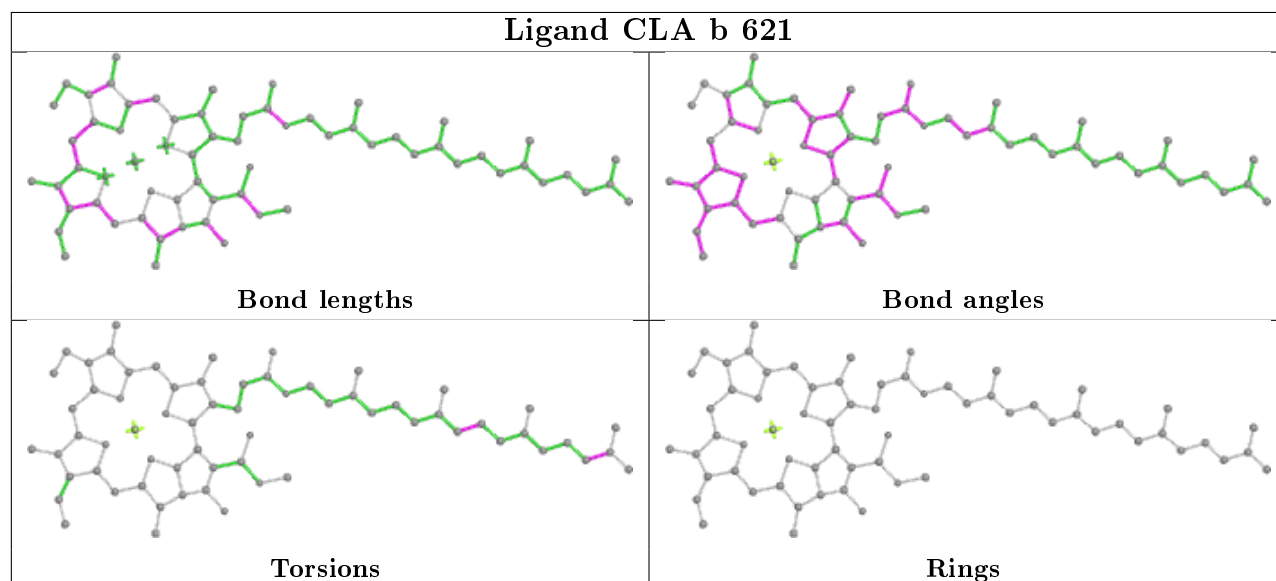




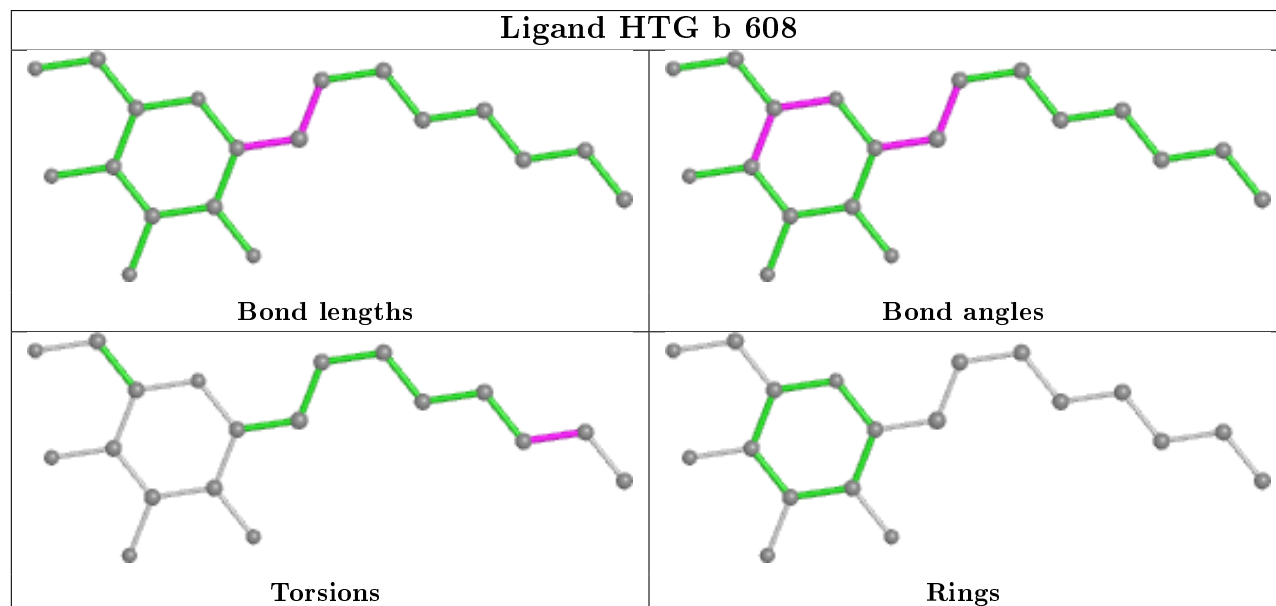
Ligand CLA B 616



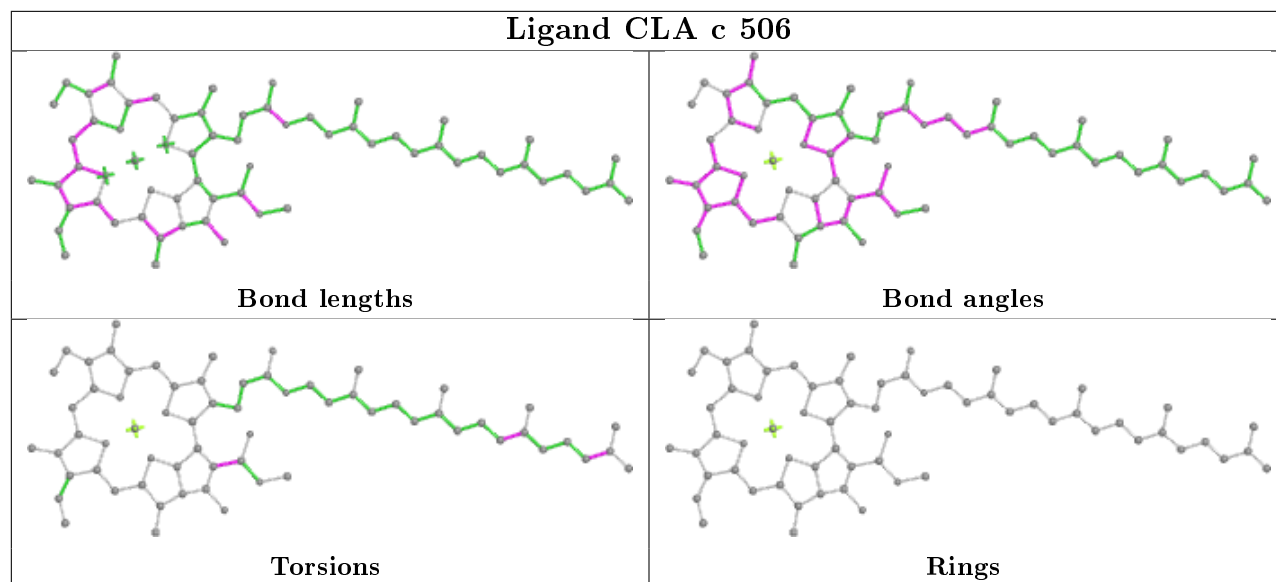
Ligand CLA b 621



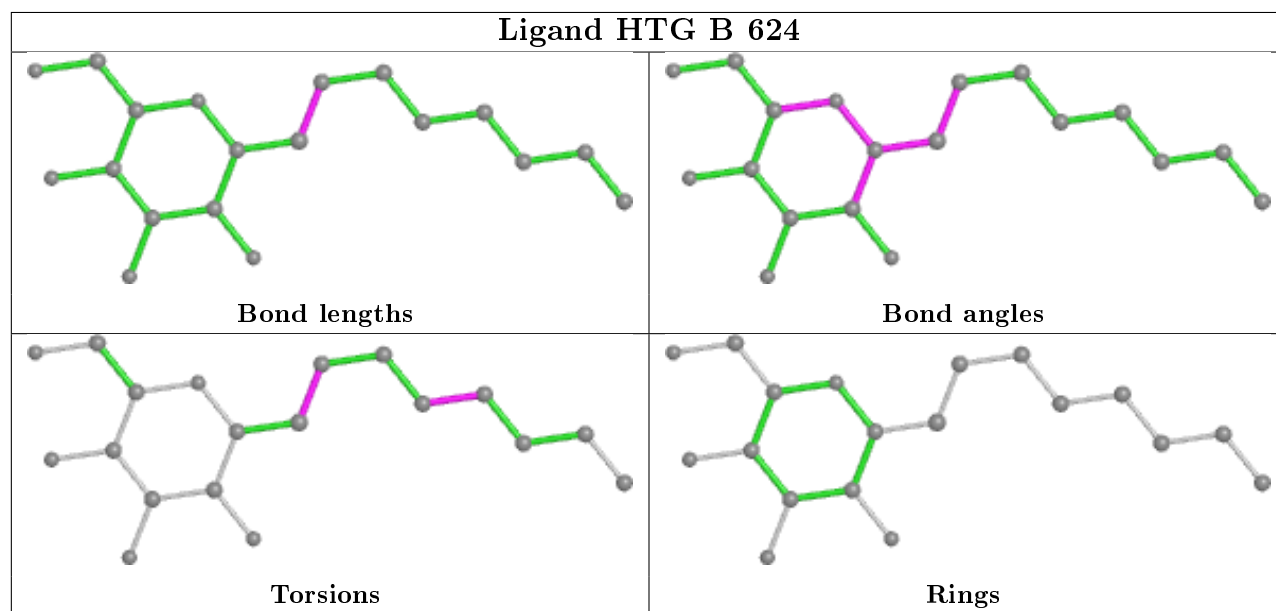
Ligand HTG b 608

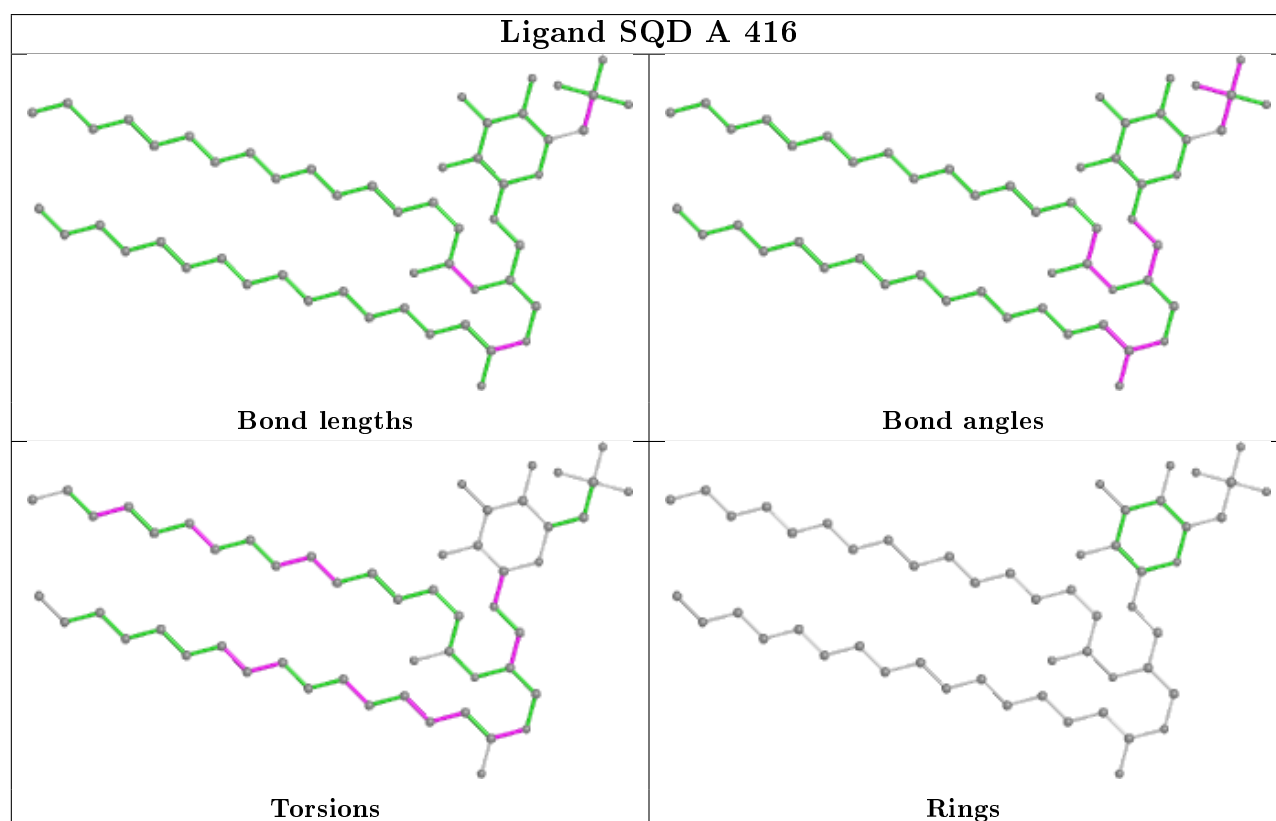
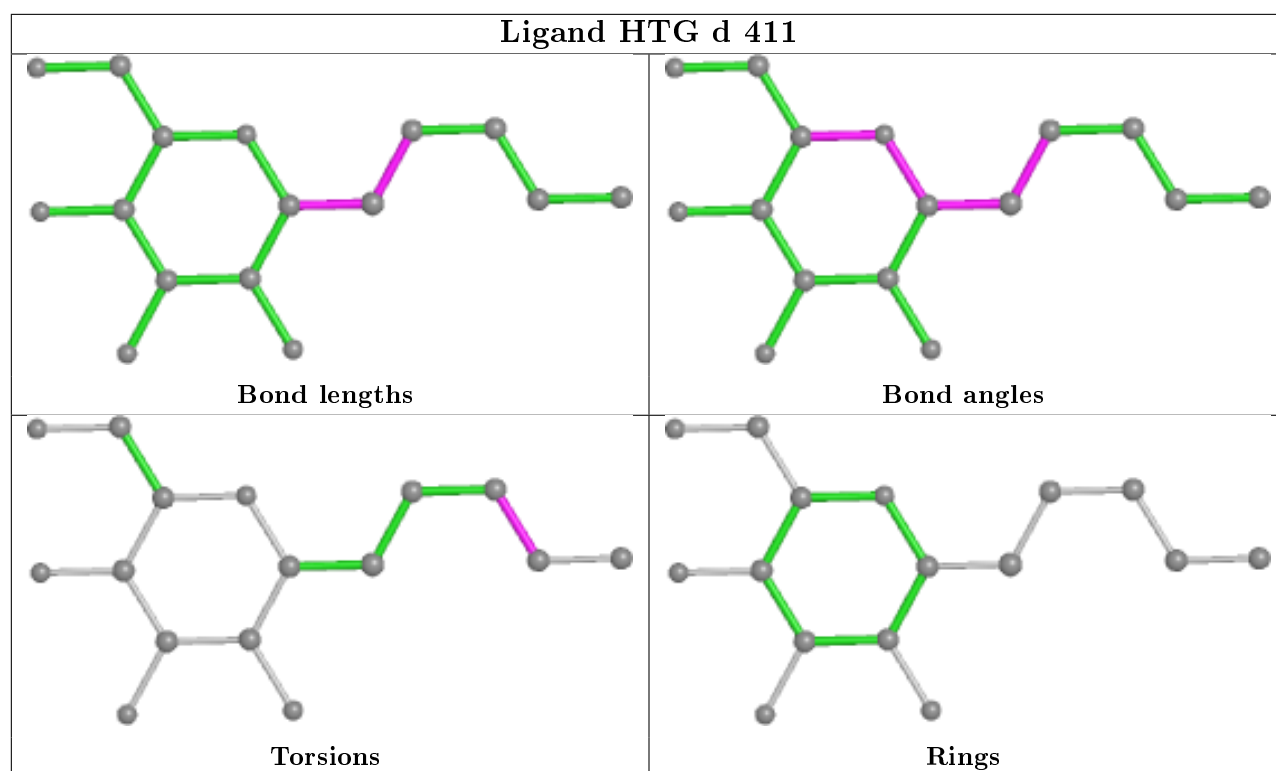


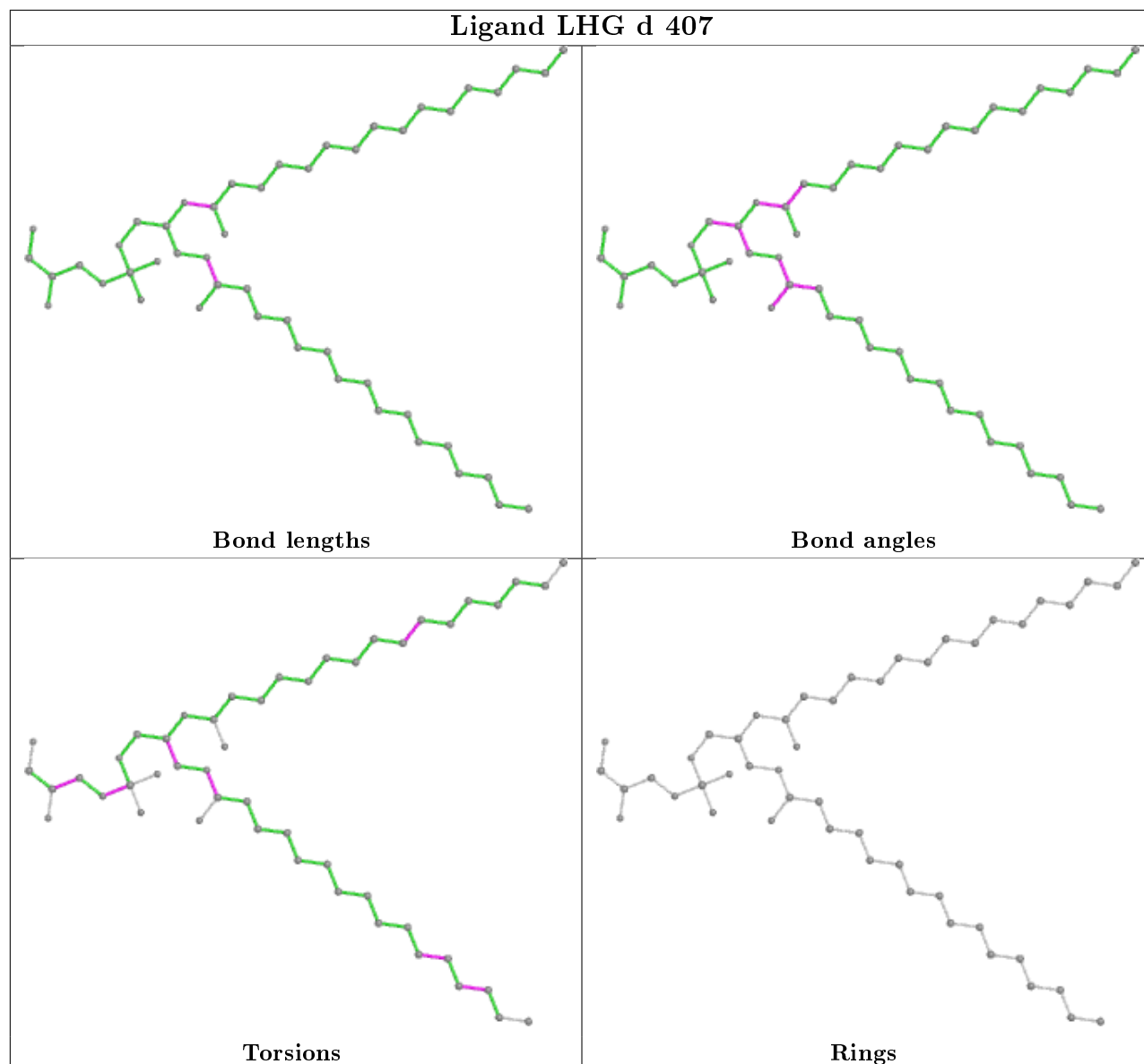
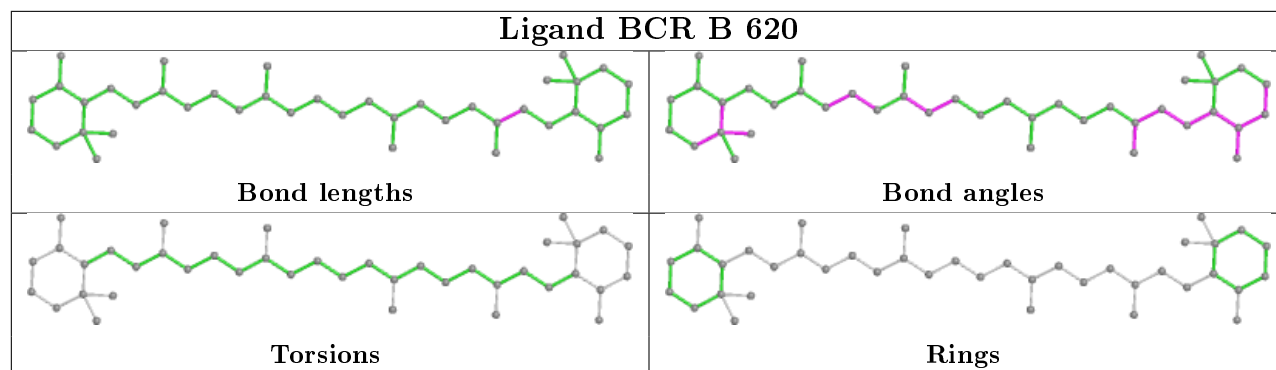
Ligand CLA c 506

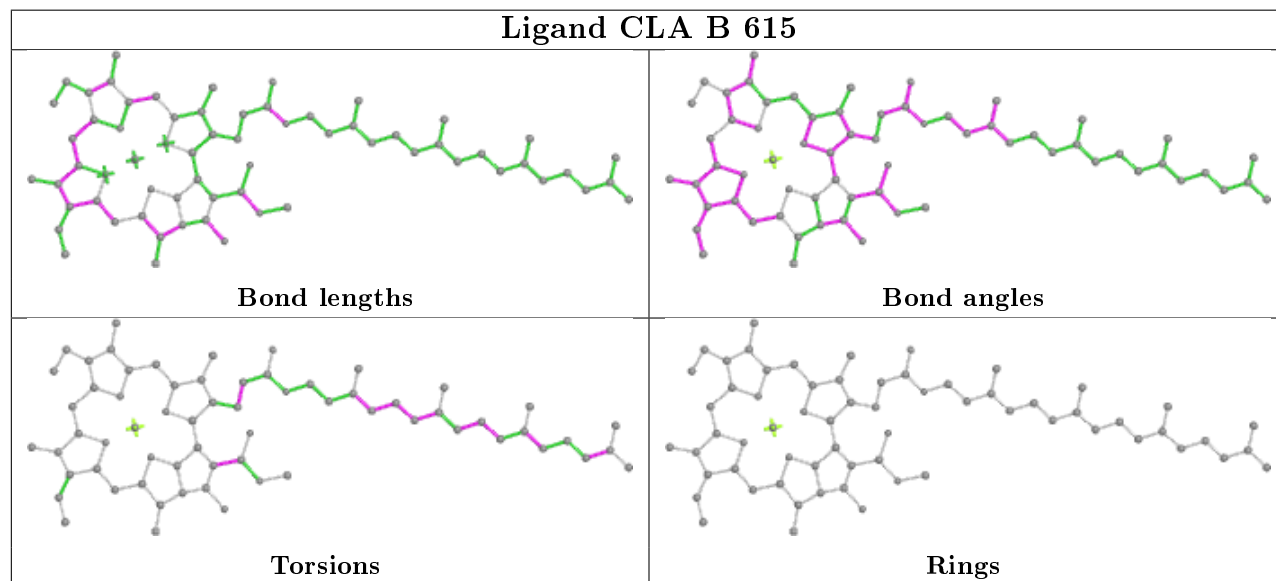
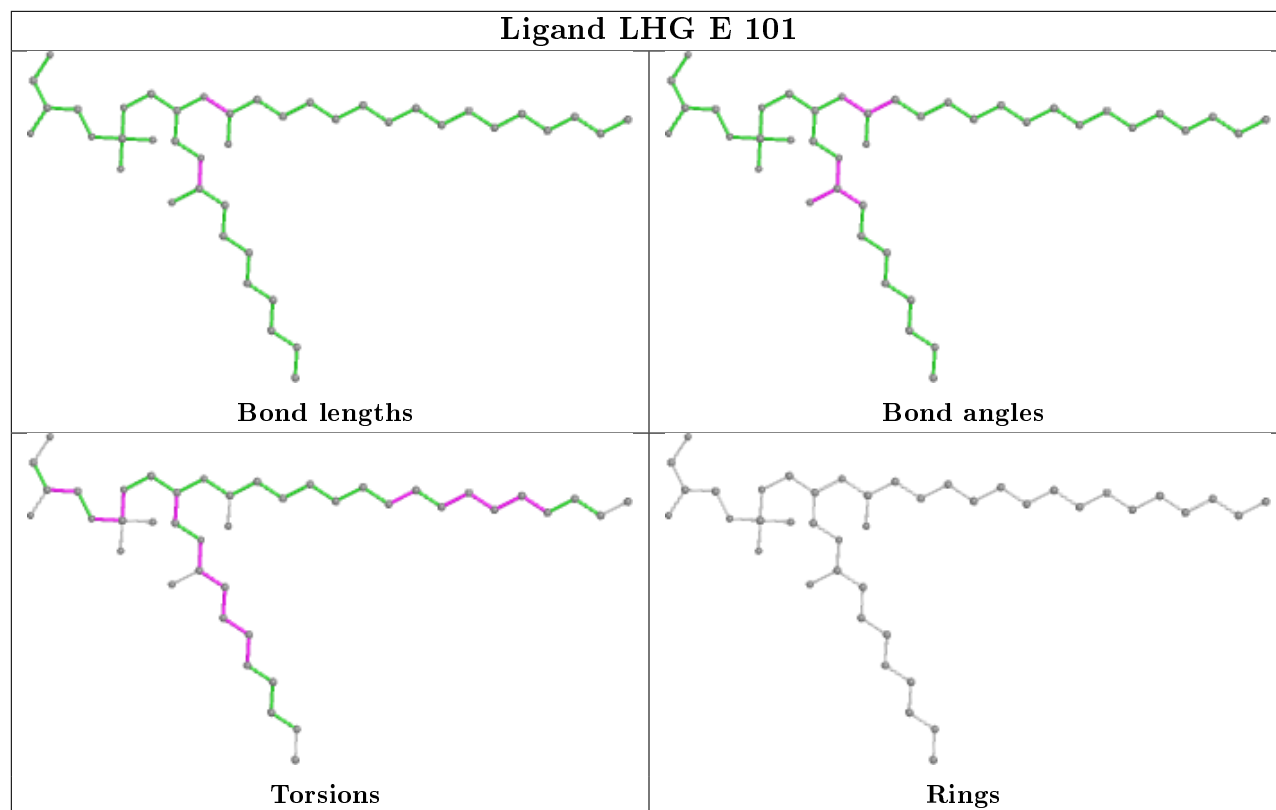


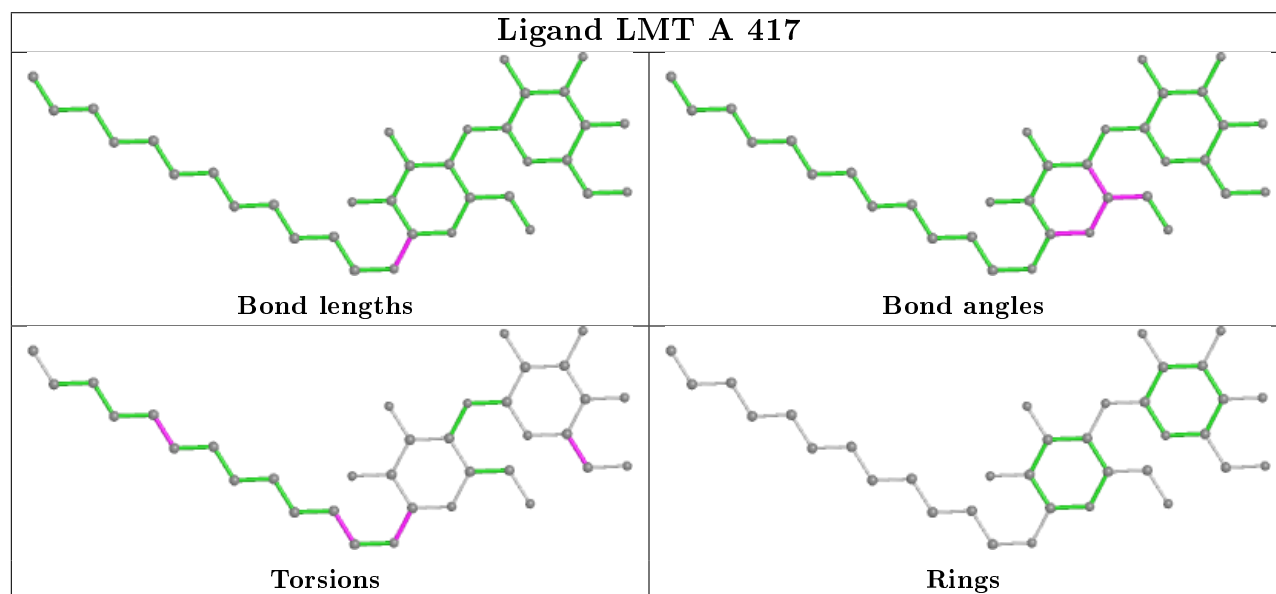
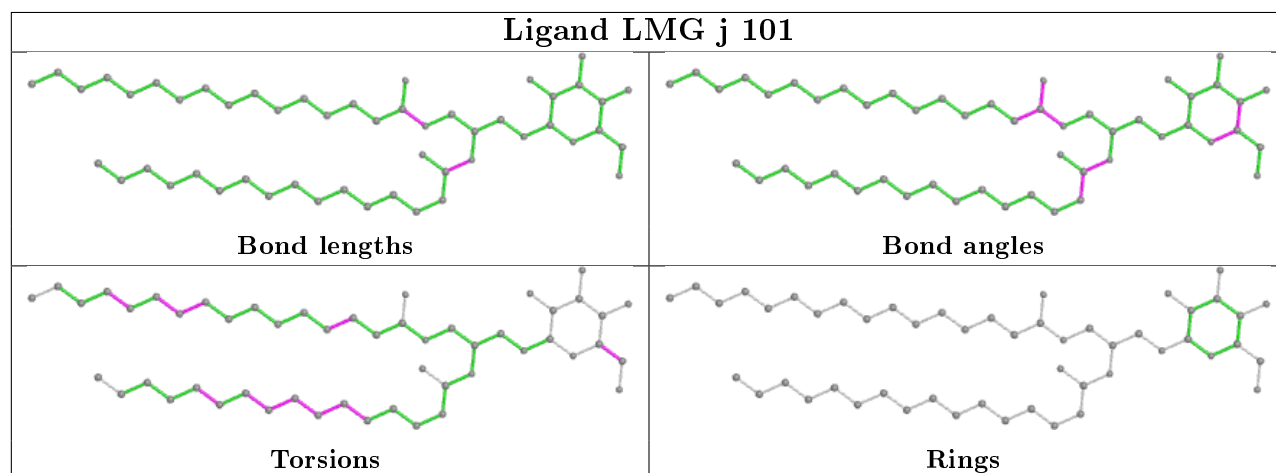
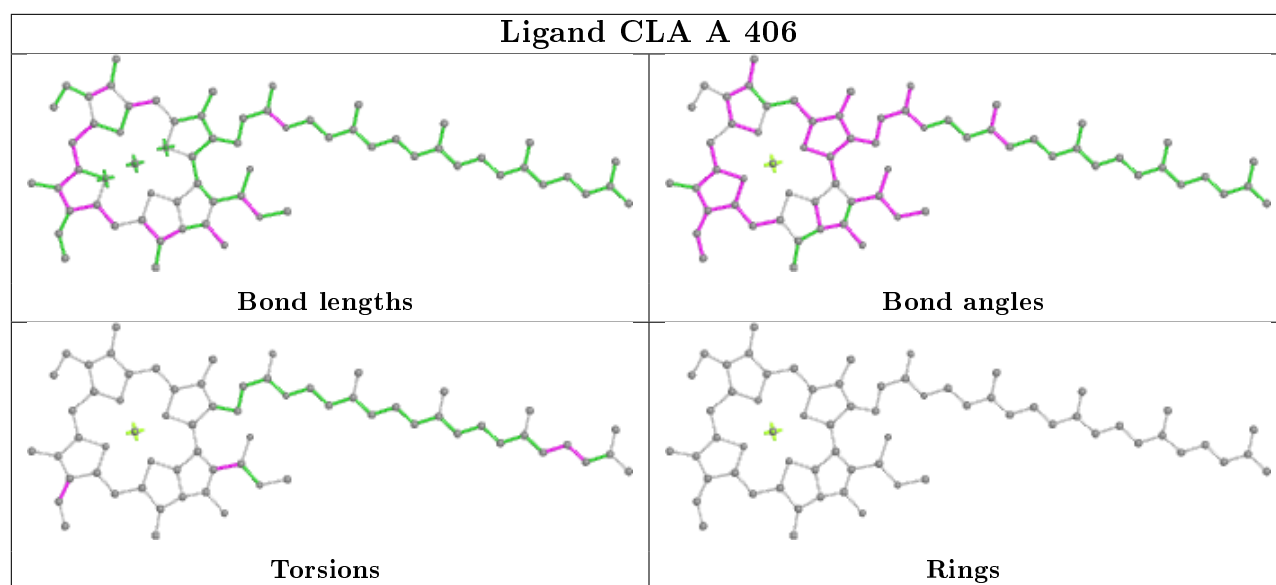
Ligand HTG B 624

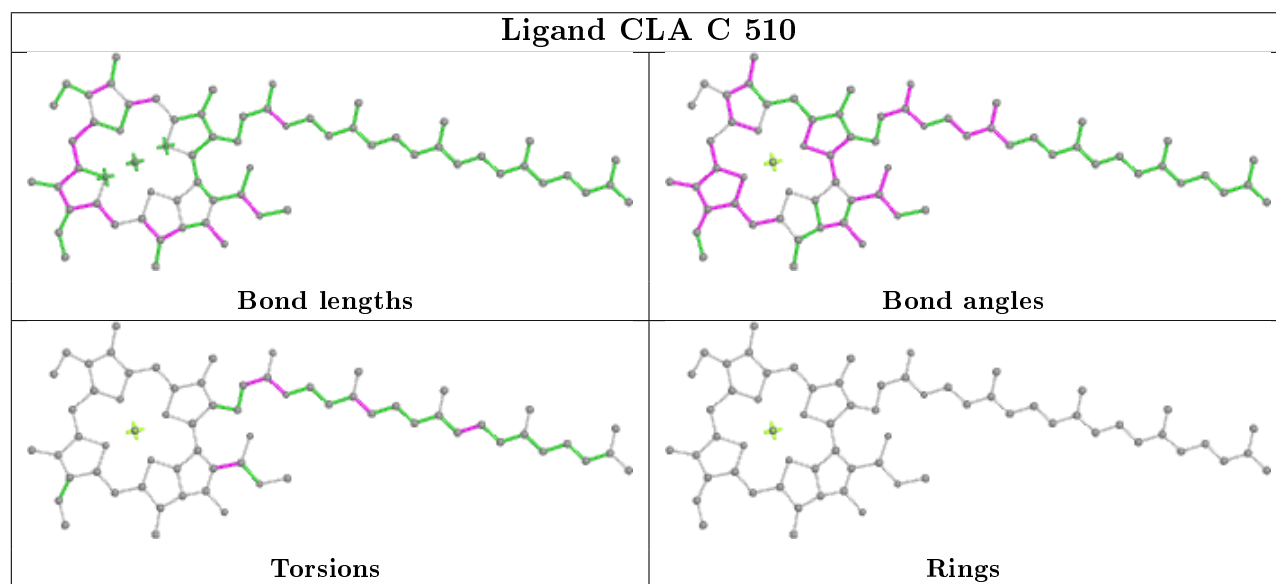
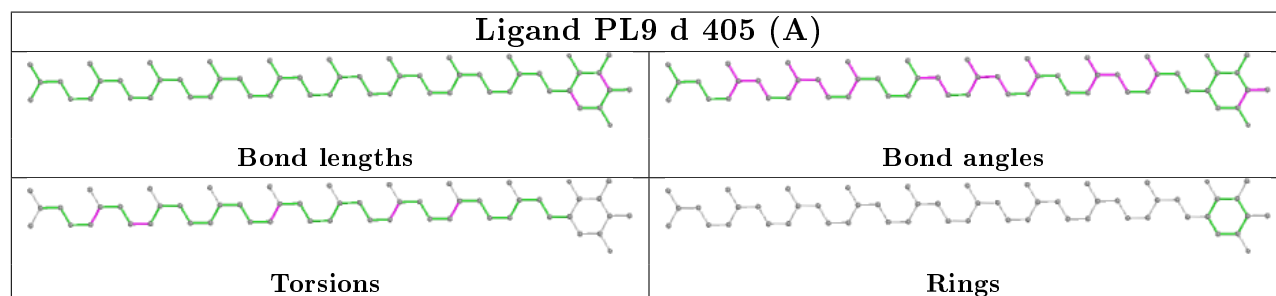
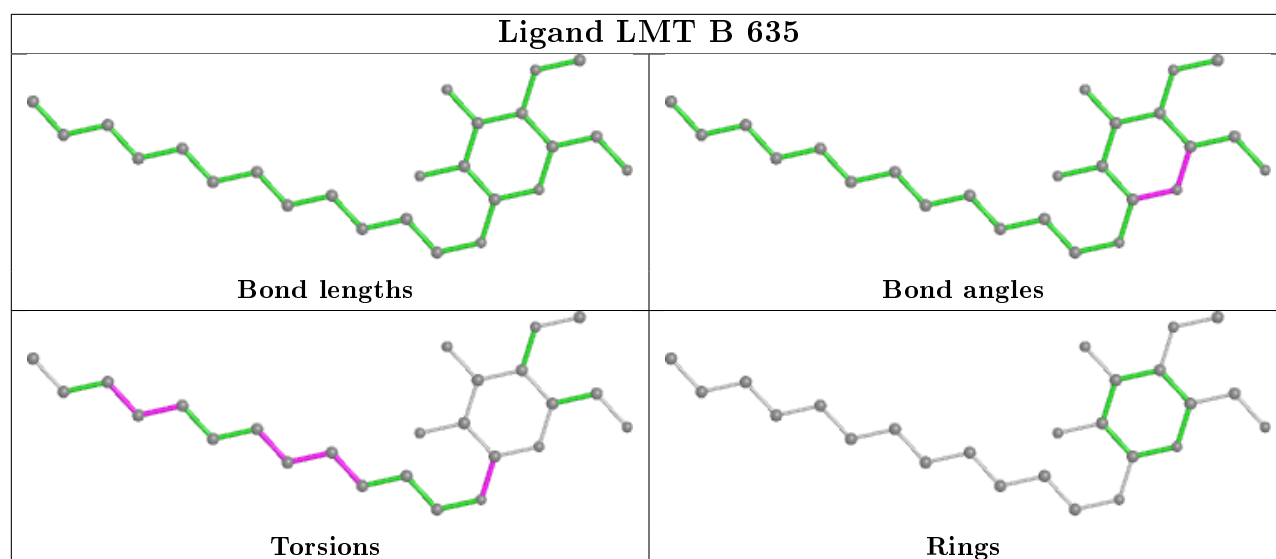


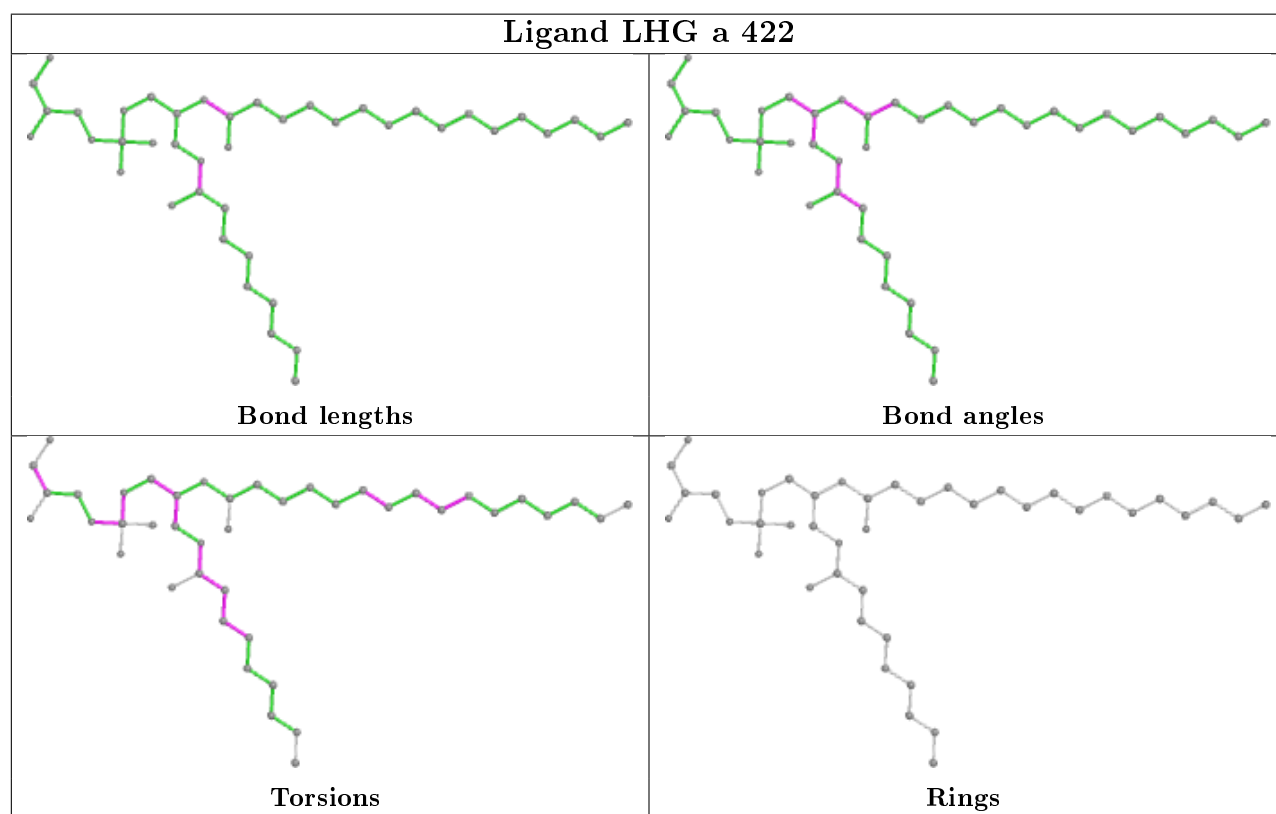
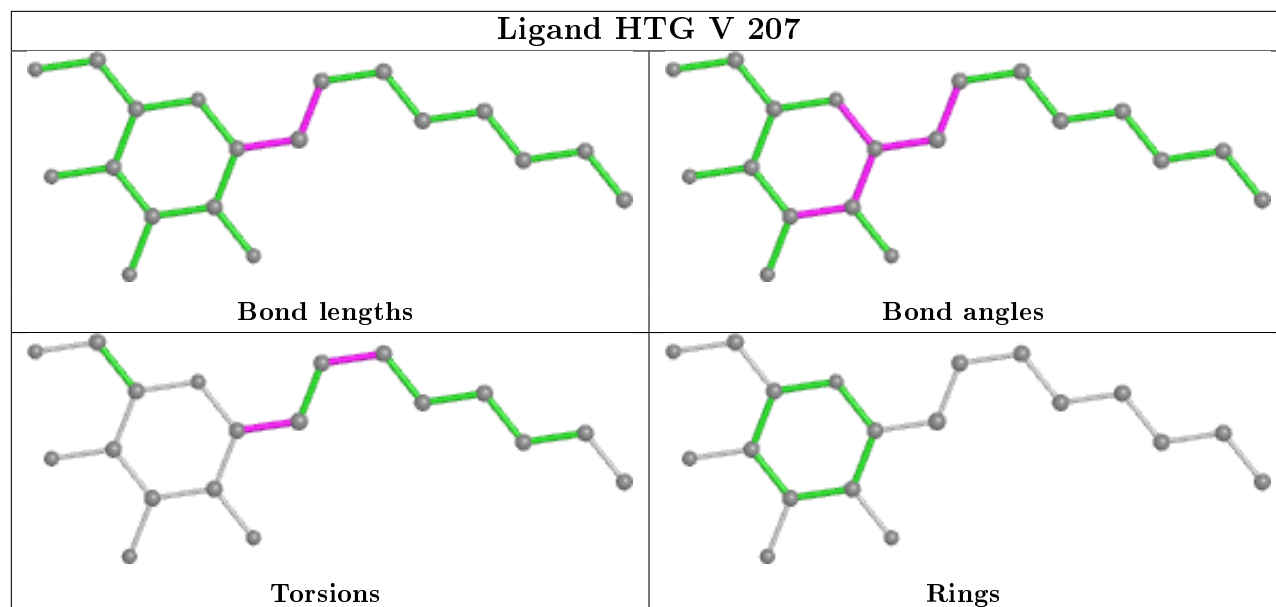


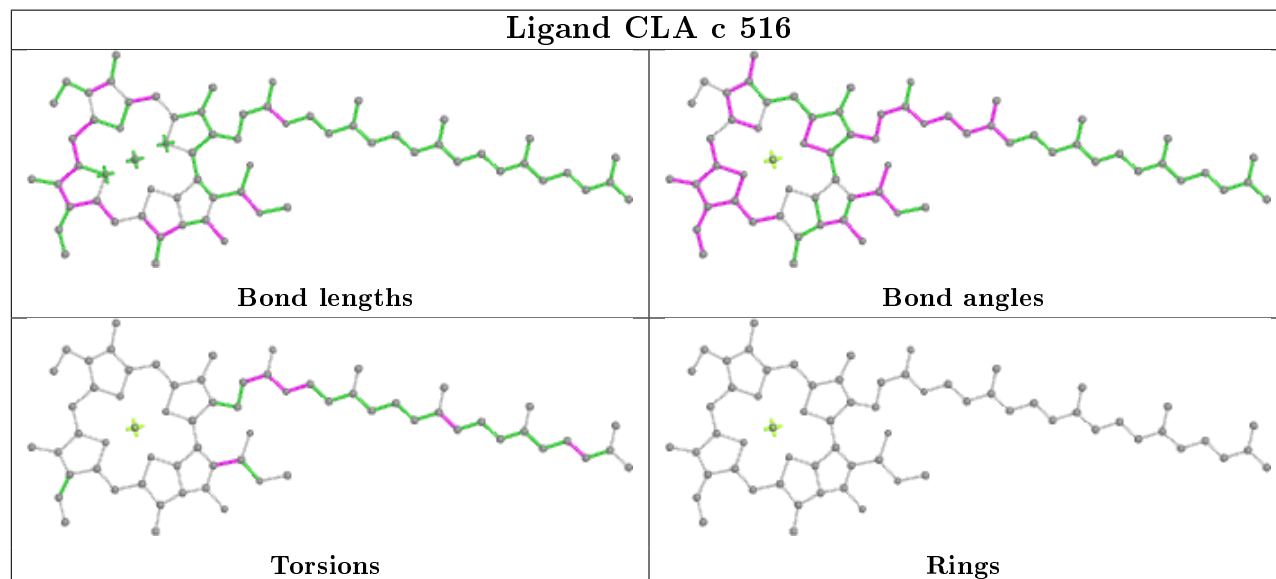
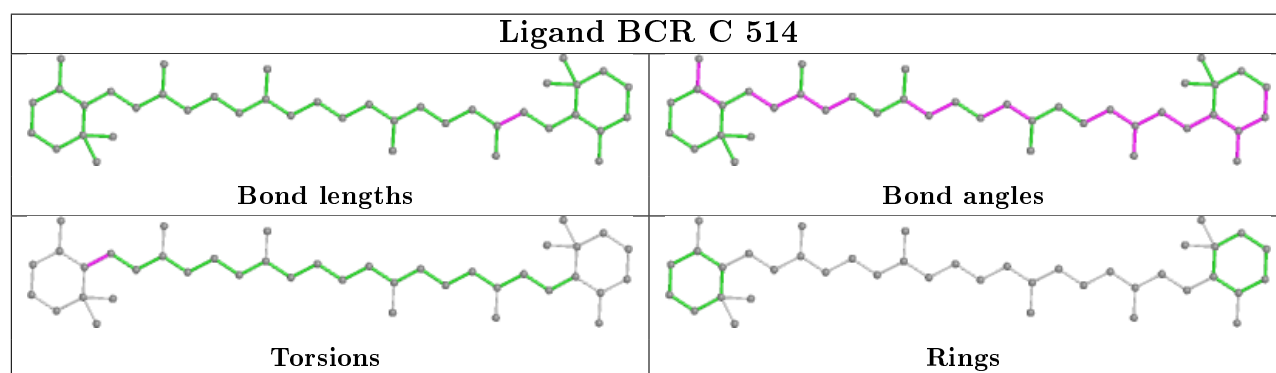
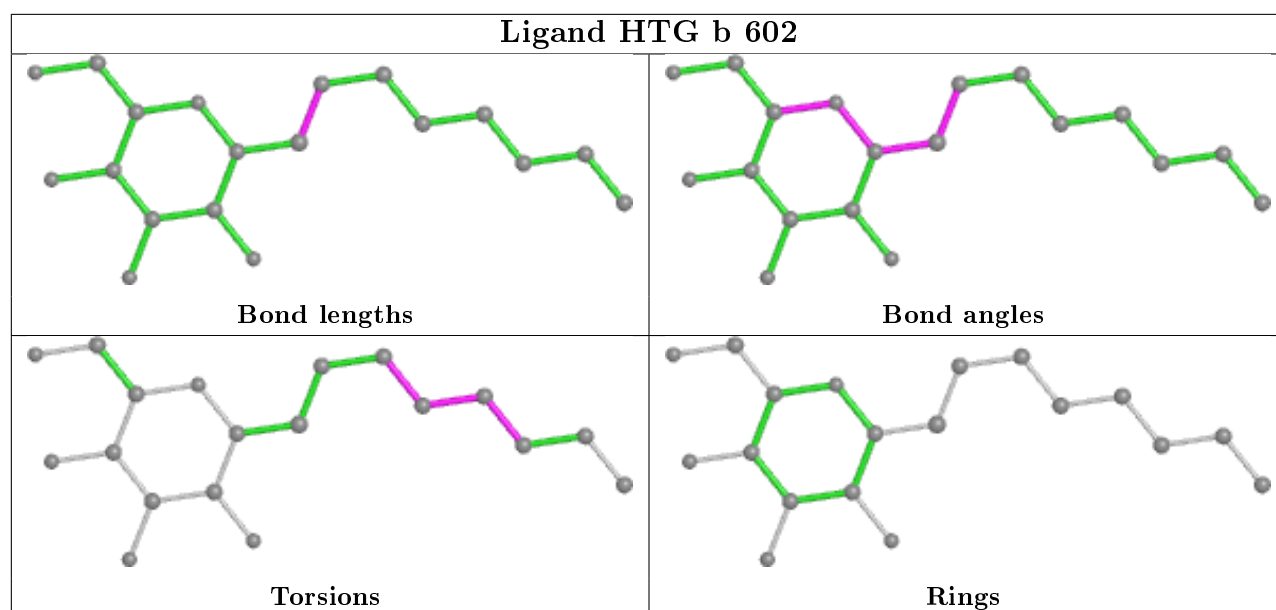


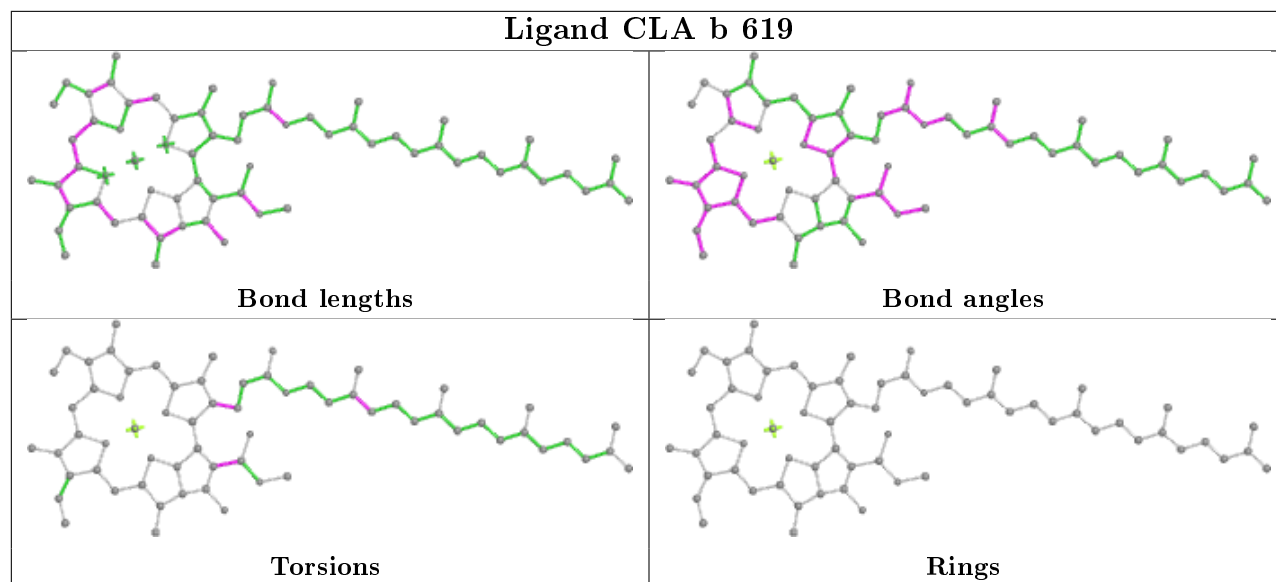
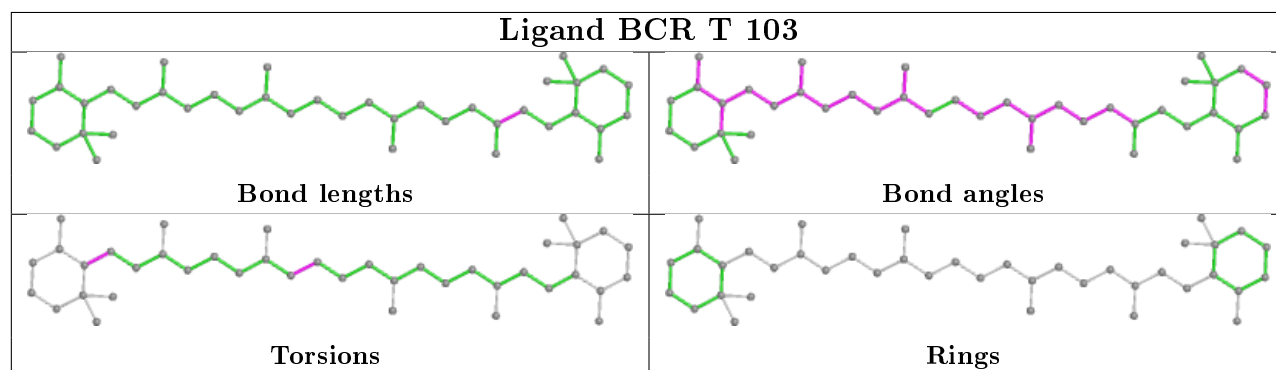
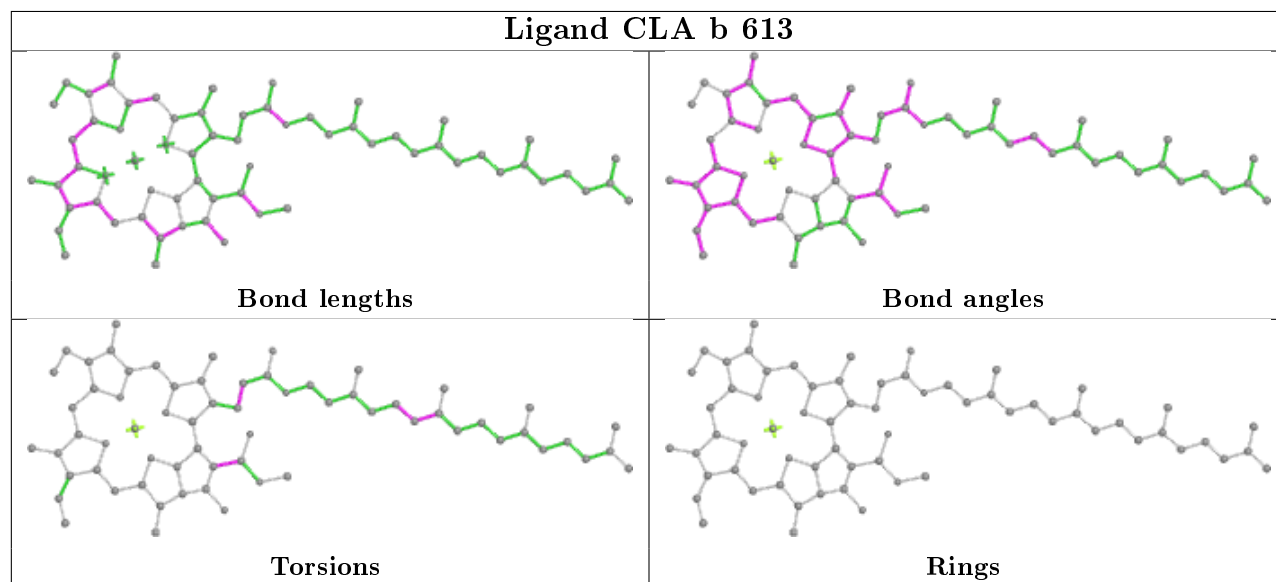




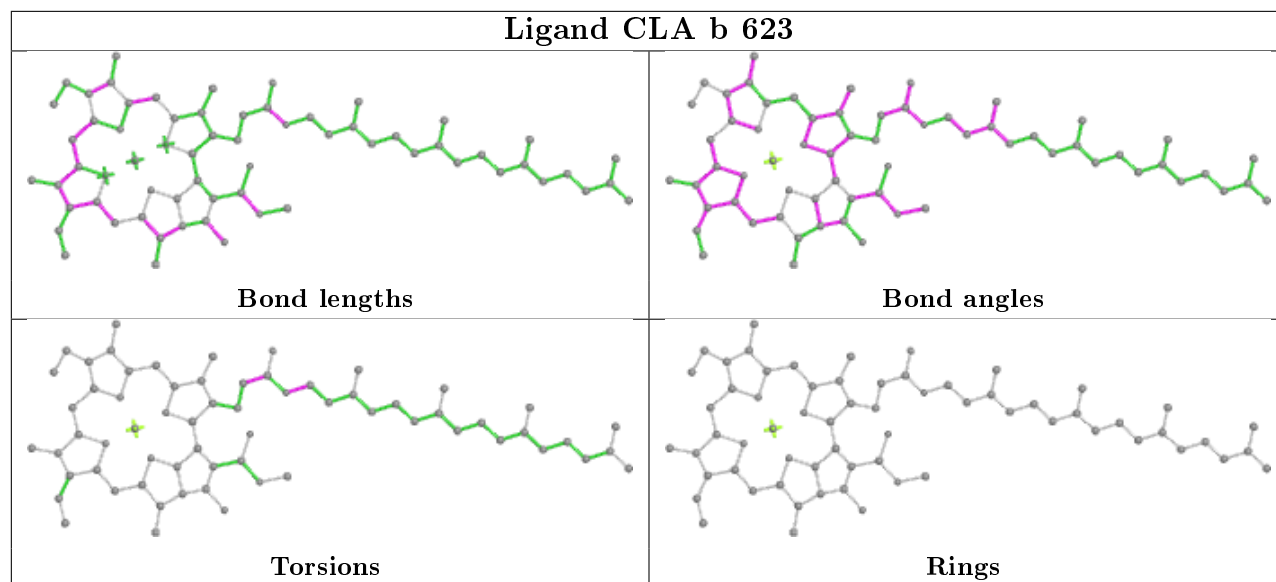




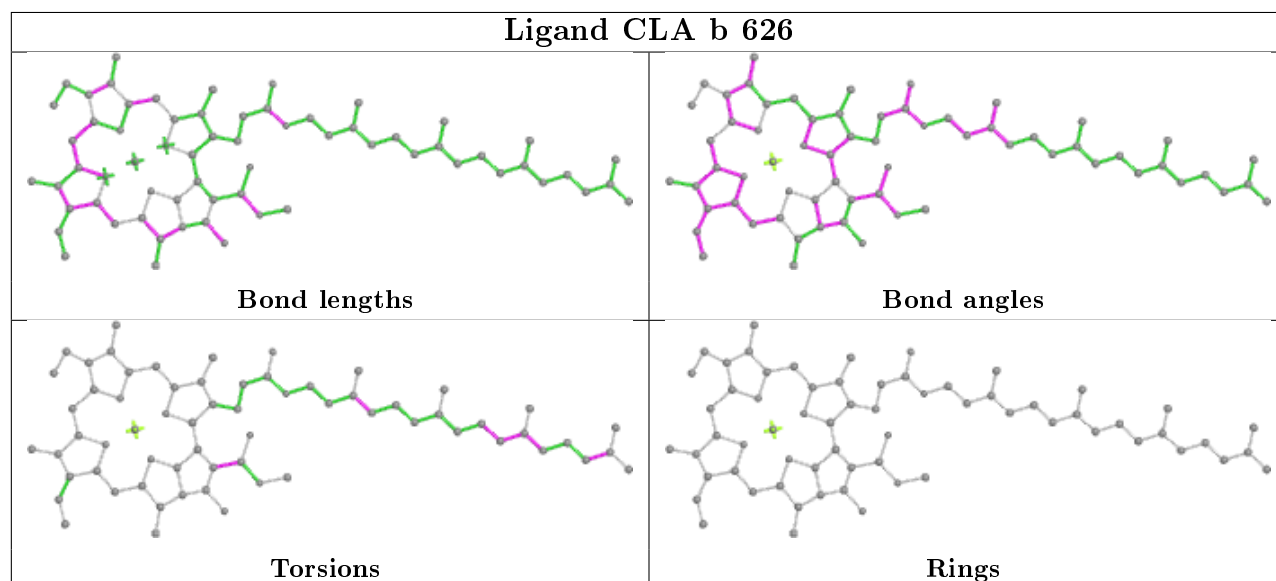


Ligand CLA b 619**Ligand BCR T 103****Ligand CLA b 613**

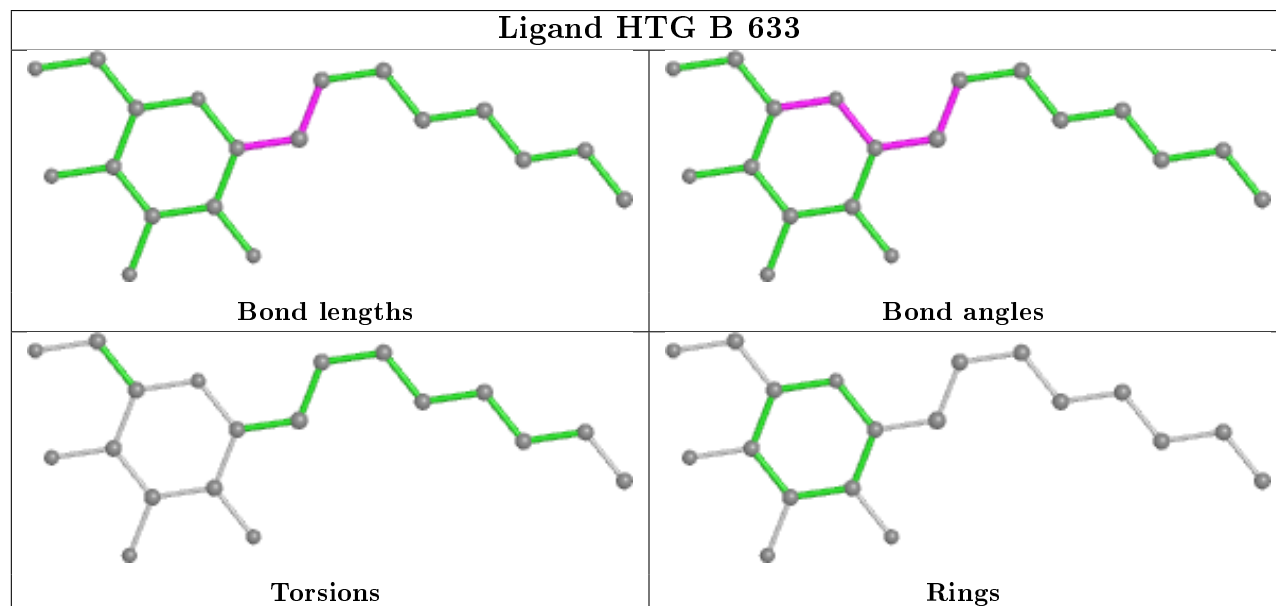
Ligand CLA b 623

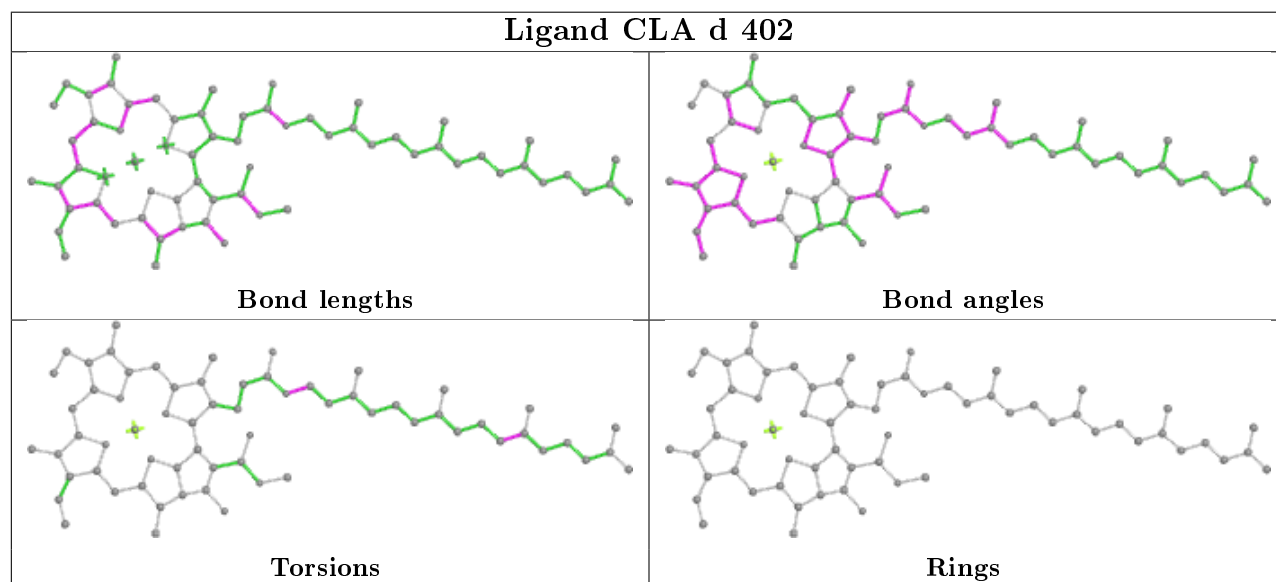
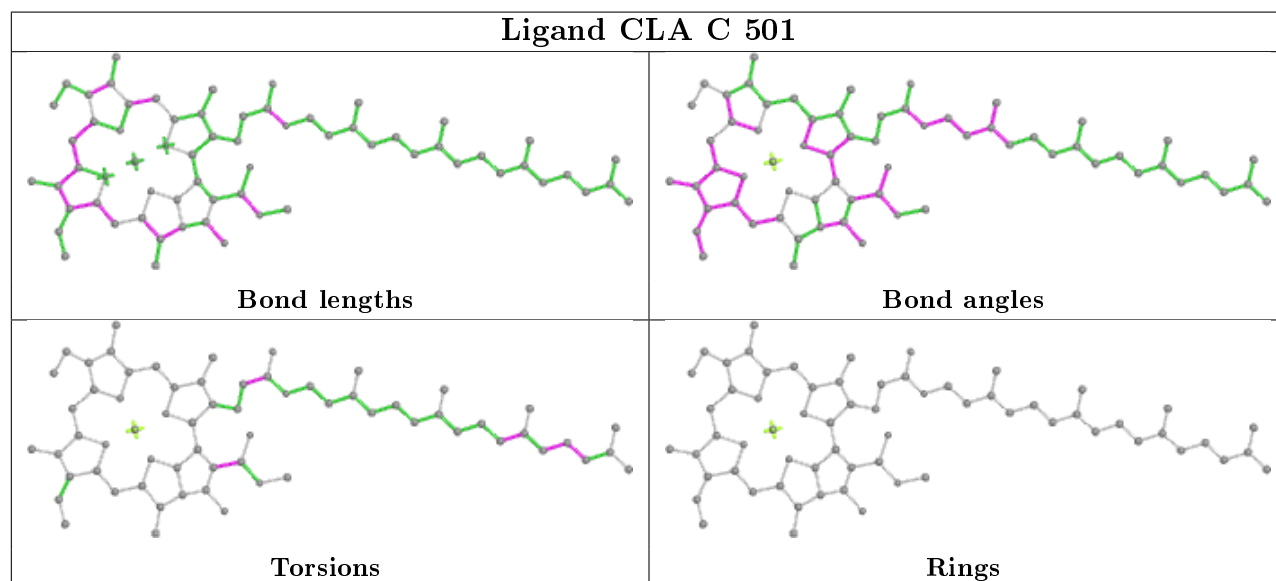
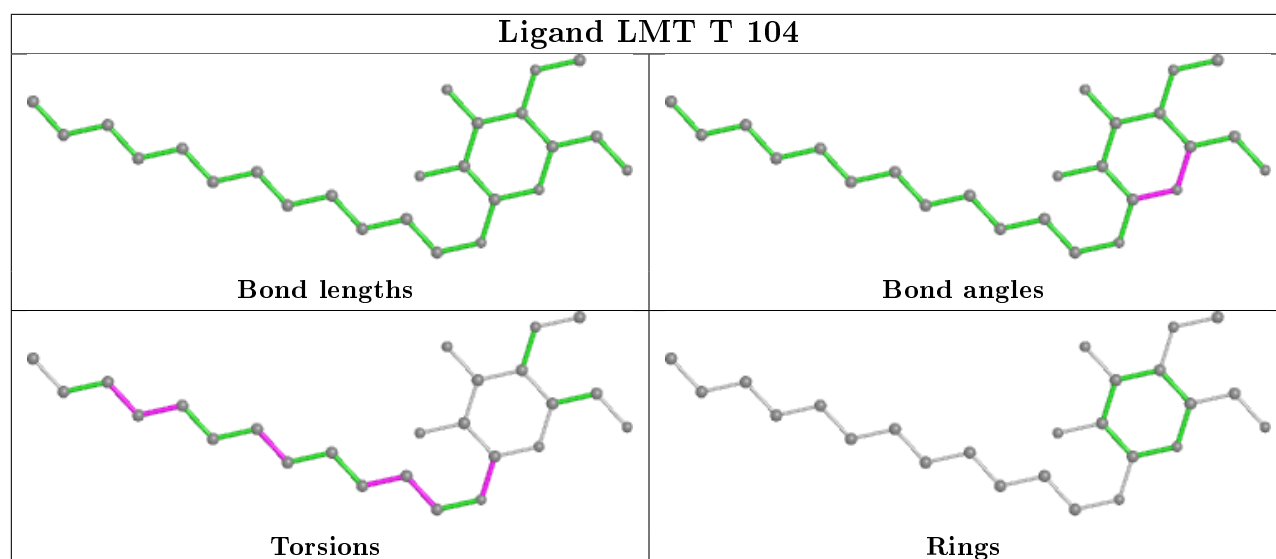


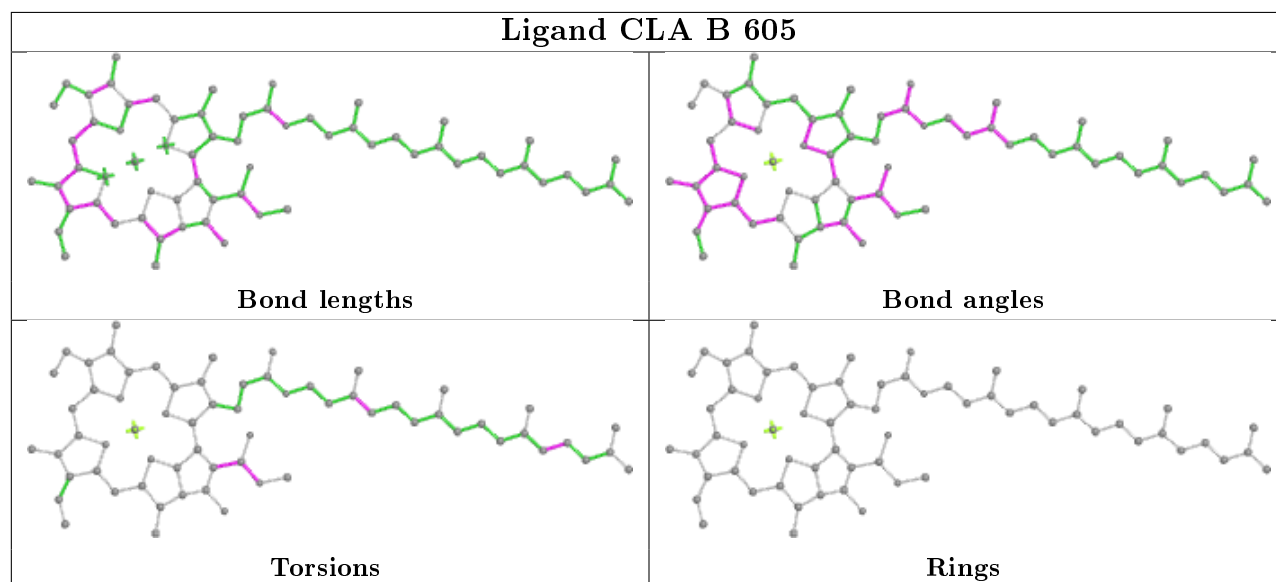
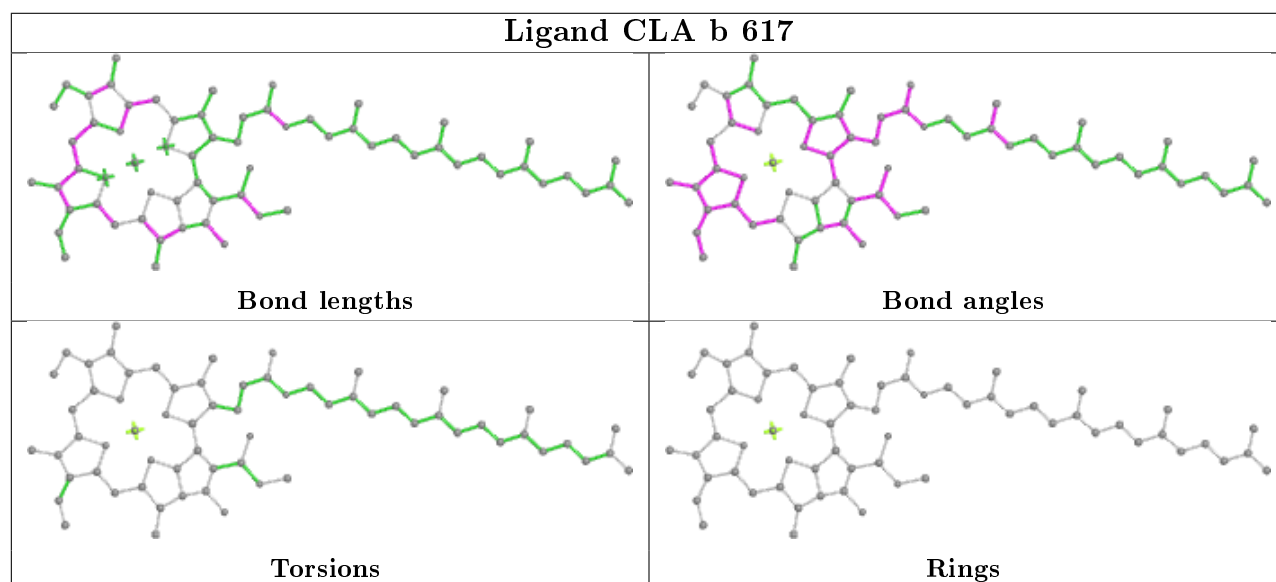
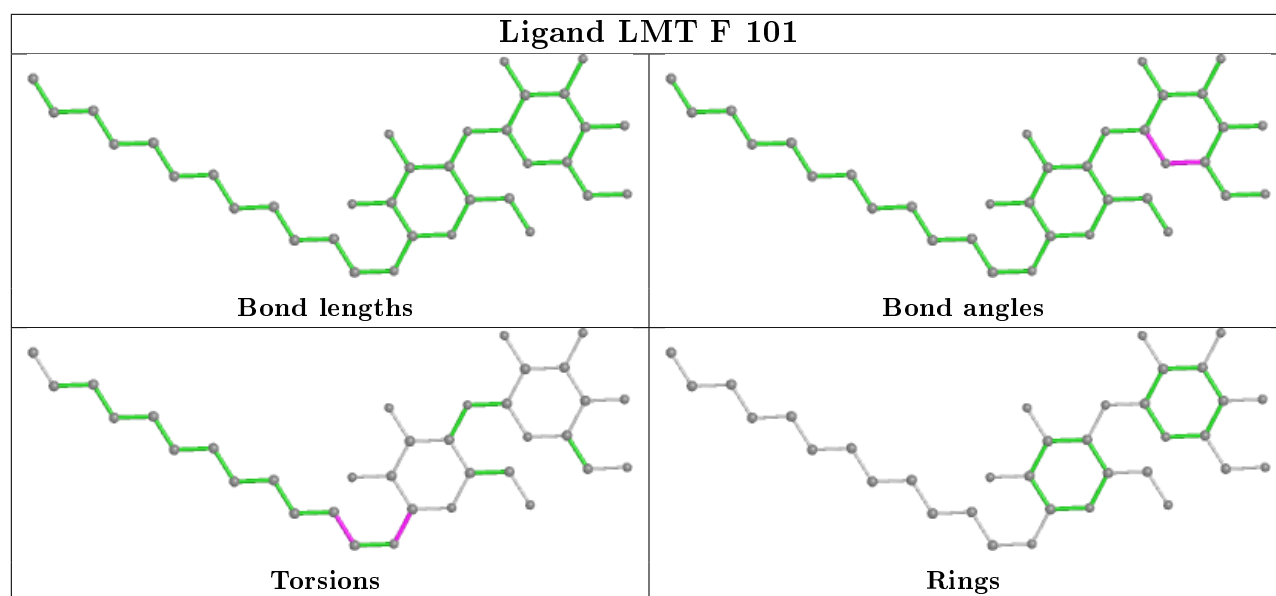
Ligand CLA b 626

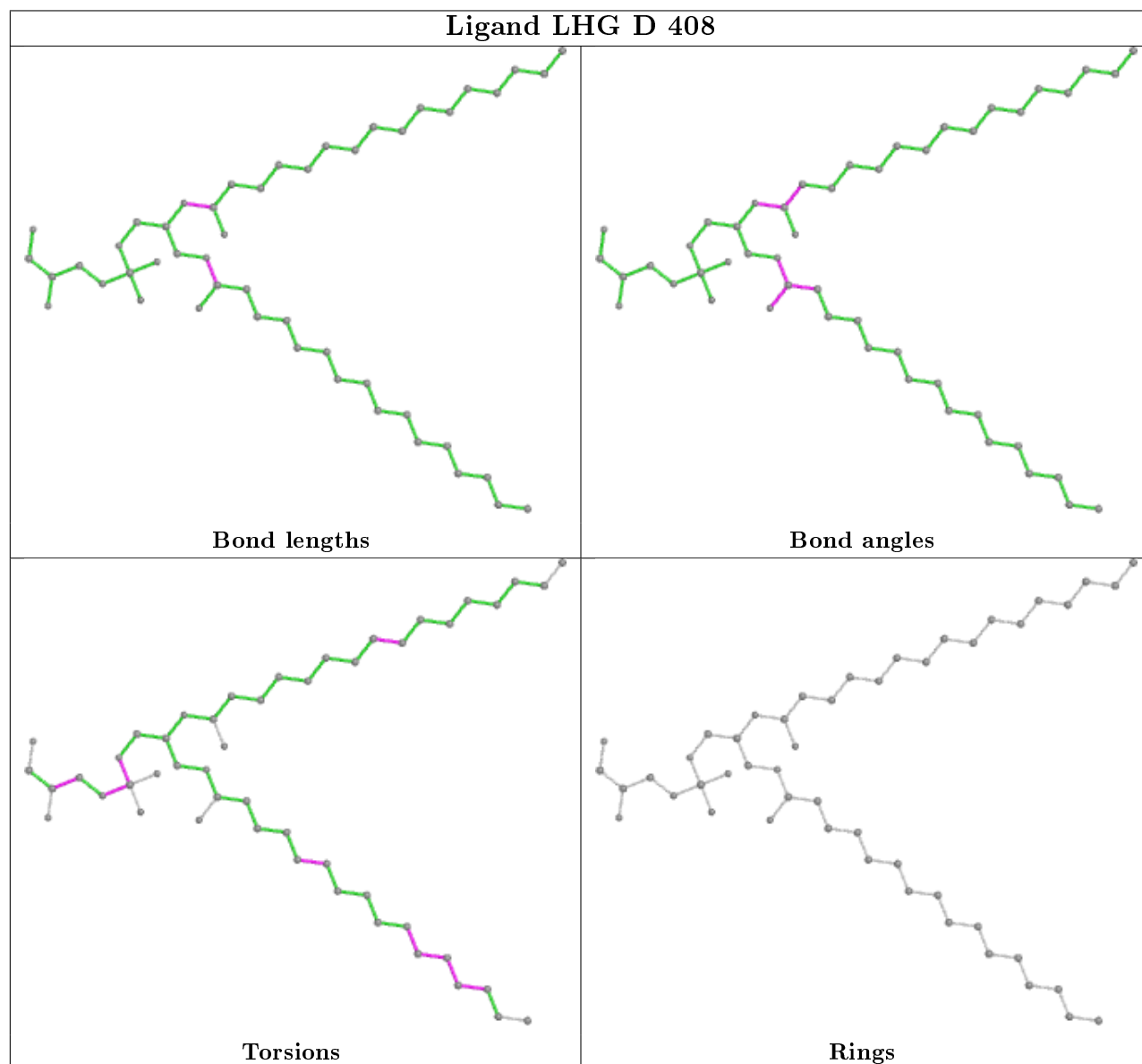
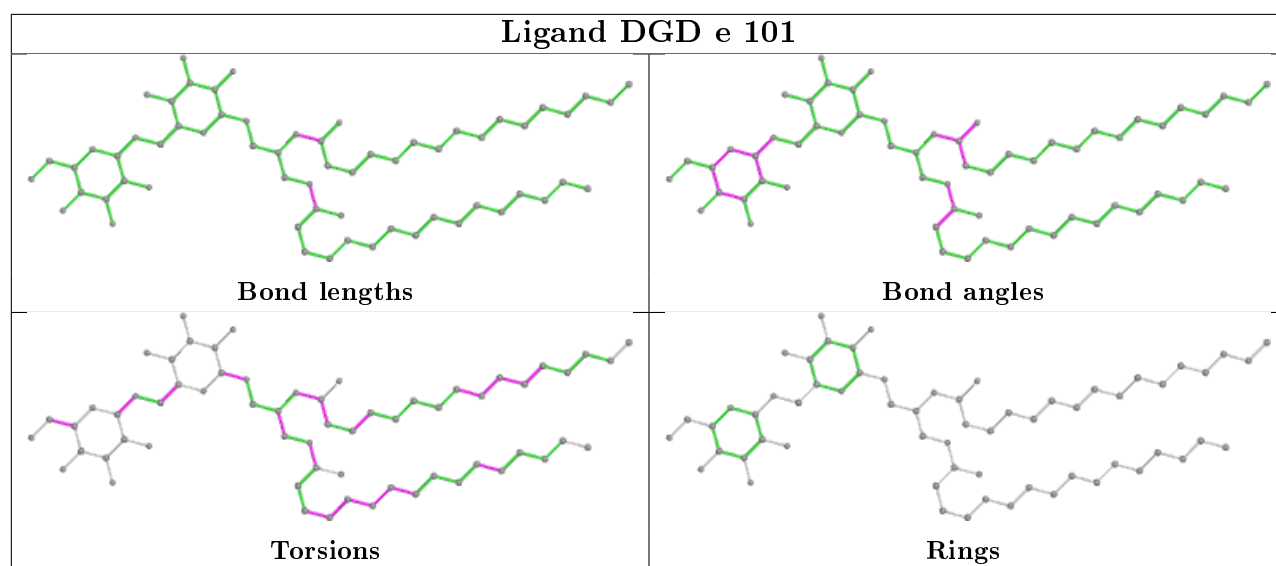


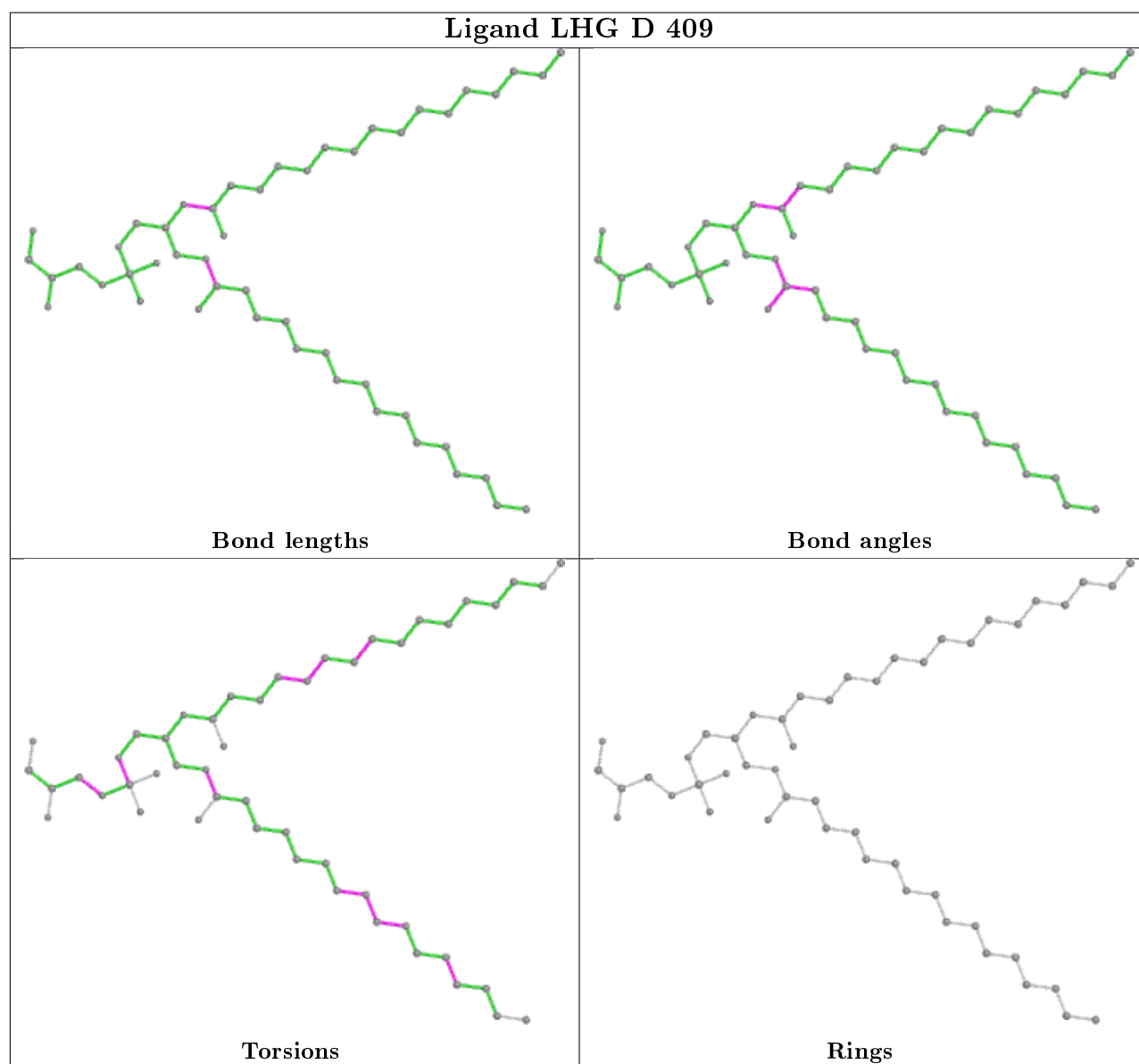
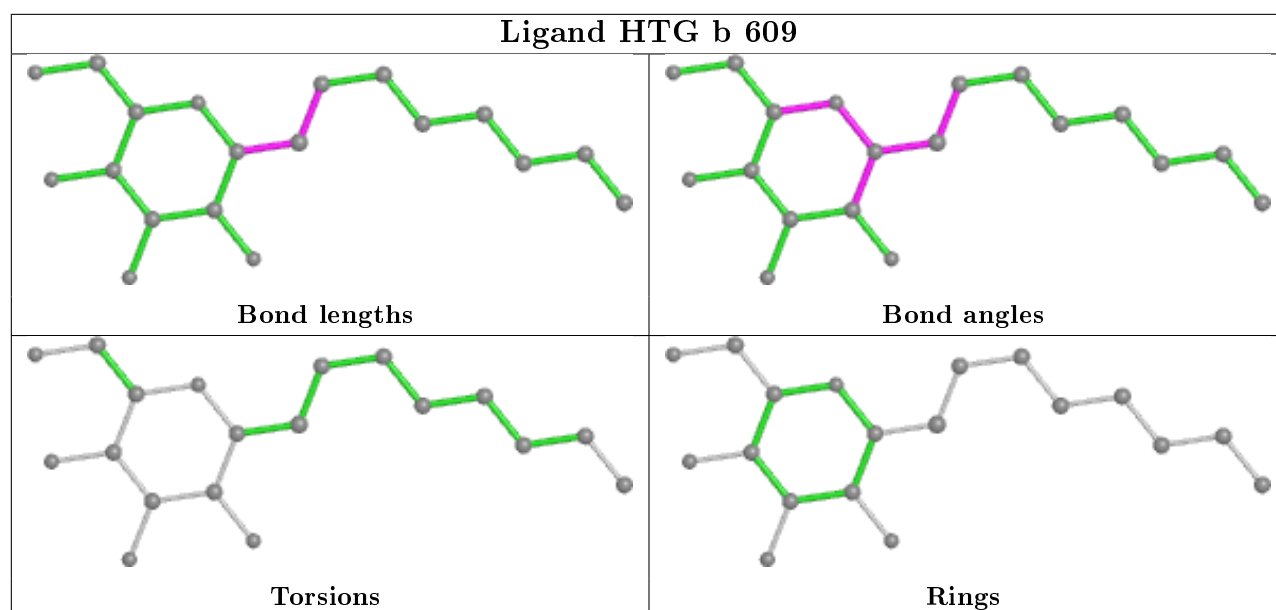
Ligand HTG B 633



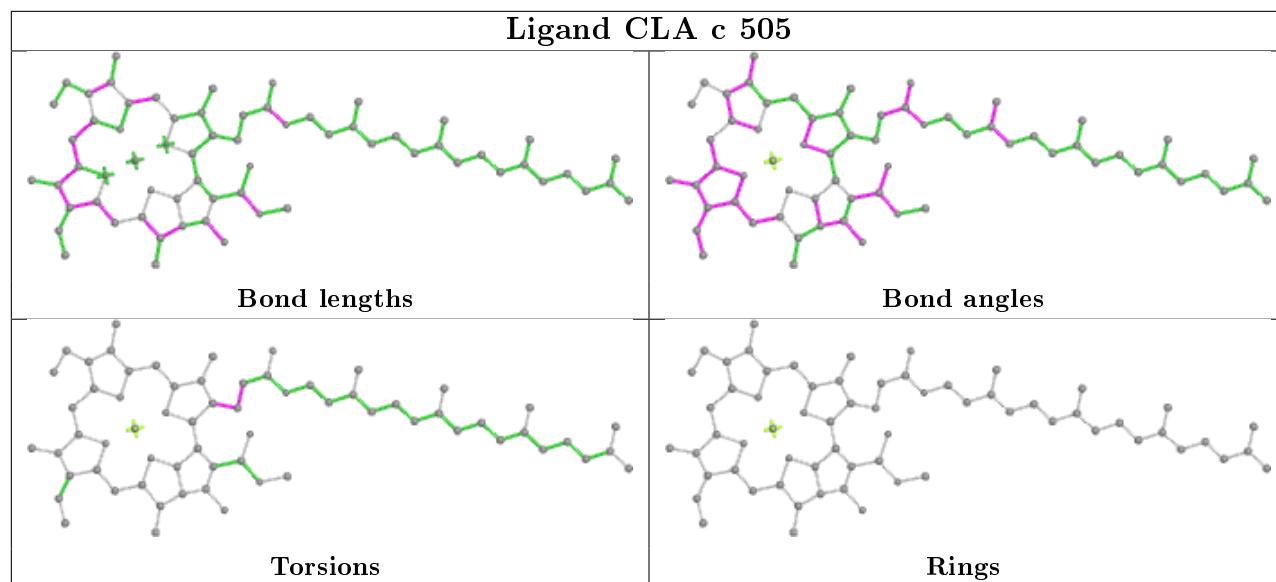




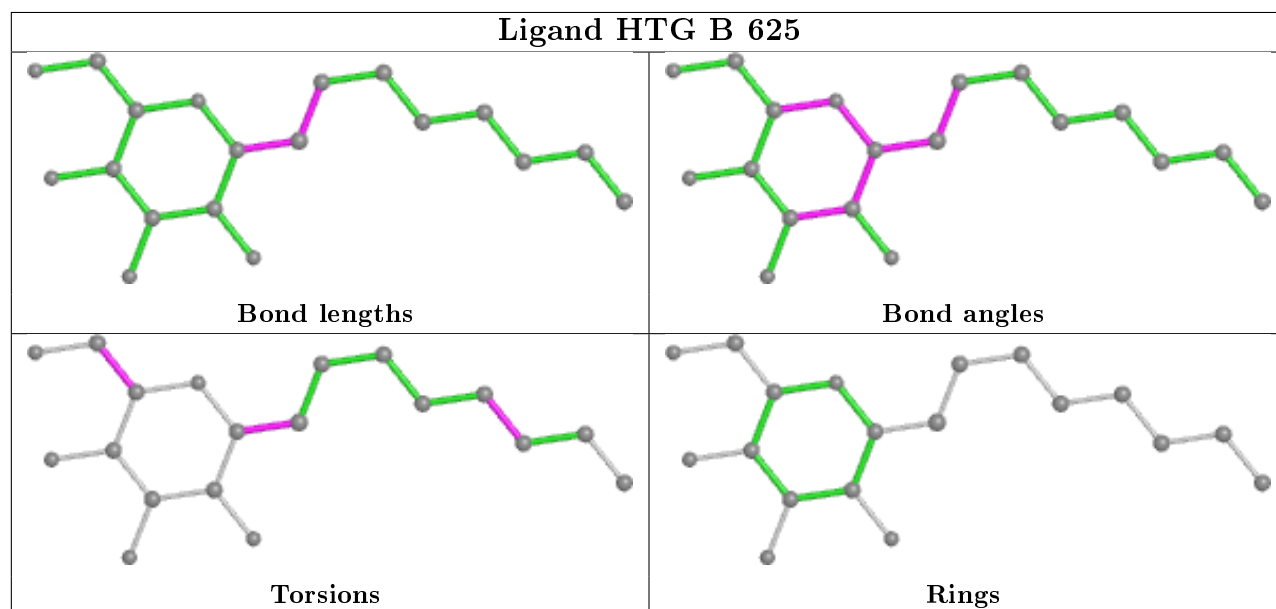




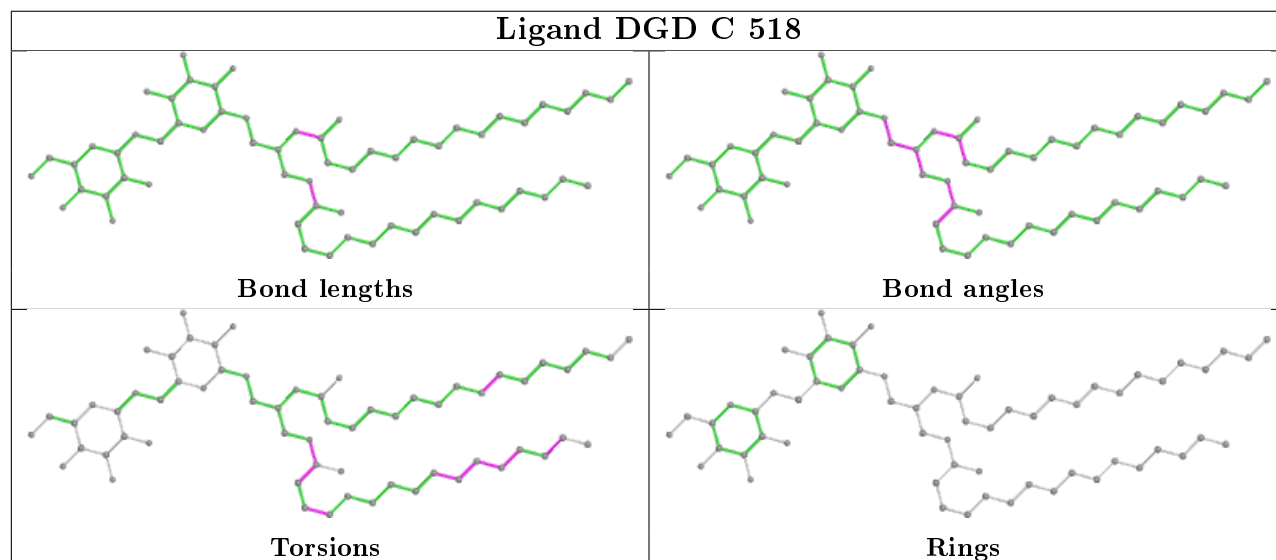
Ligand CLA c 505

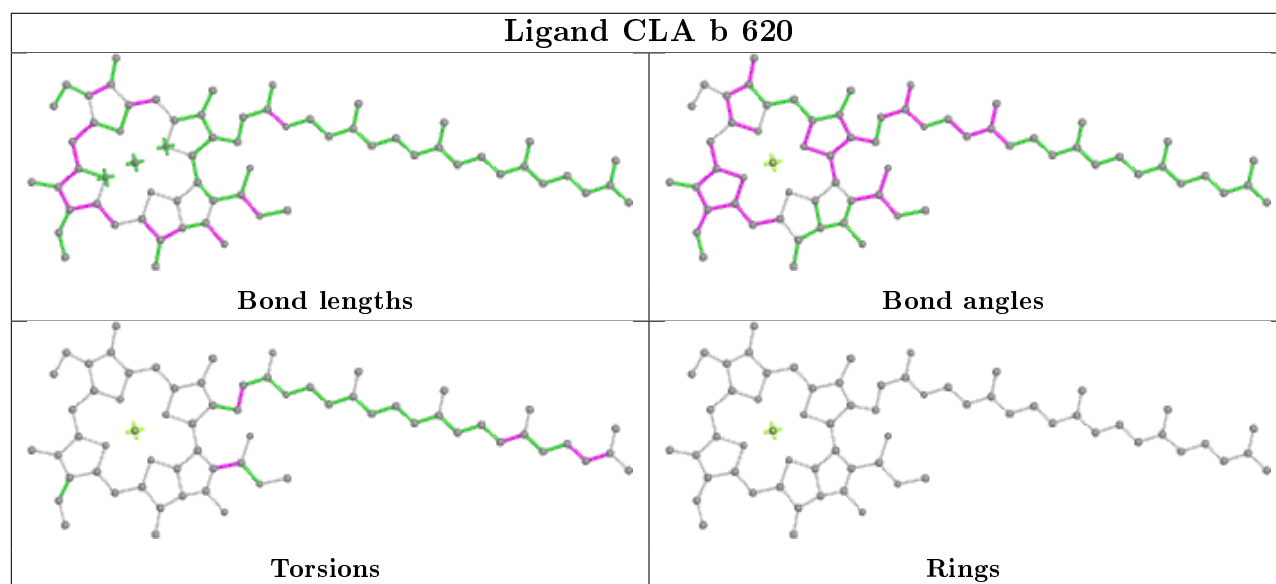
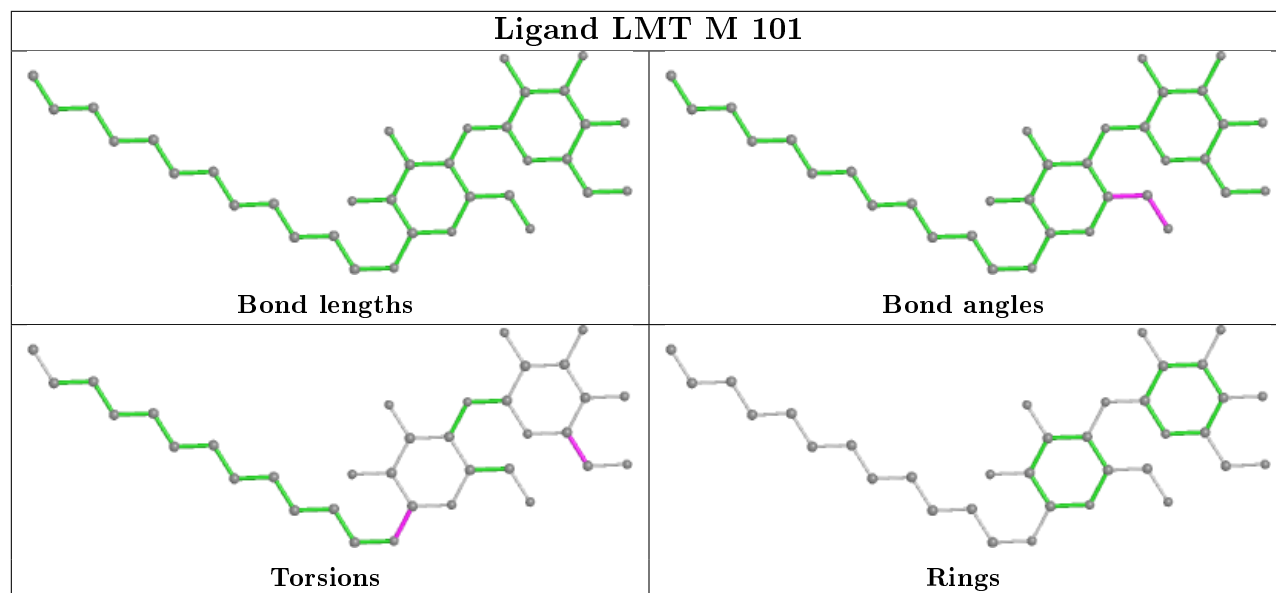


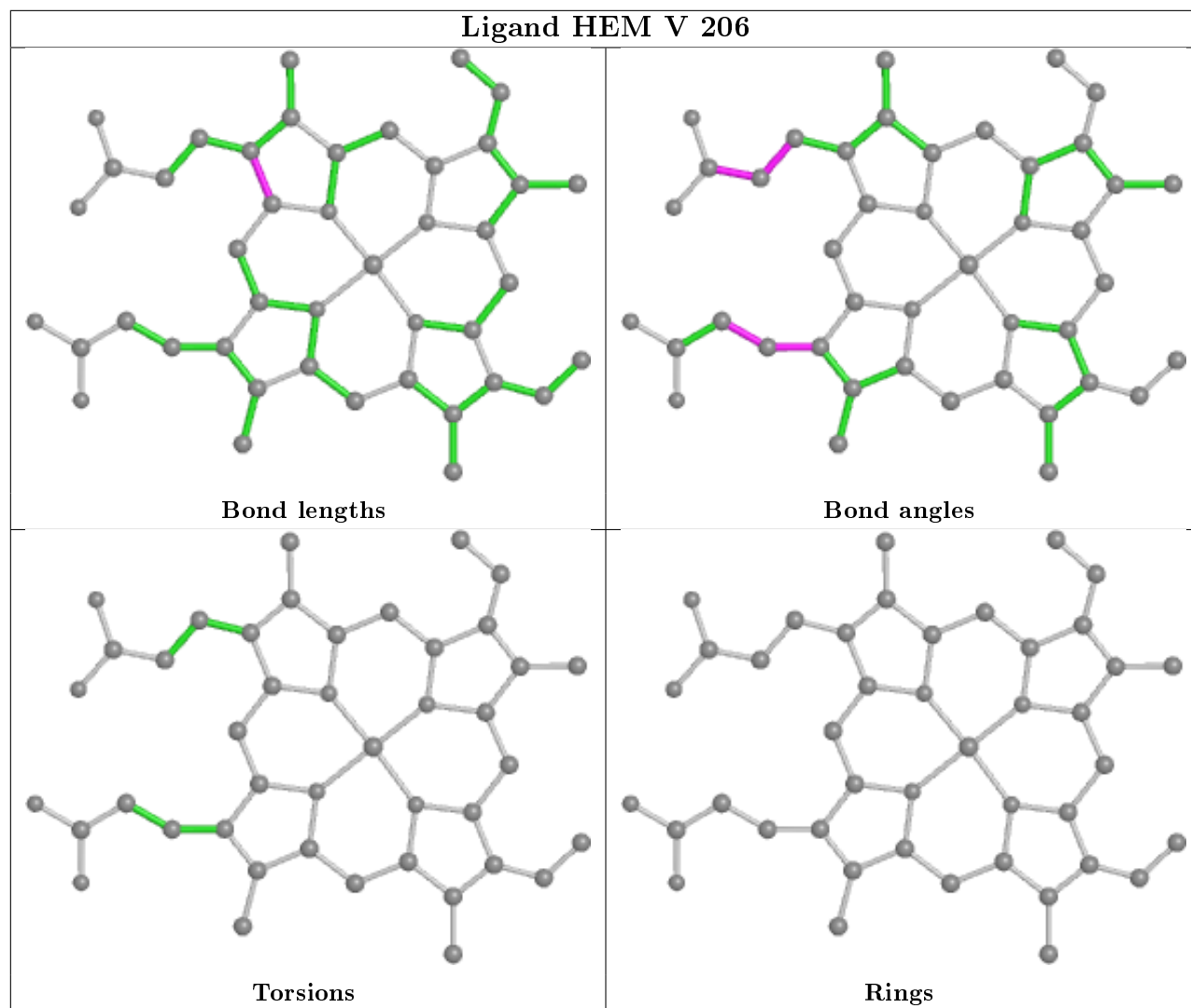
Ligand HTG B 625

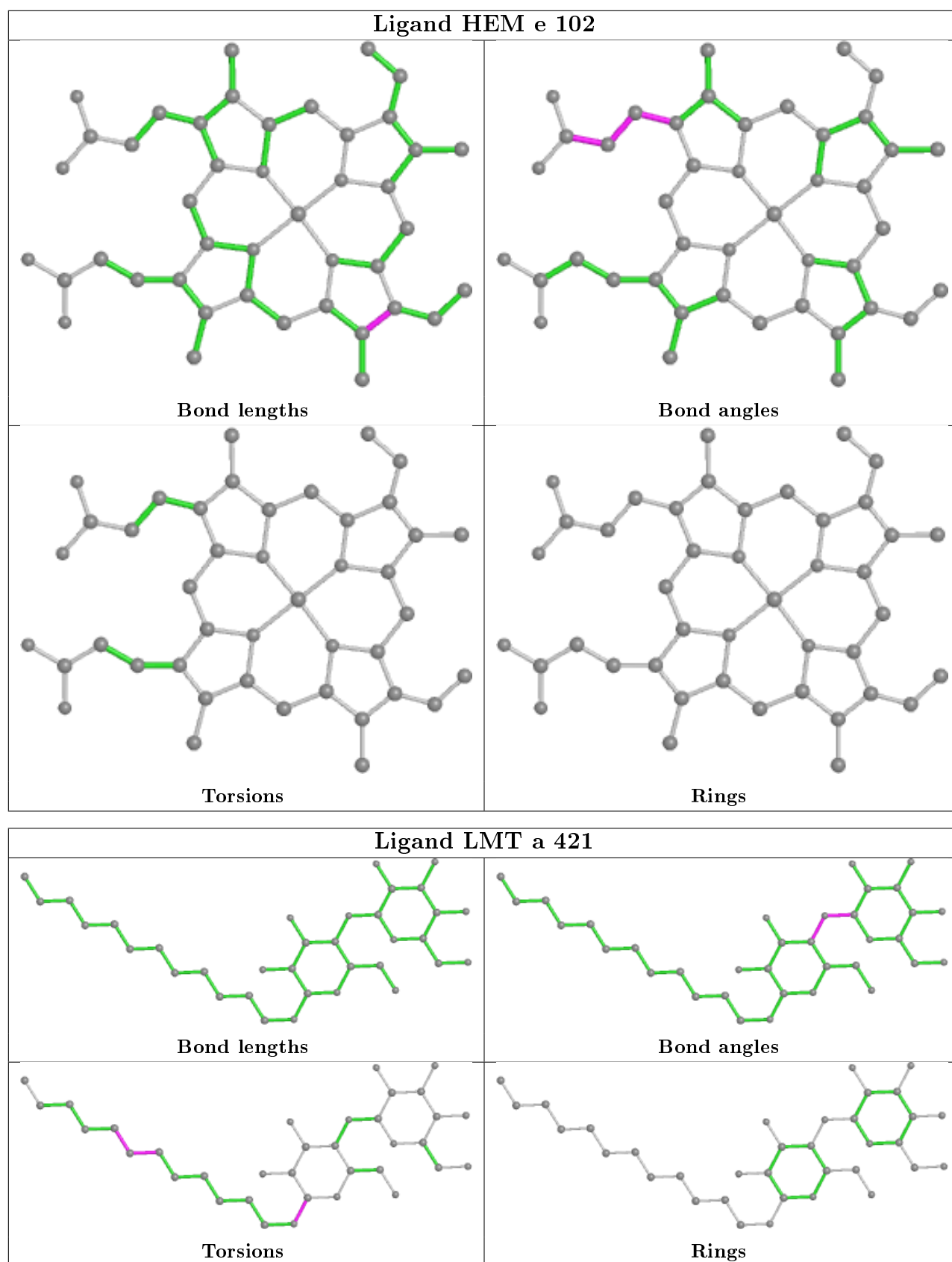


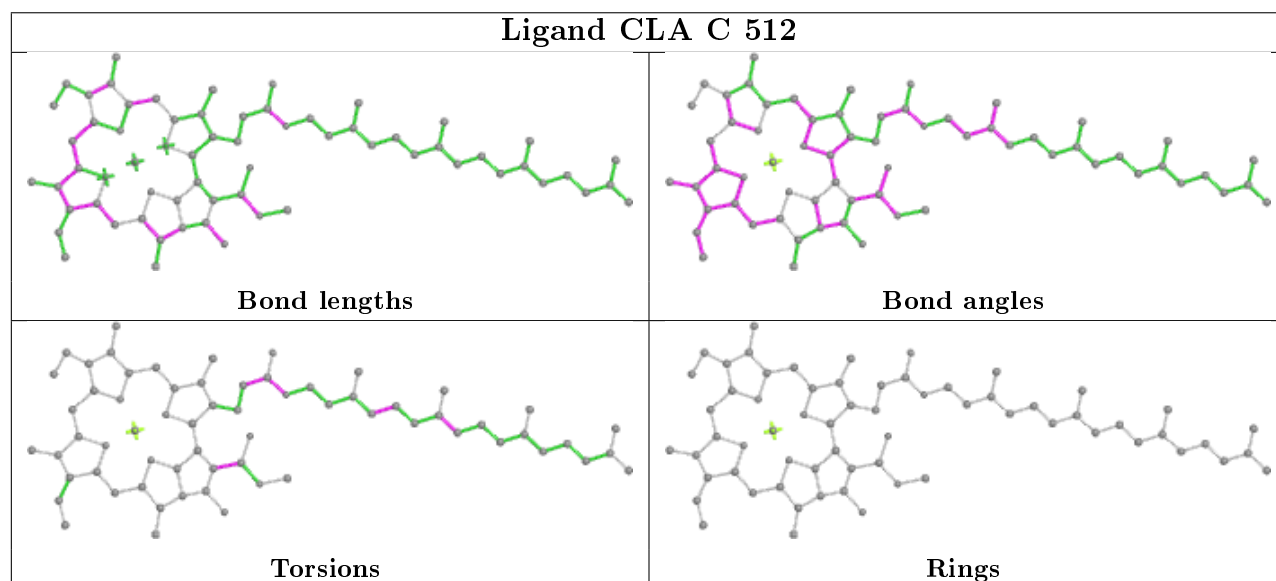
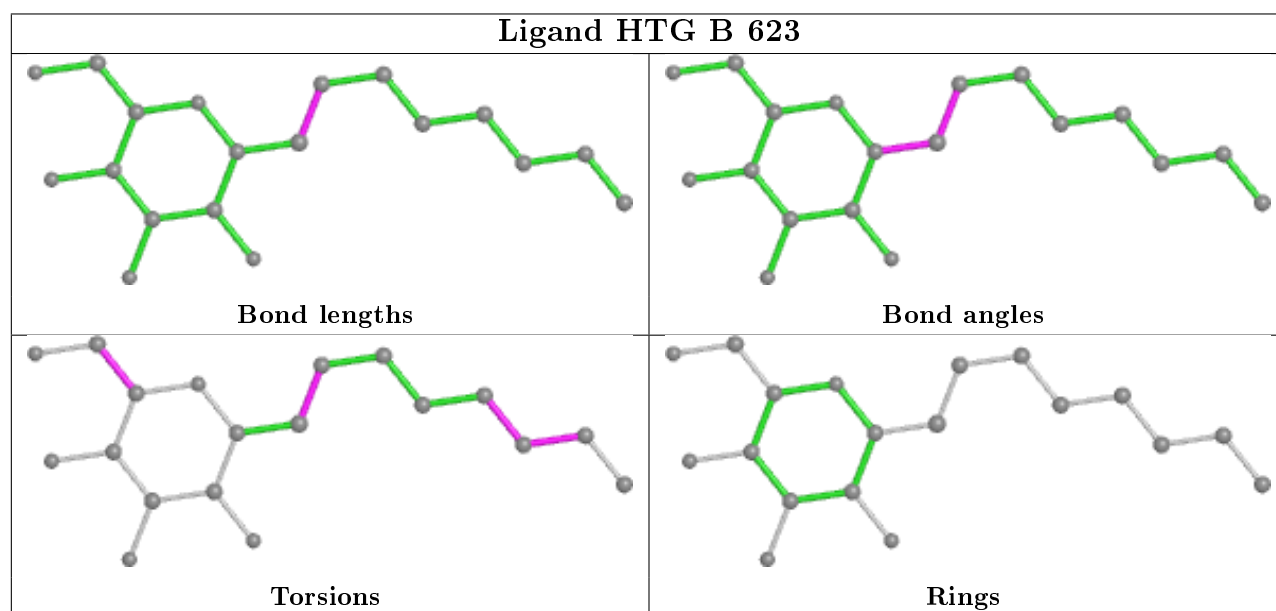
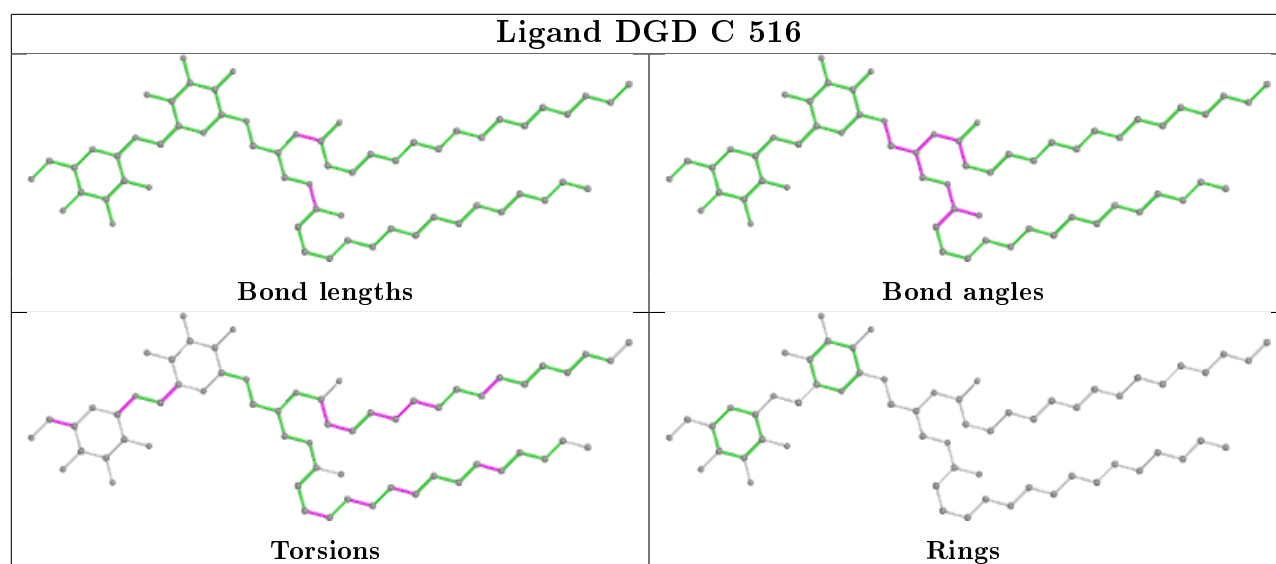
Ligand DGD C 518

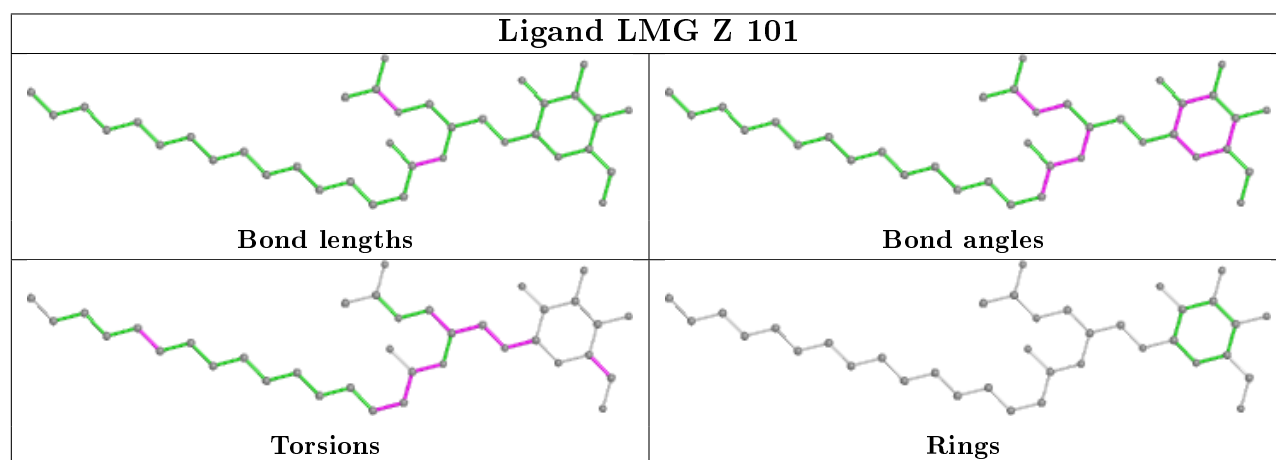
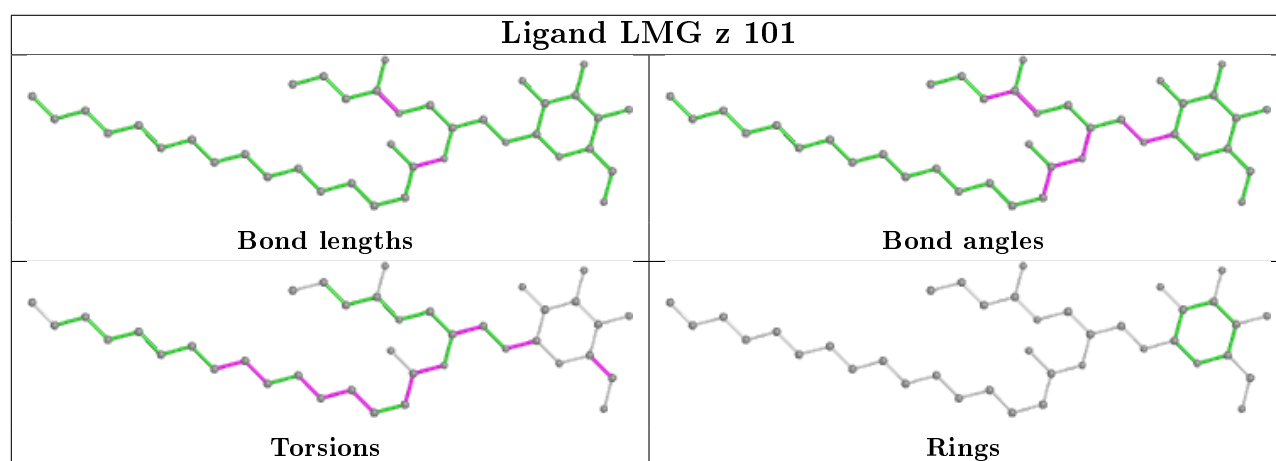
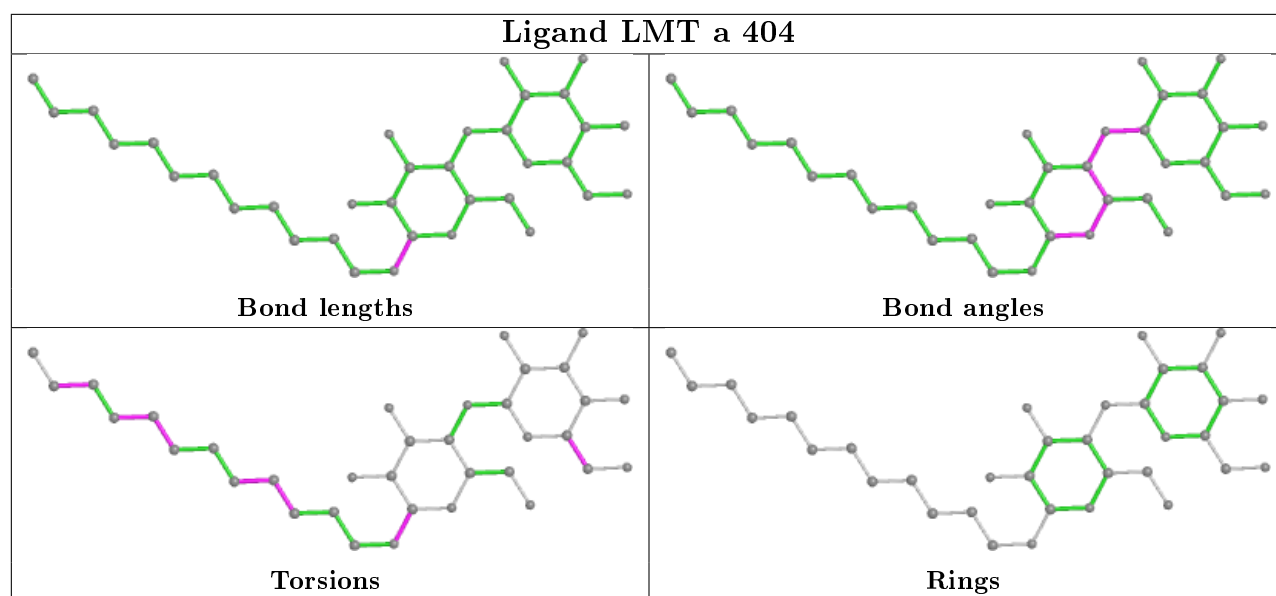


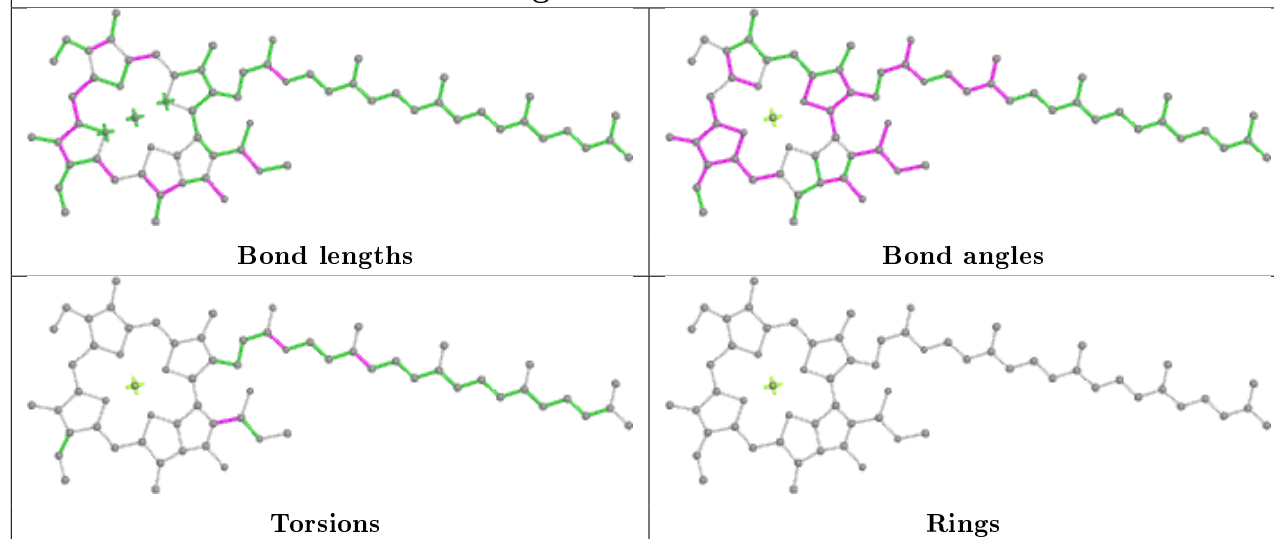
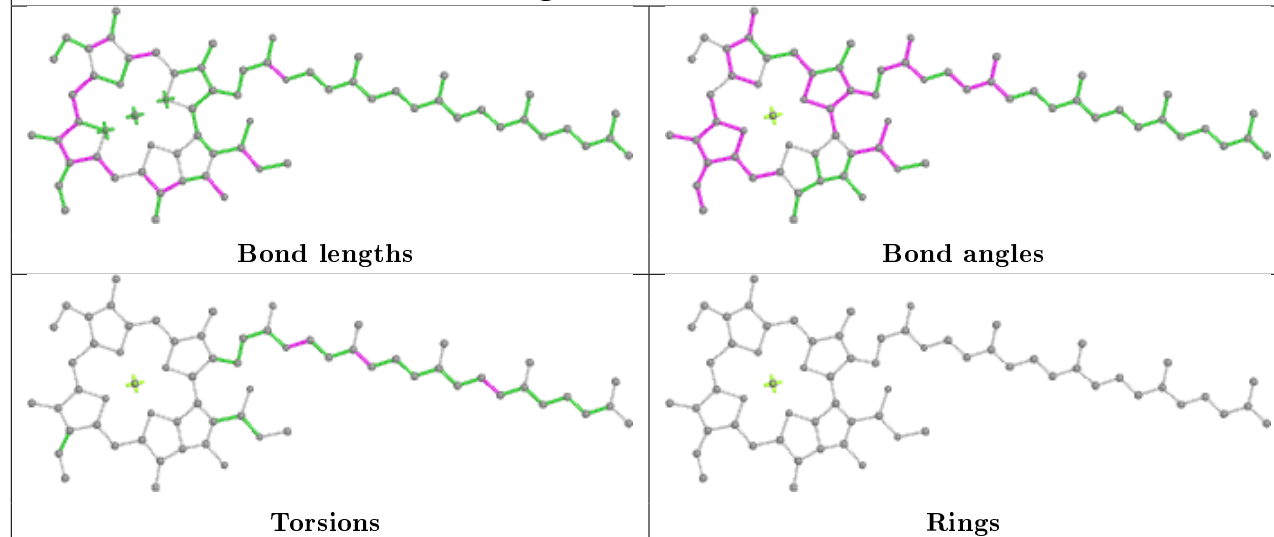


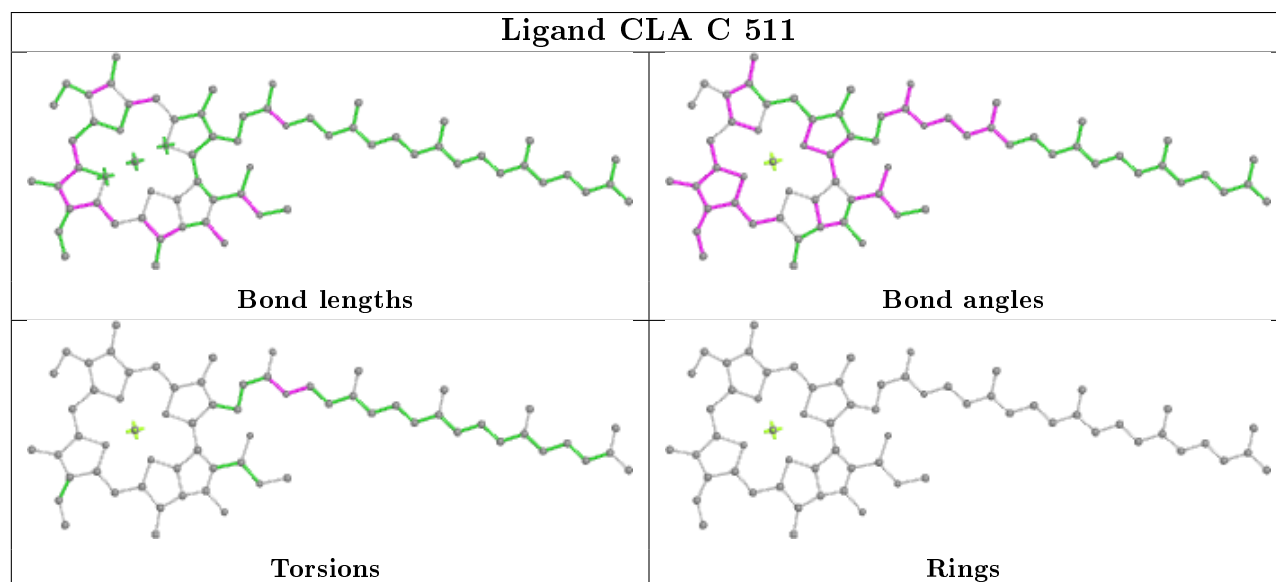
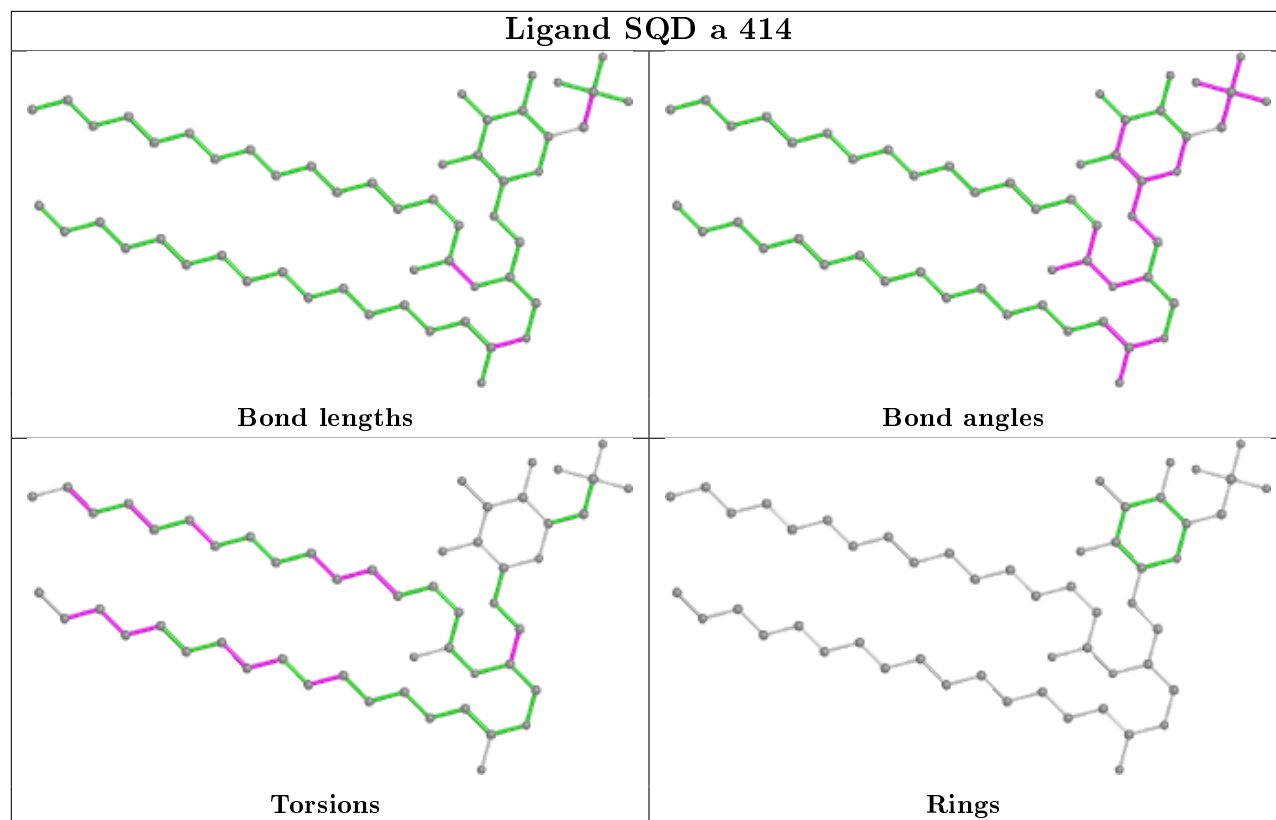


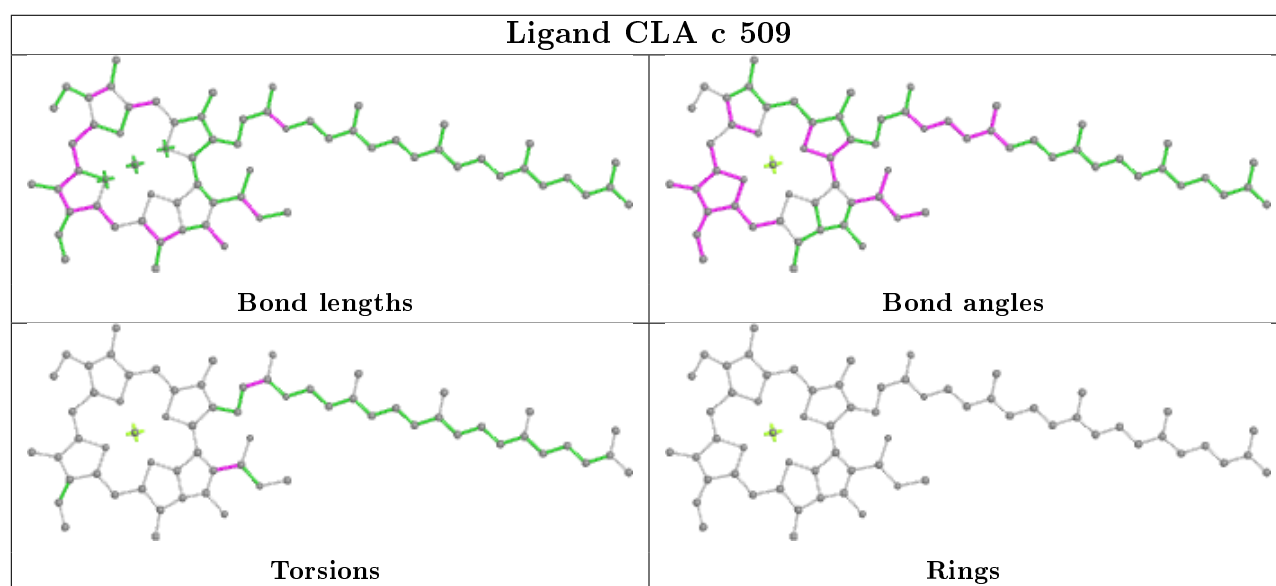
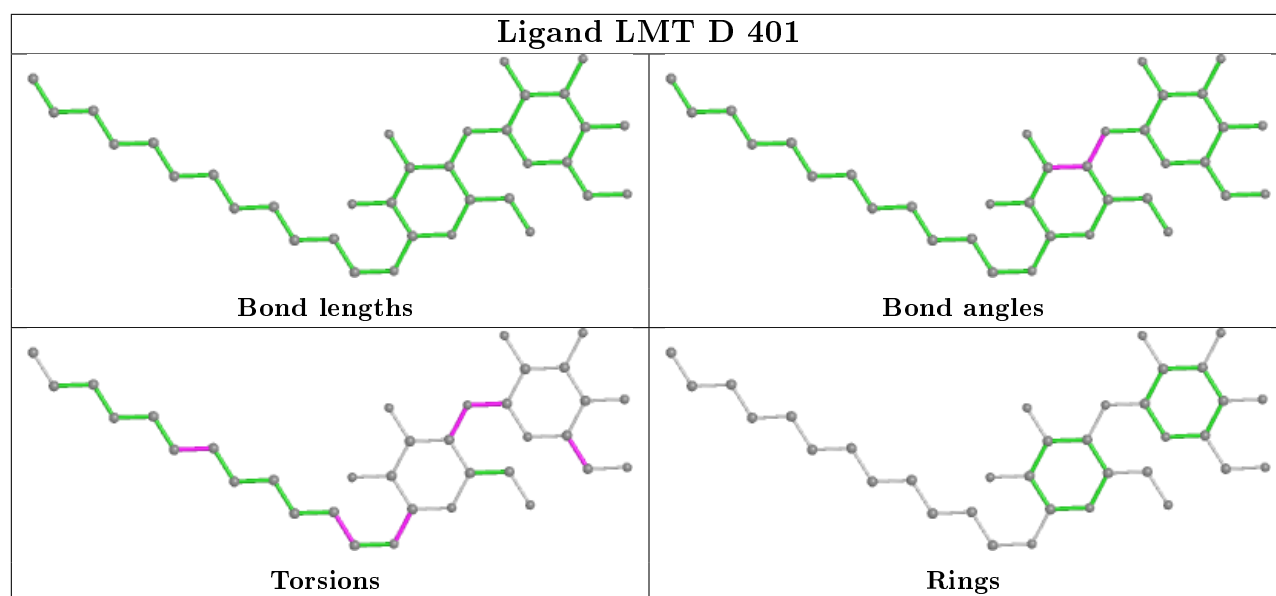


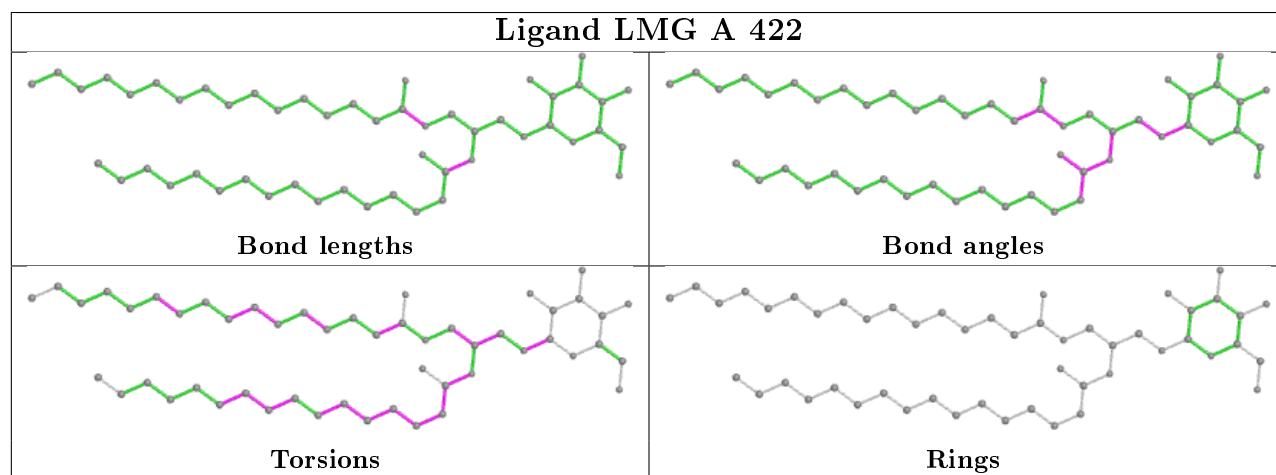
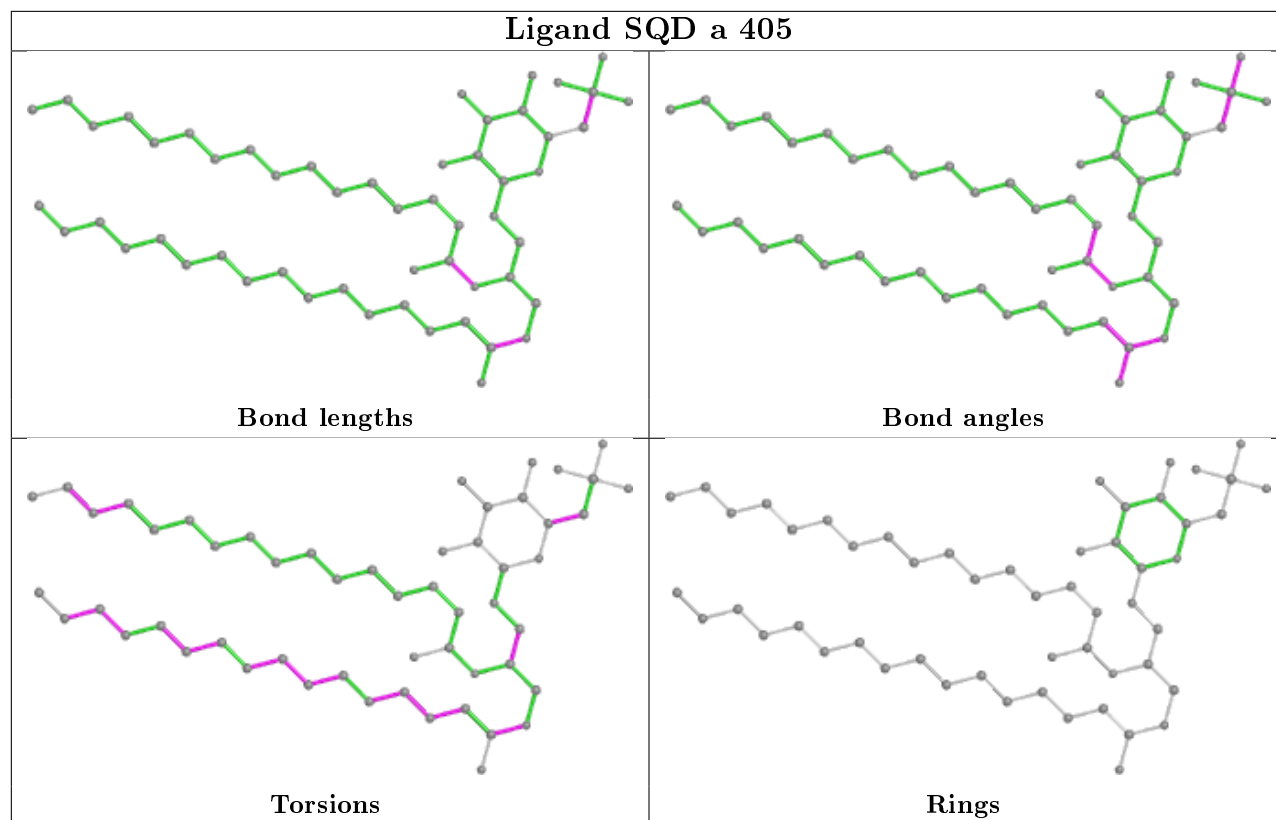


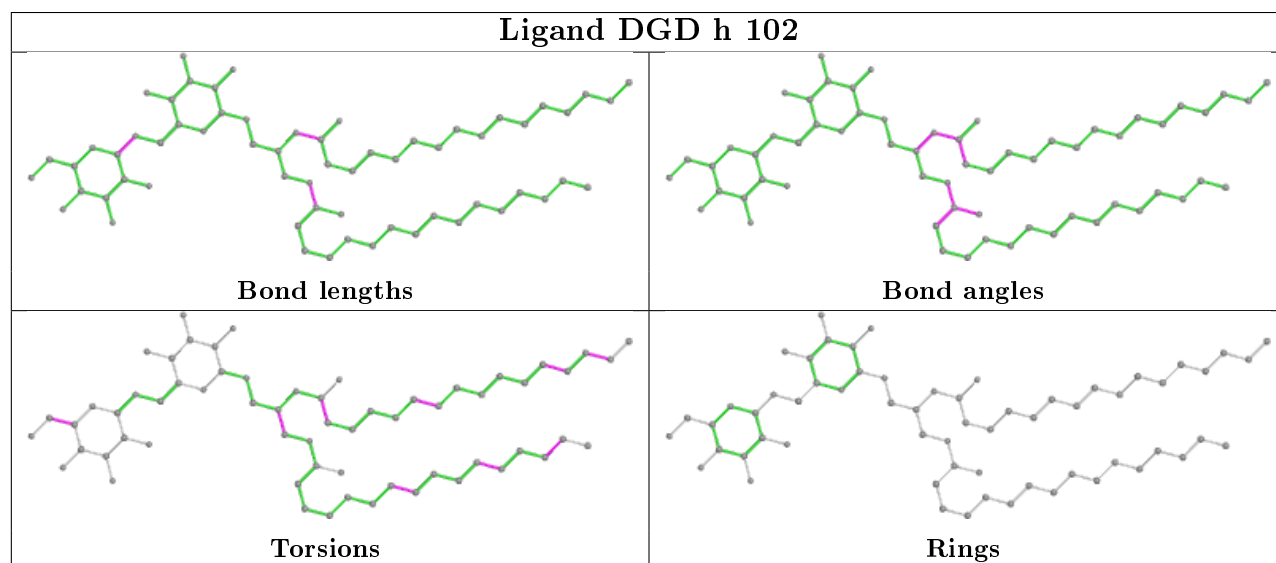
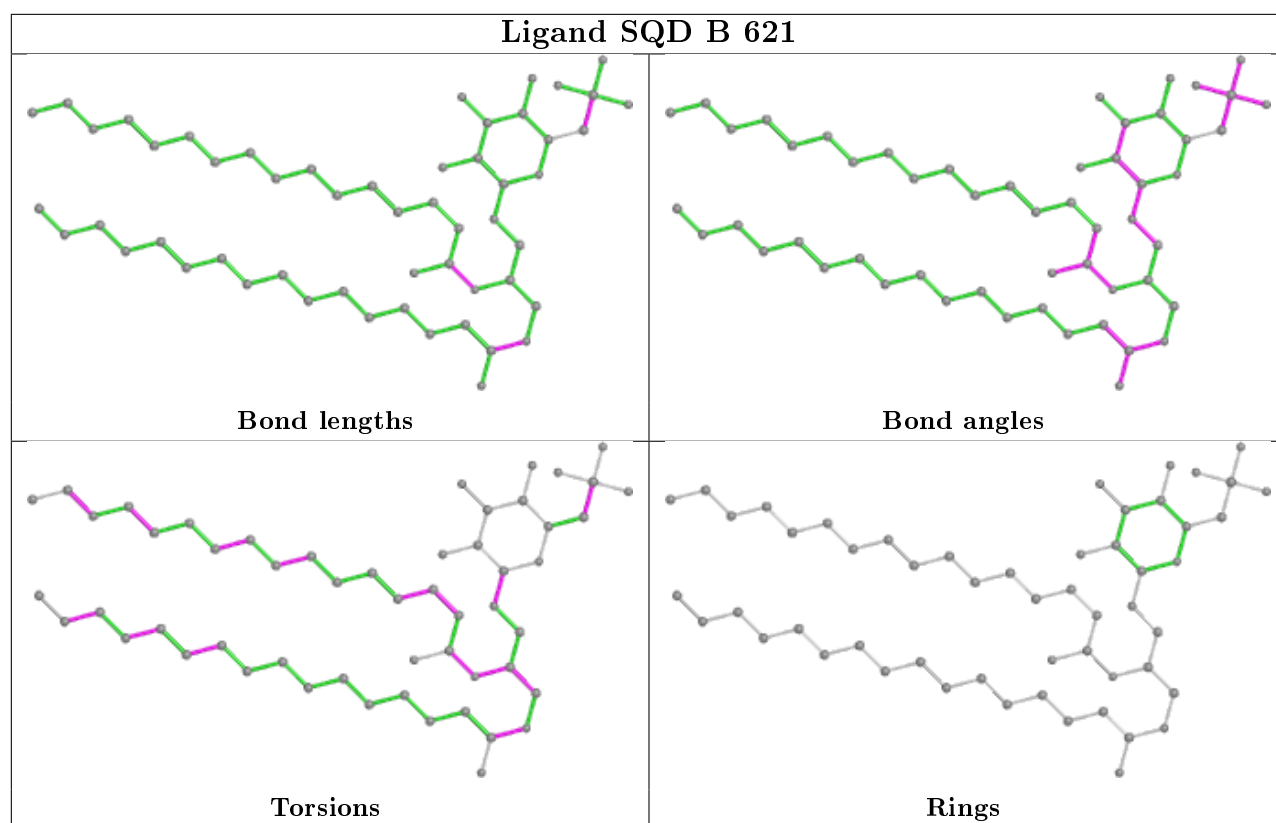


Ligand CLA B 606**Ligand CLA c 517**

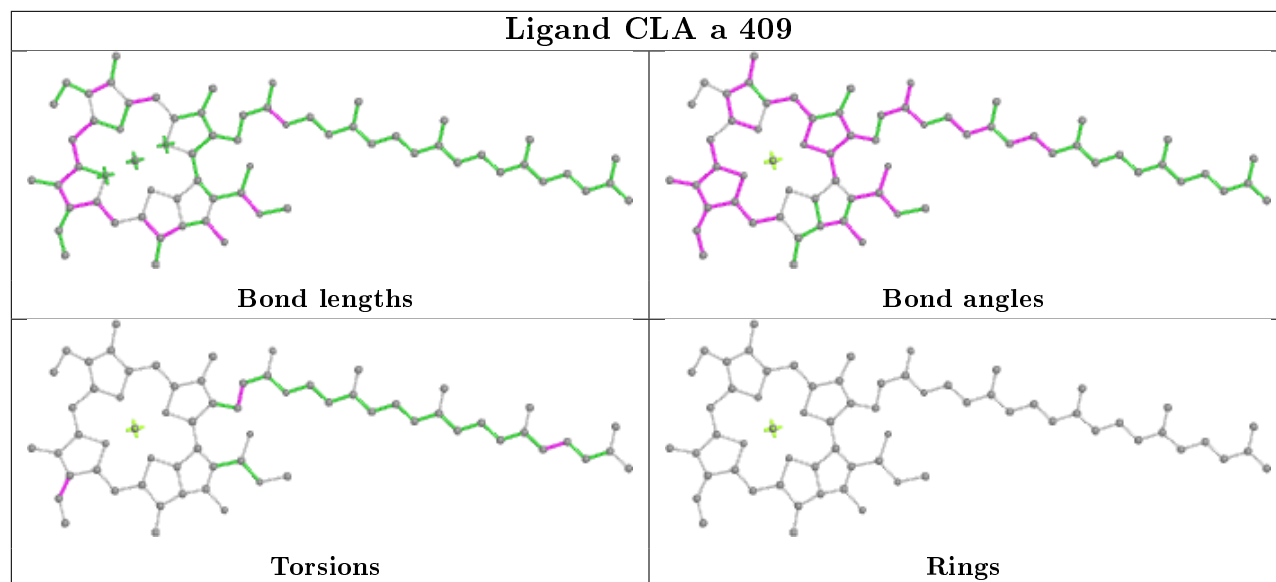




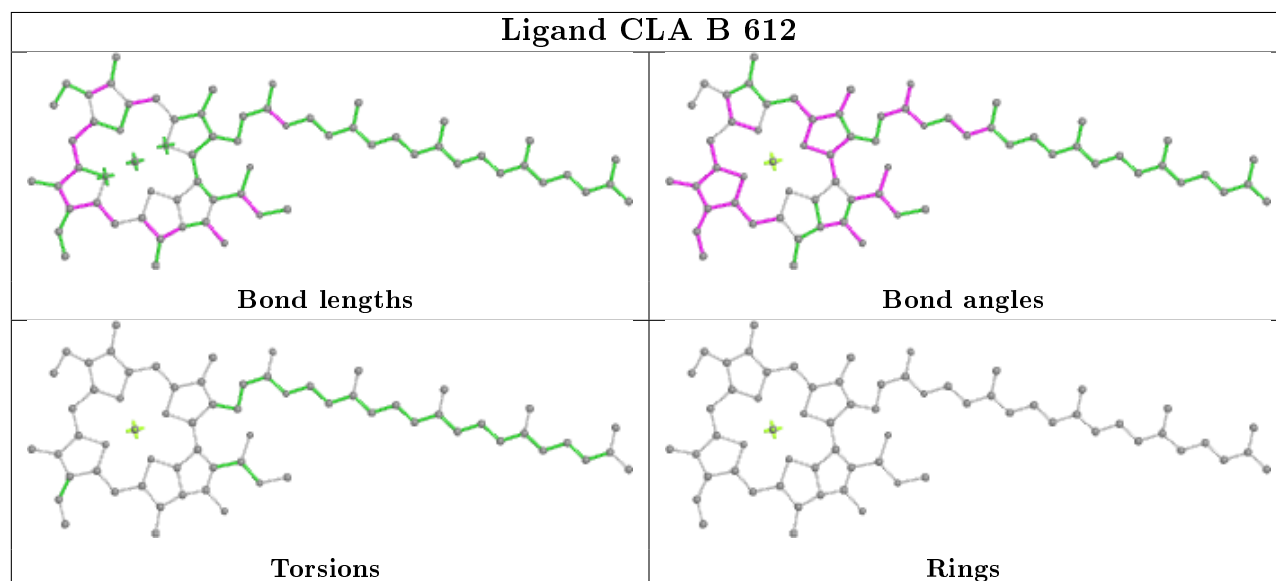




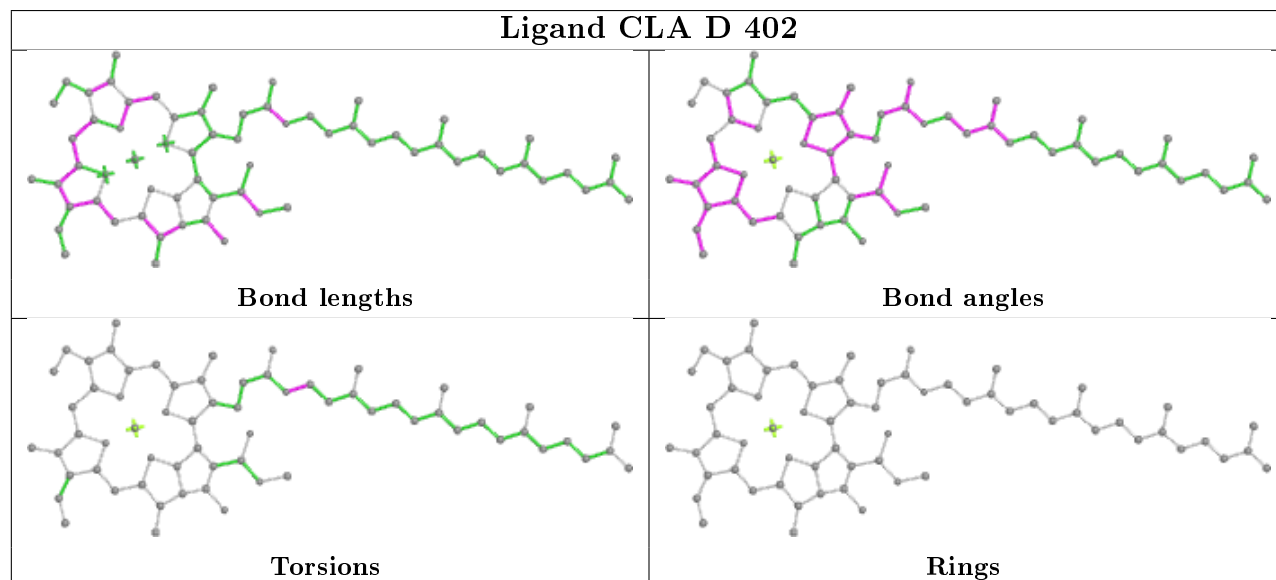
Ligand CLA a 409

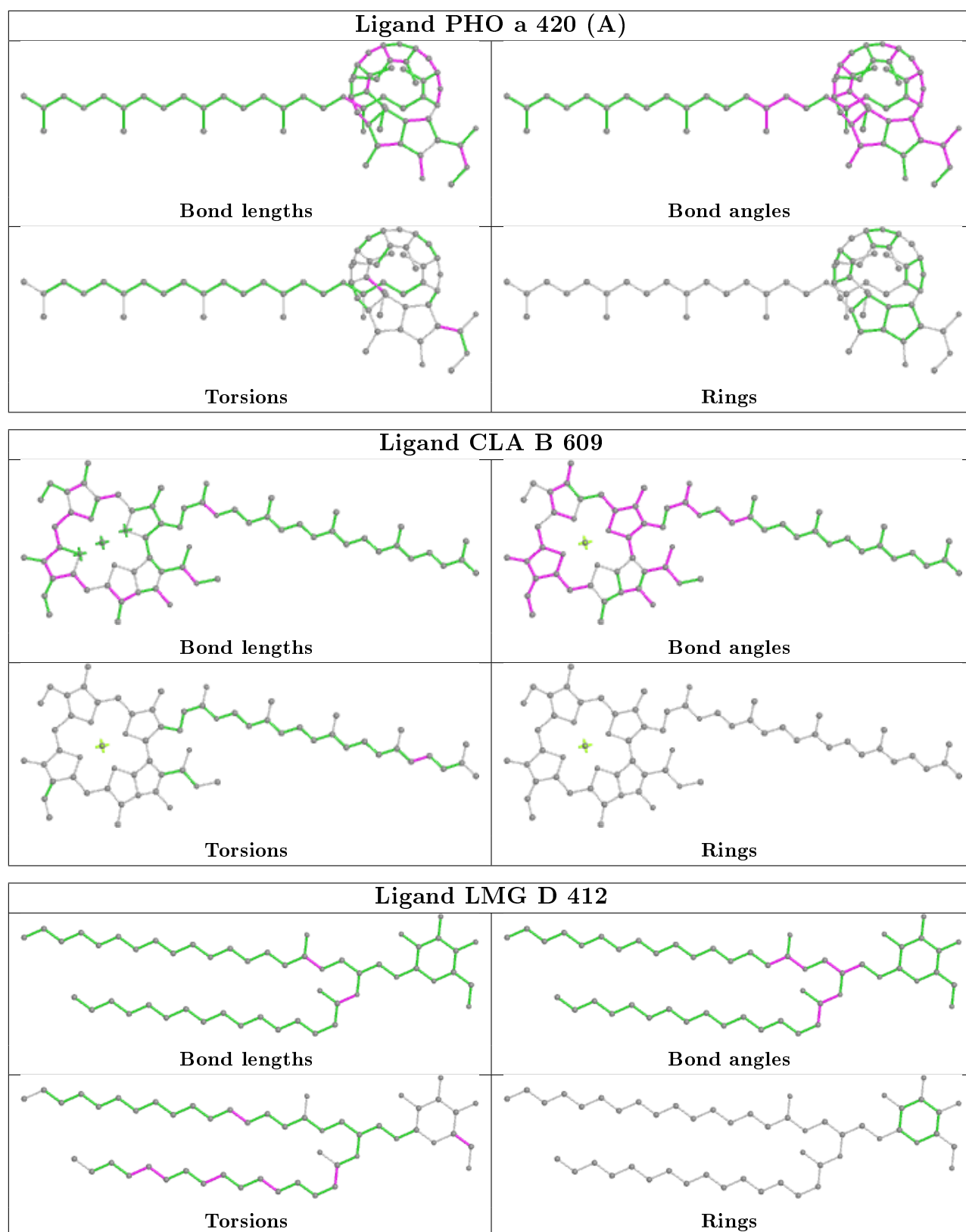


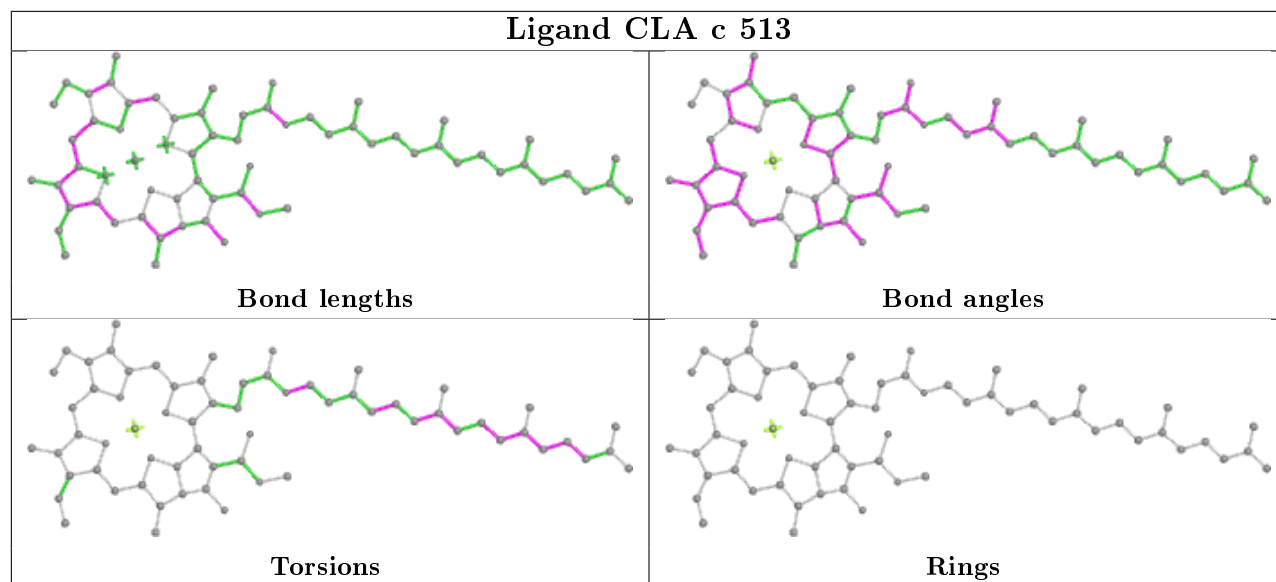
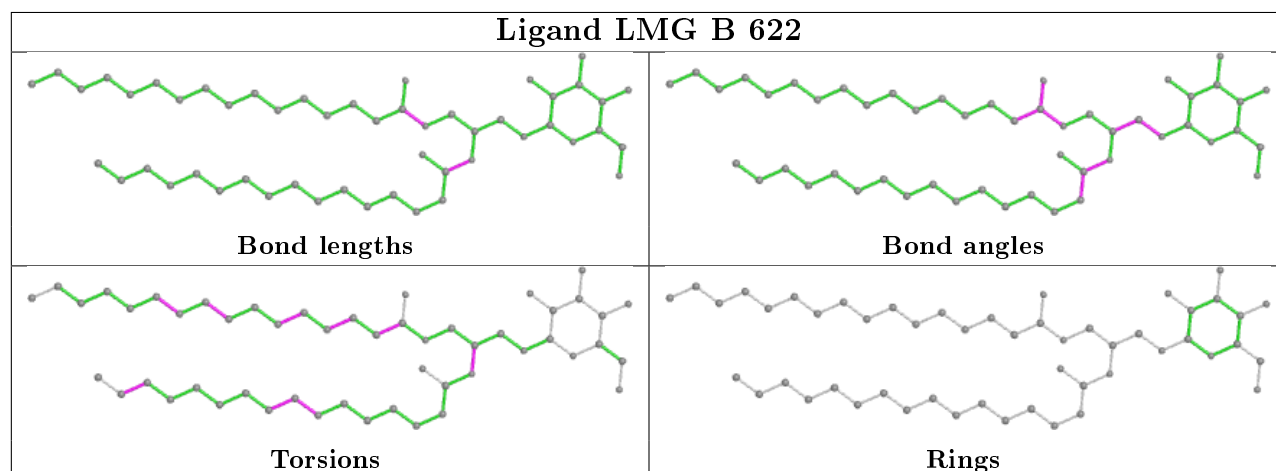
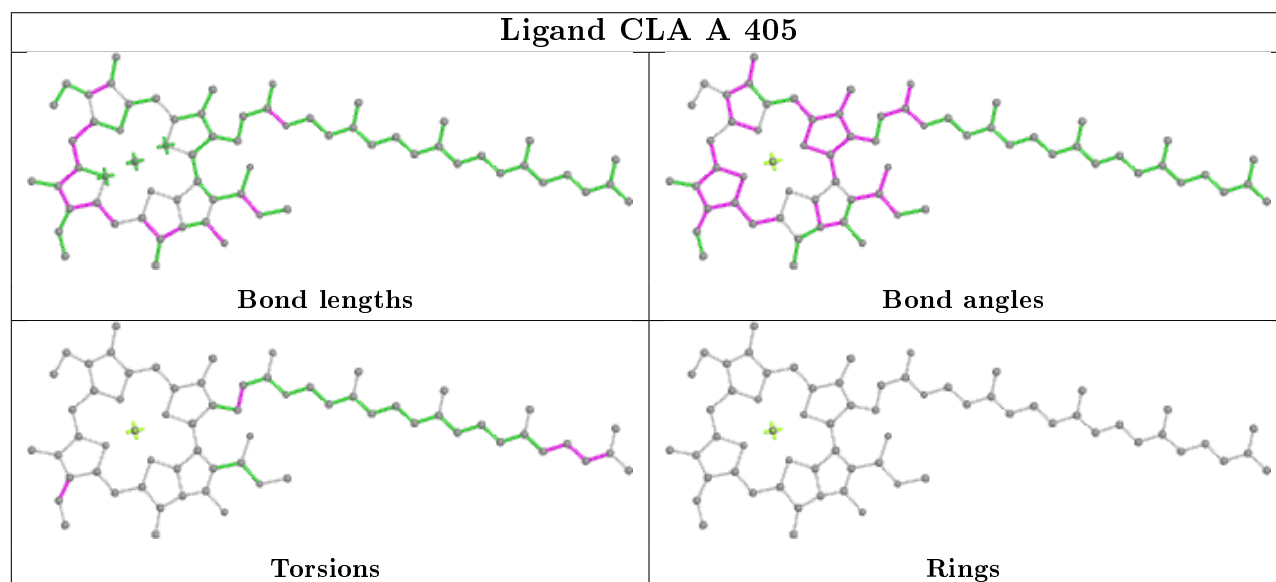
Ligand CLA B 612



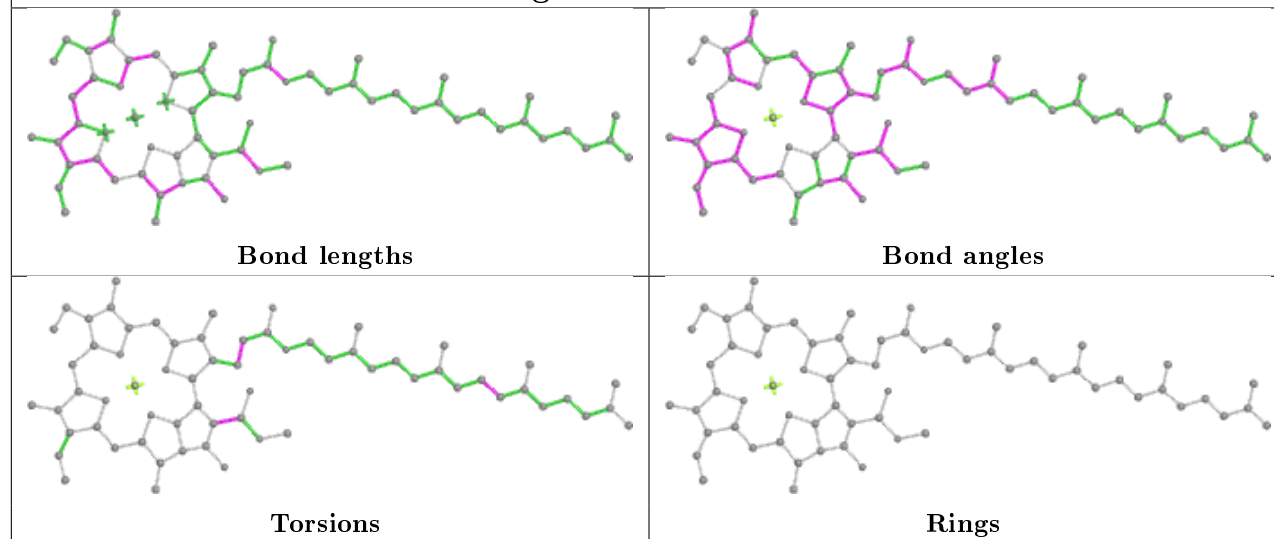
Ligand CLA D 402



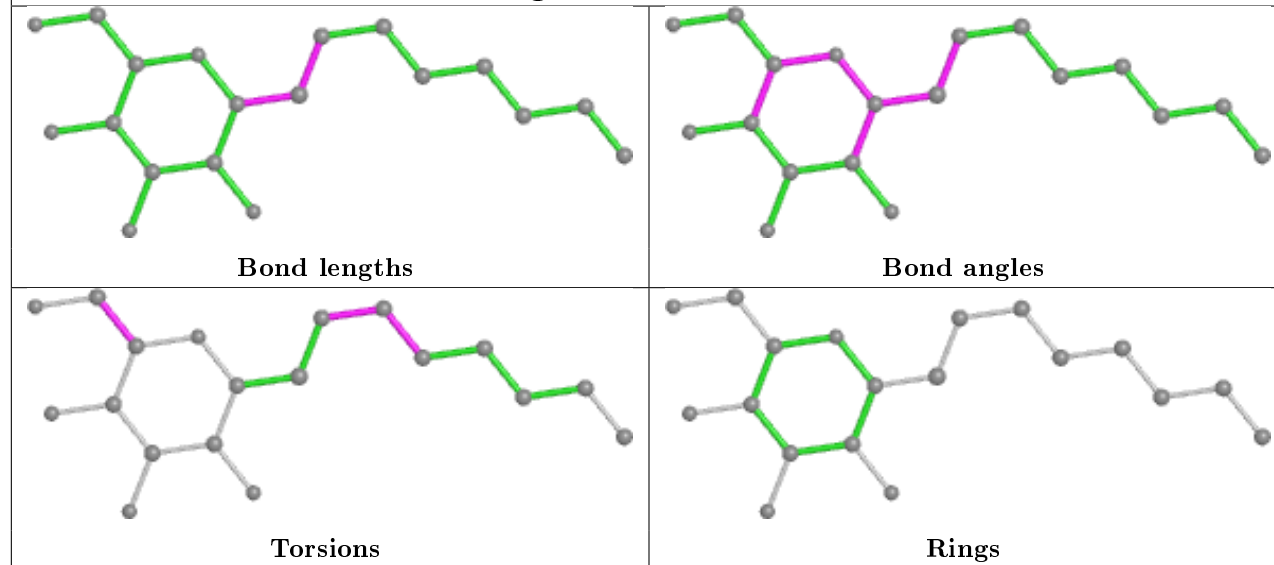


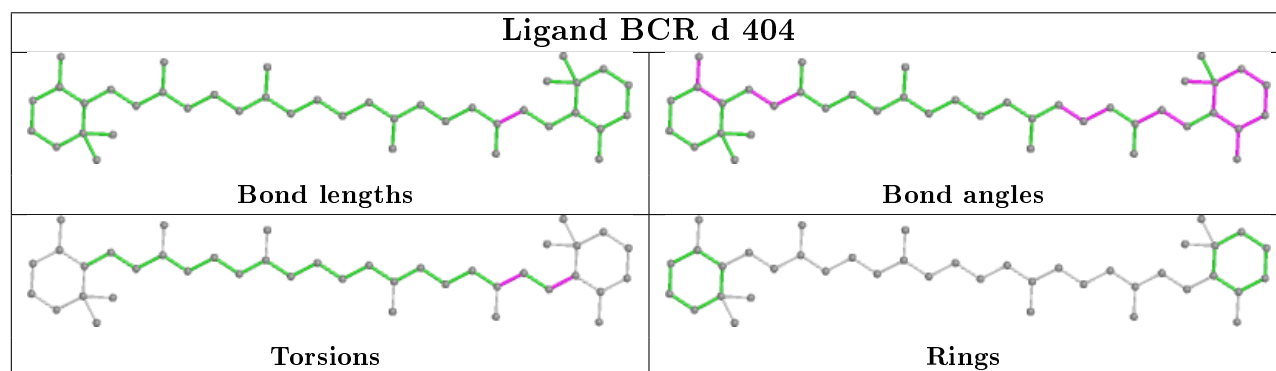
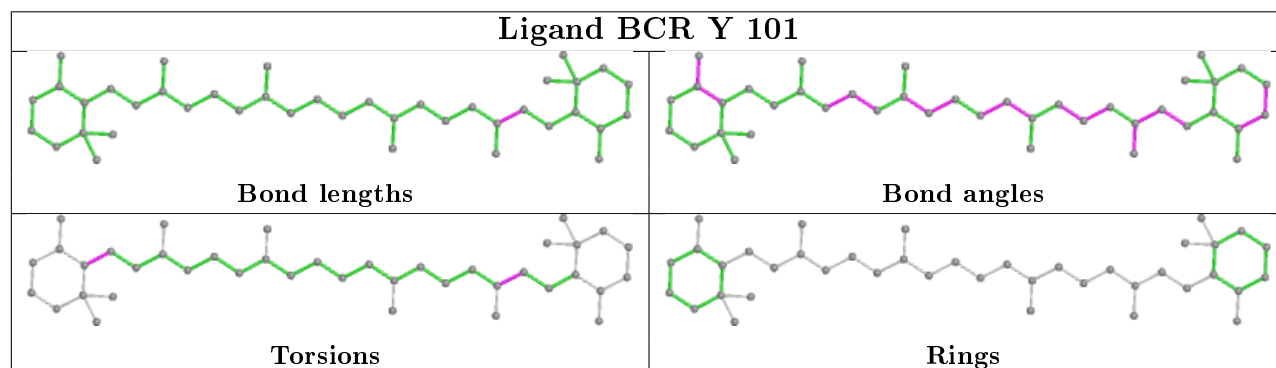
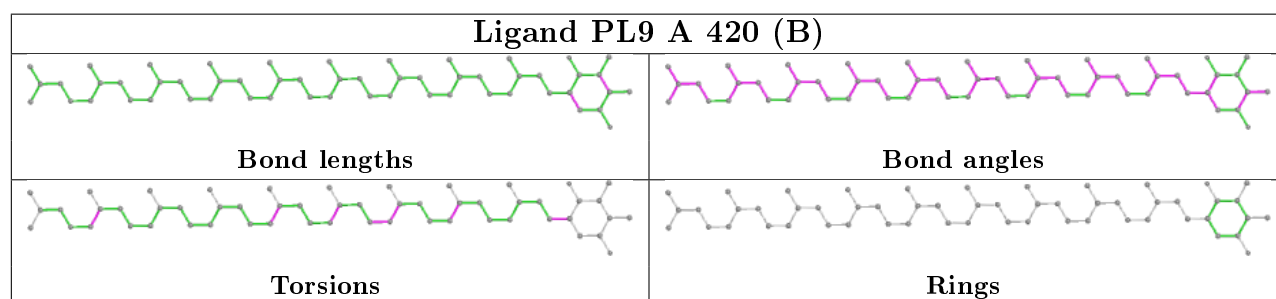
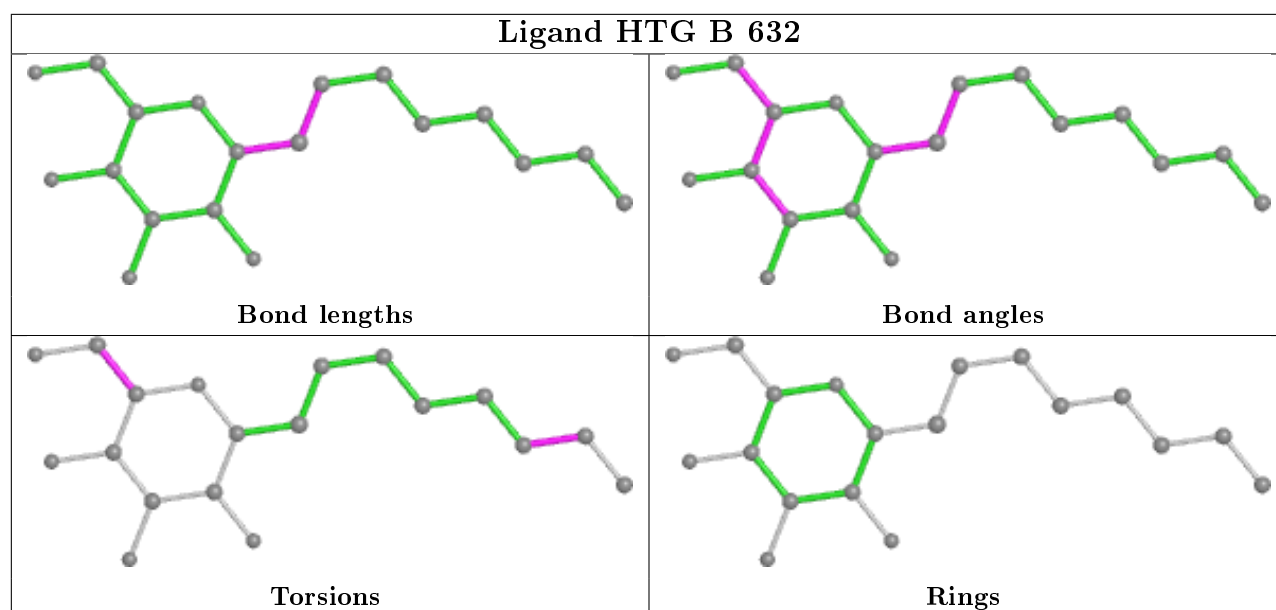
Ligand CLA c 513**Ligand LMG B 622****Ligand CLA A 405**

Ligand CLA B 607

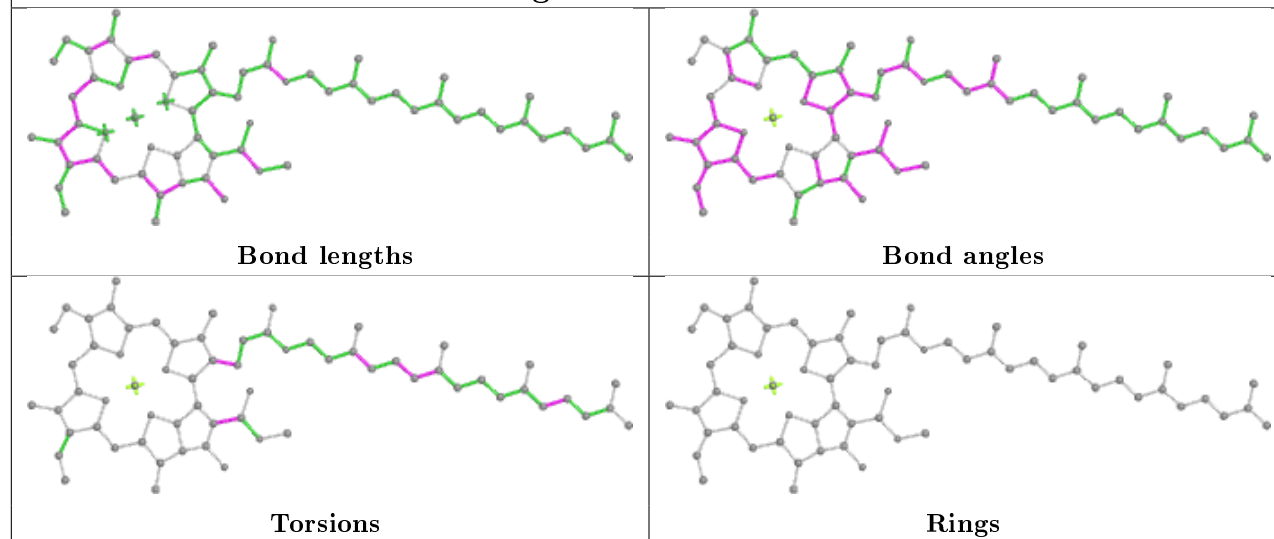


Ligand HTG C 523

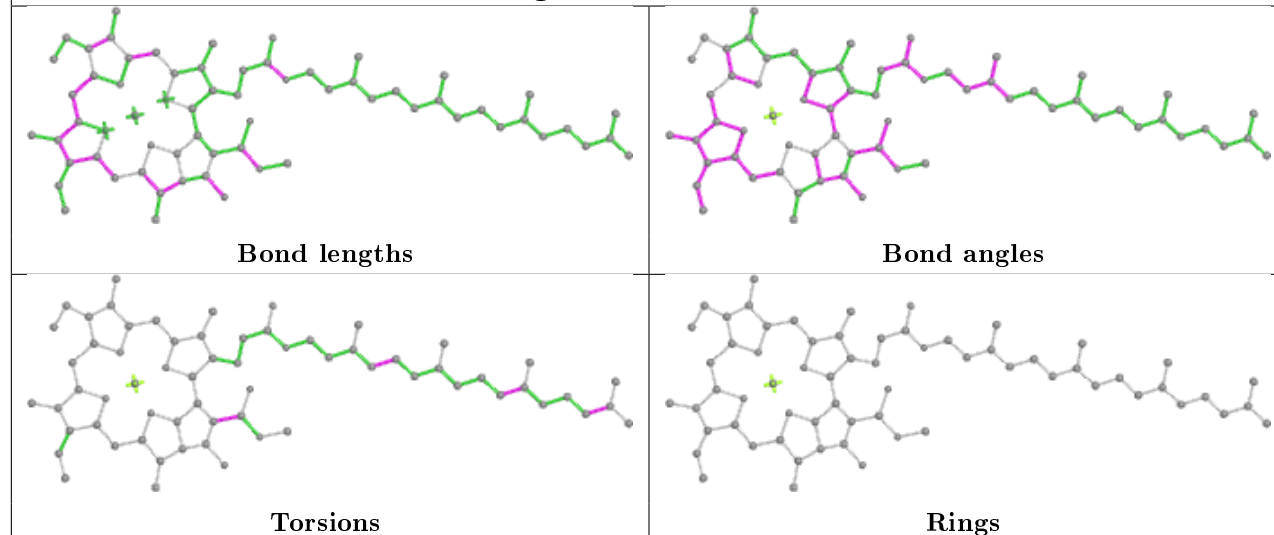




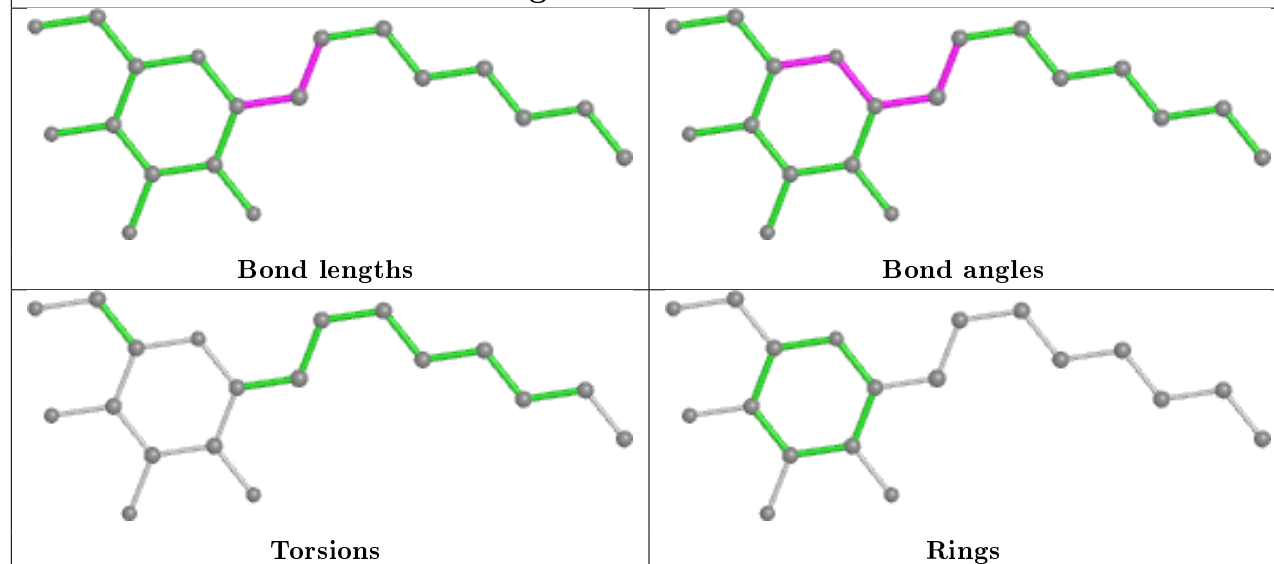
Ligand CLA C 506

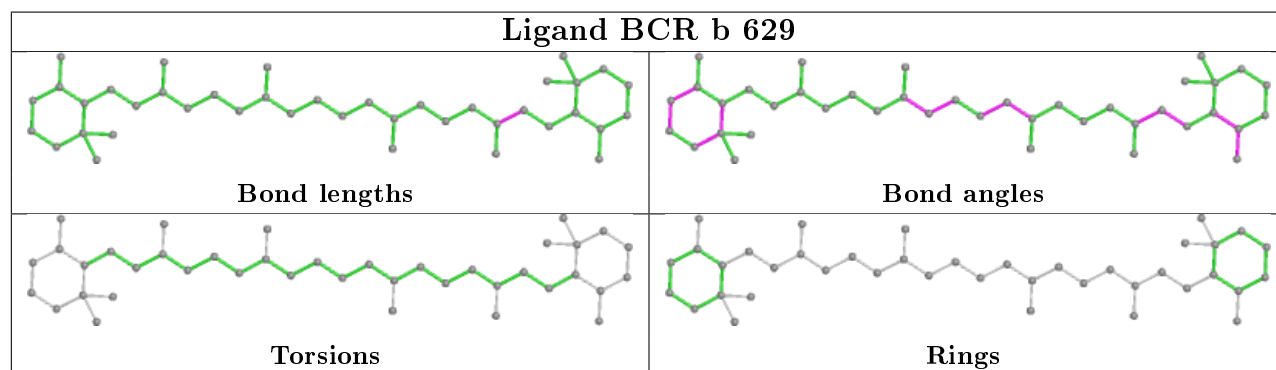
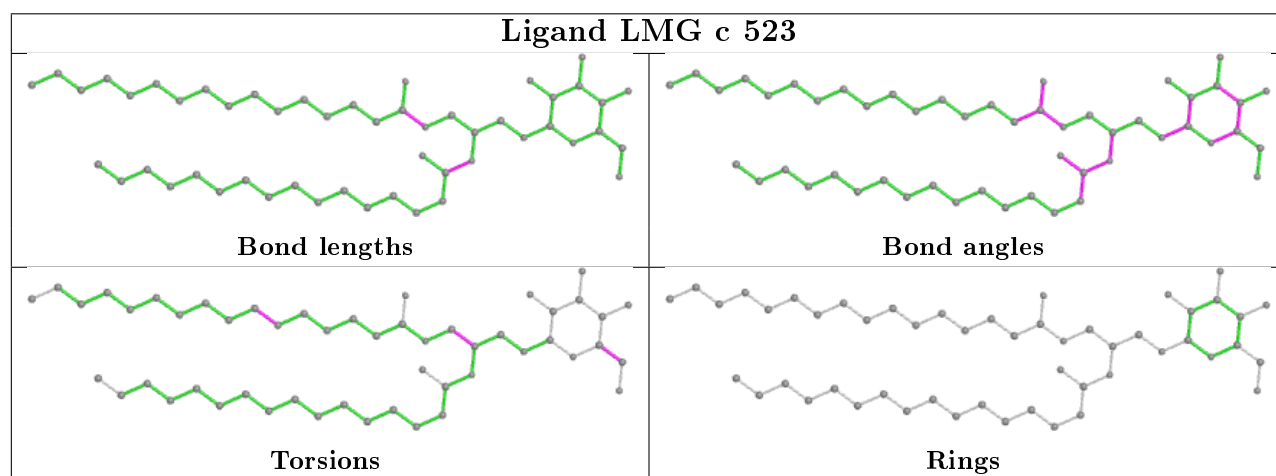
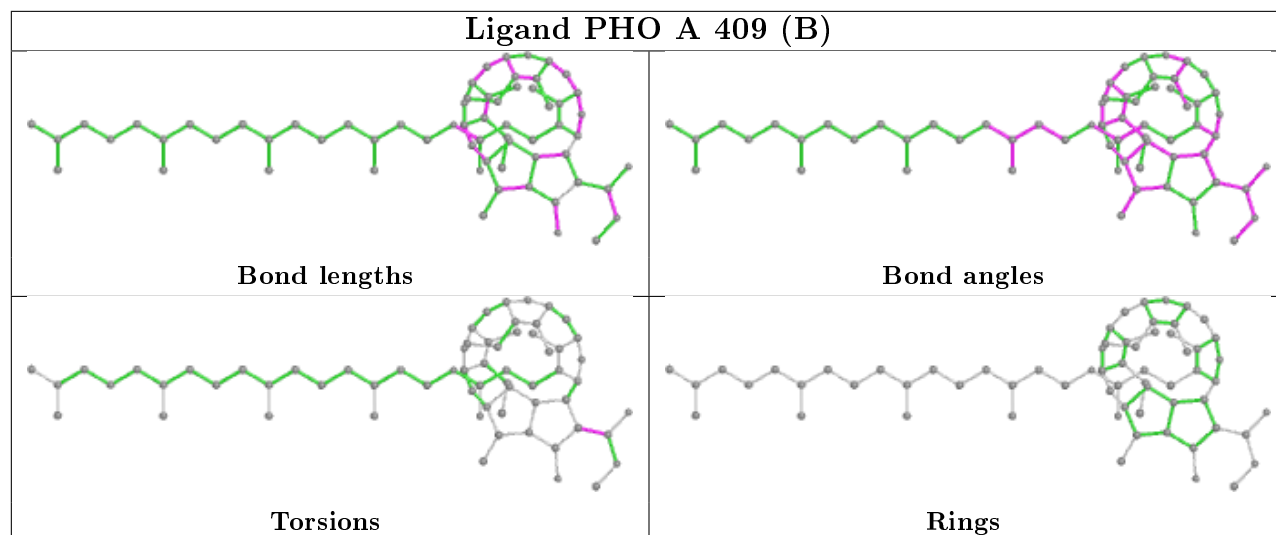


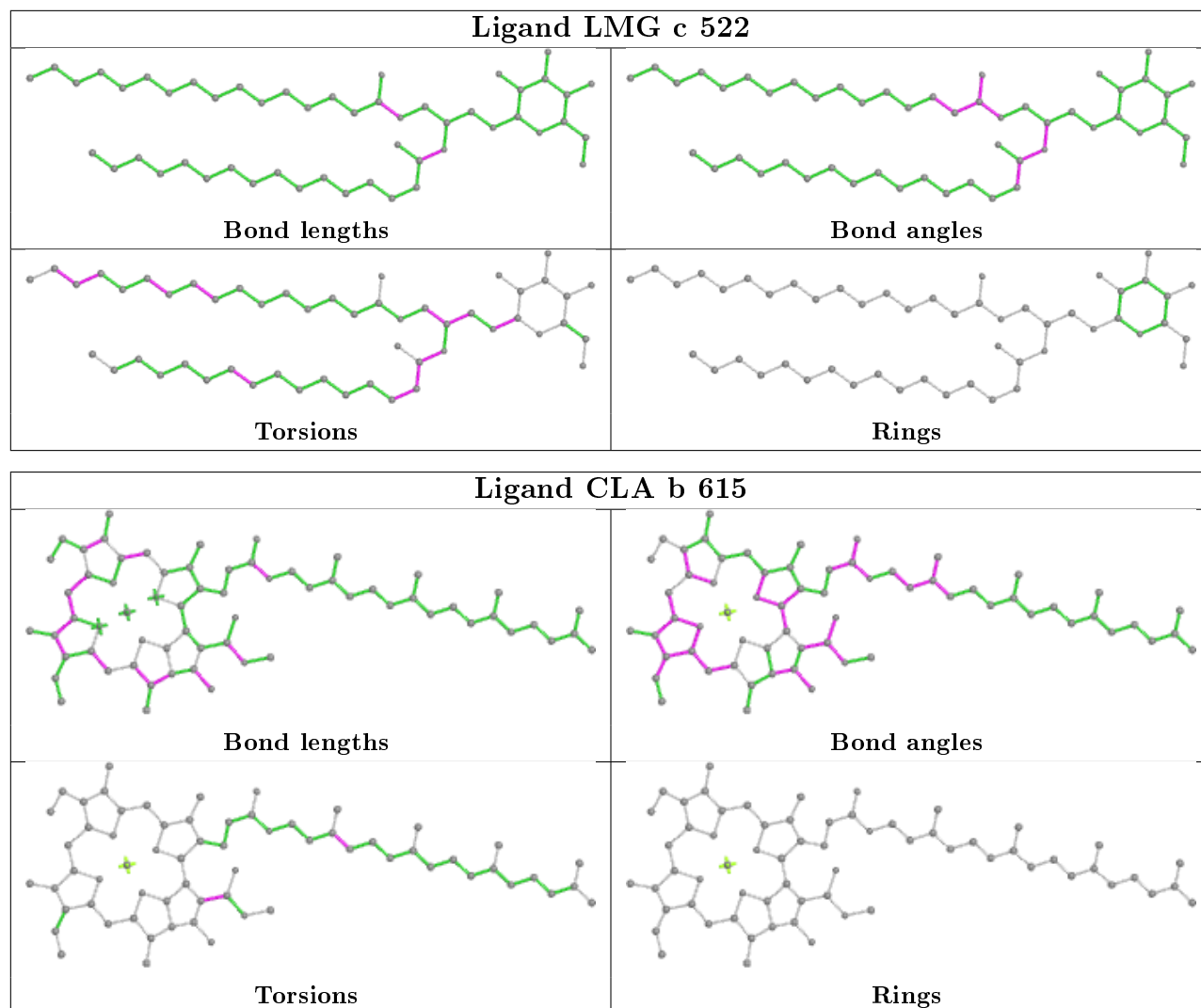
Ligand CLA C 502

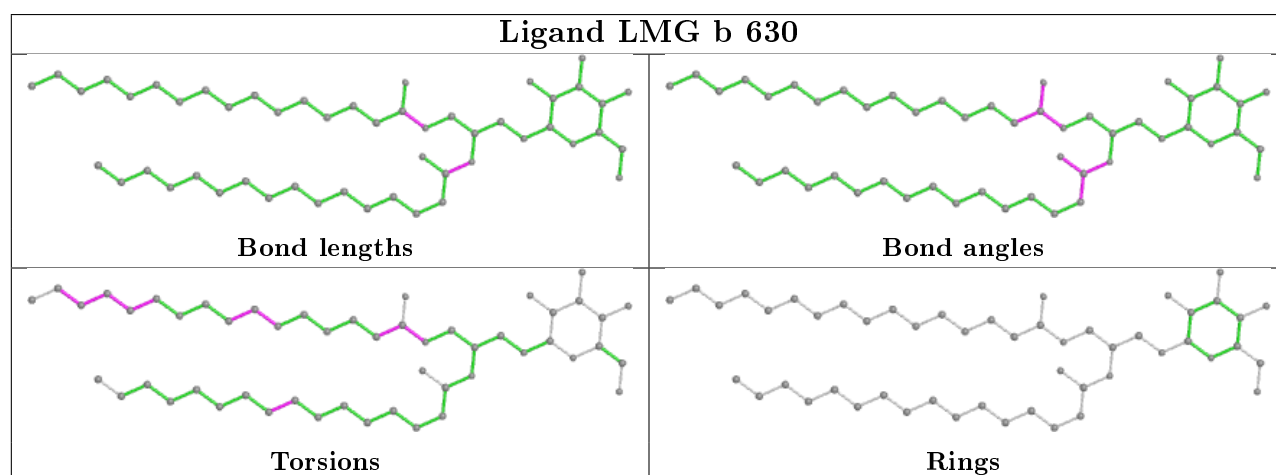
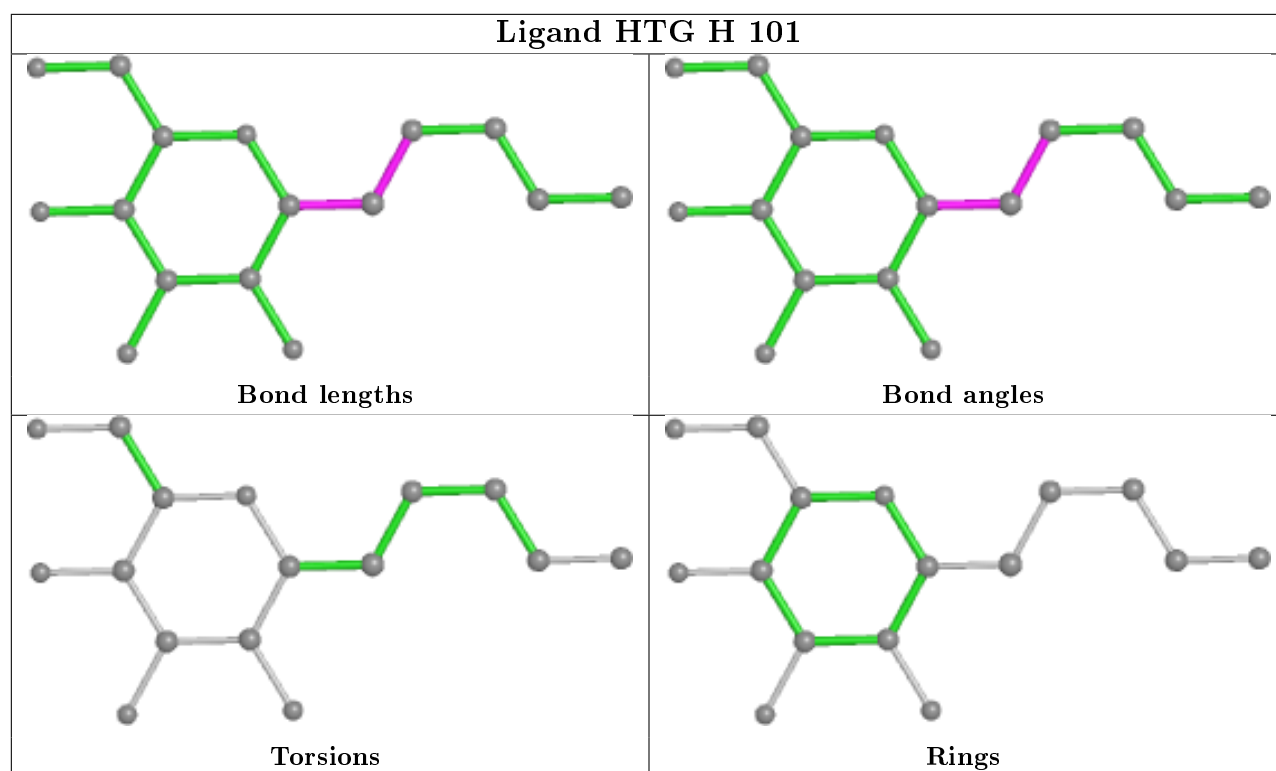


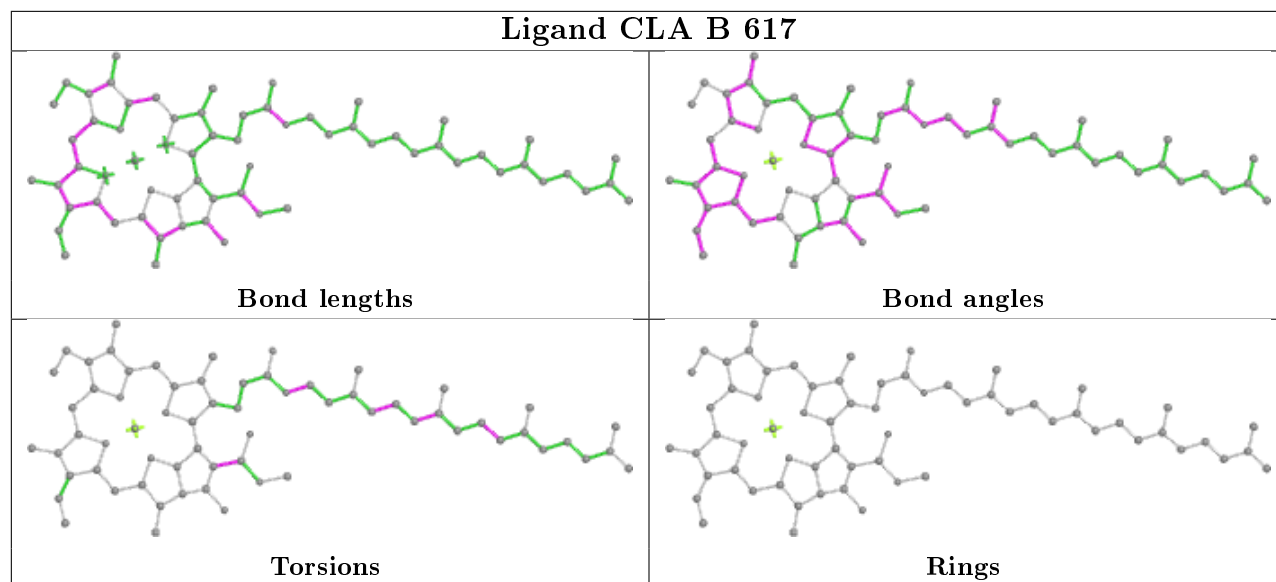
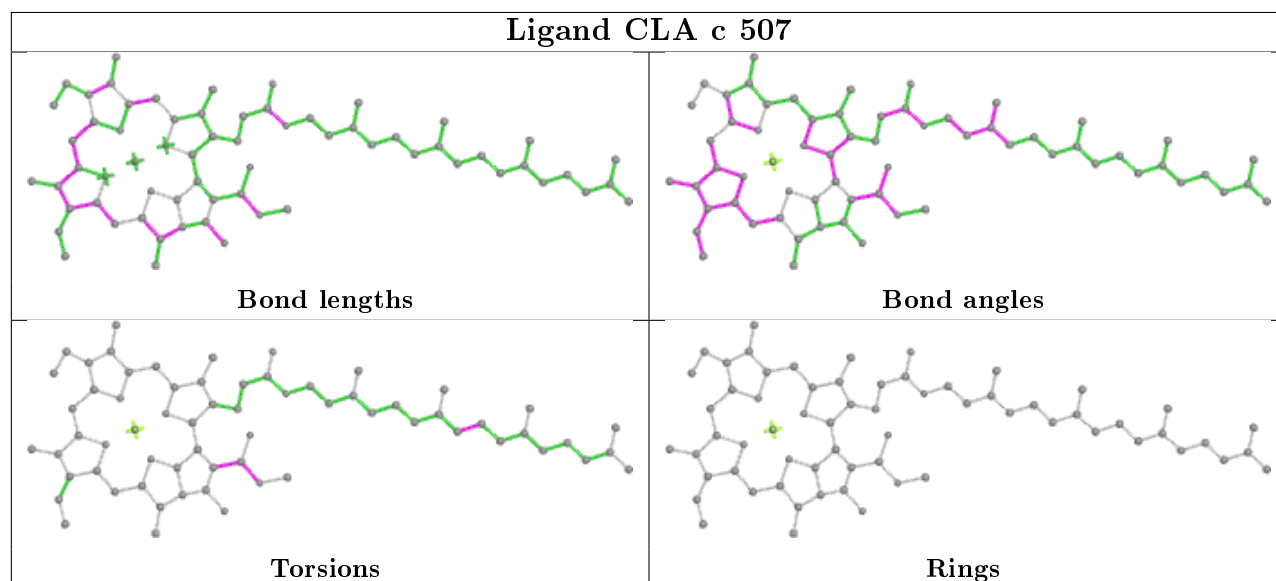
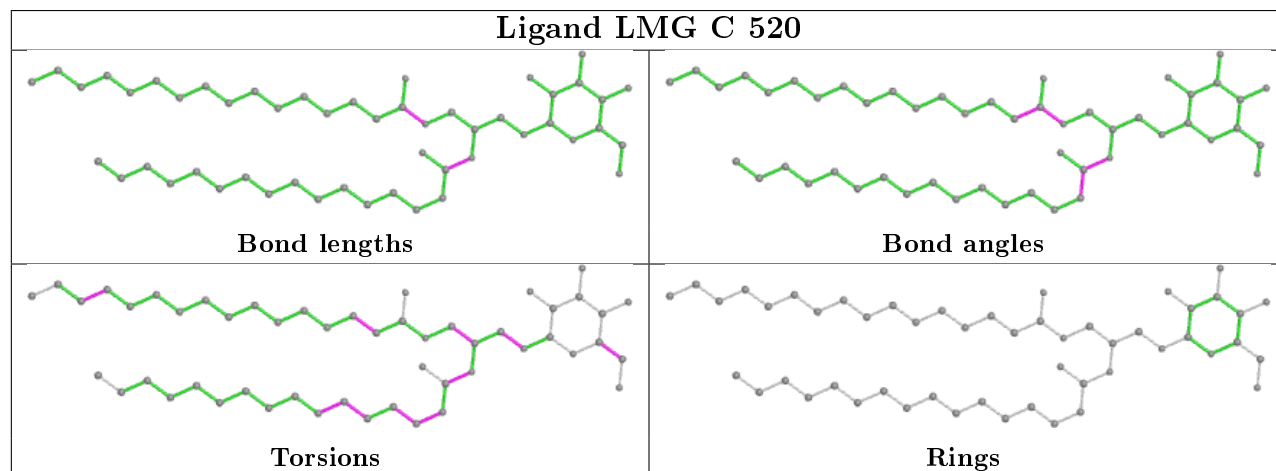
Ligand HTG C 522

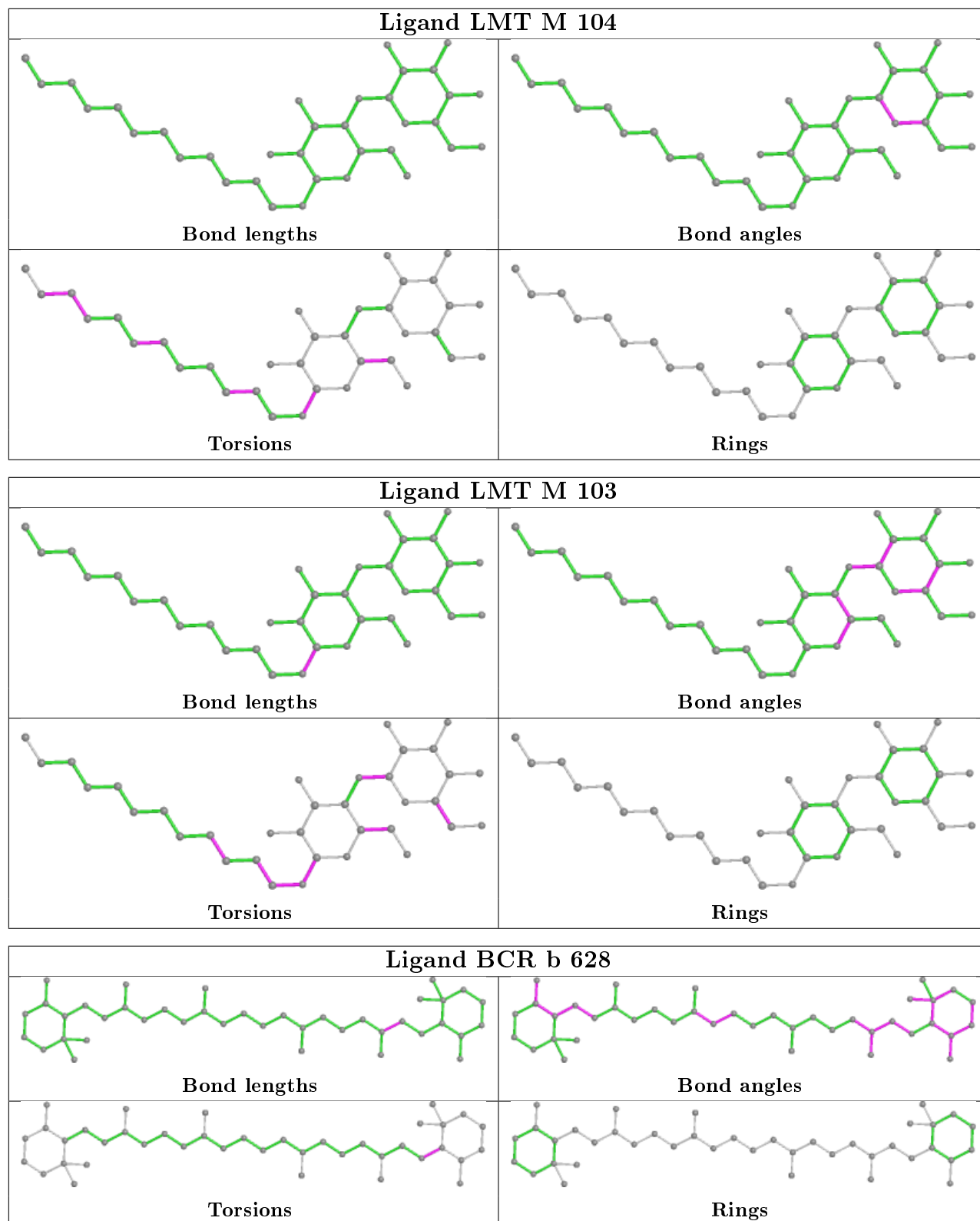


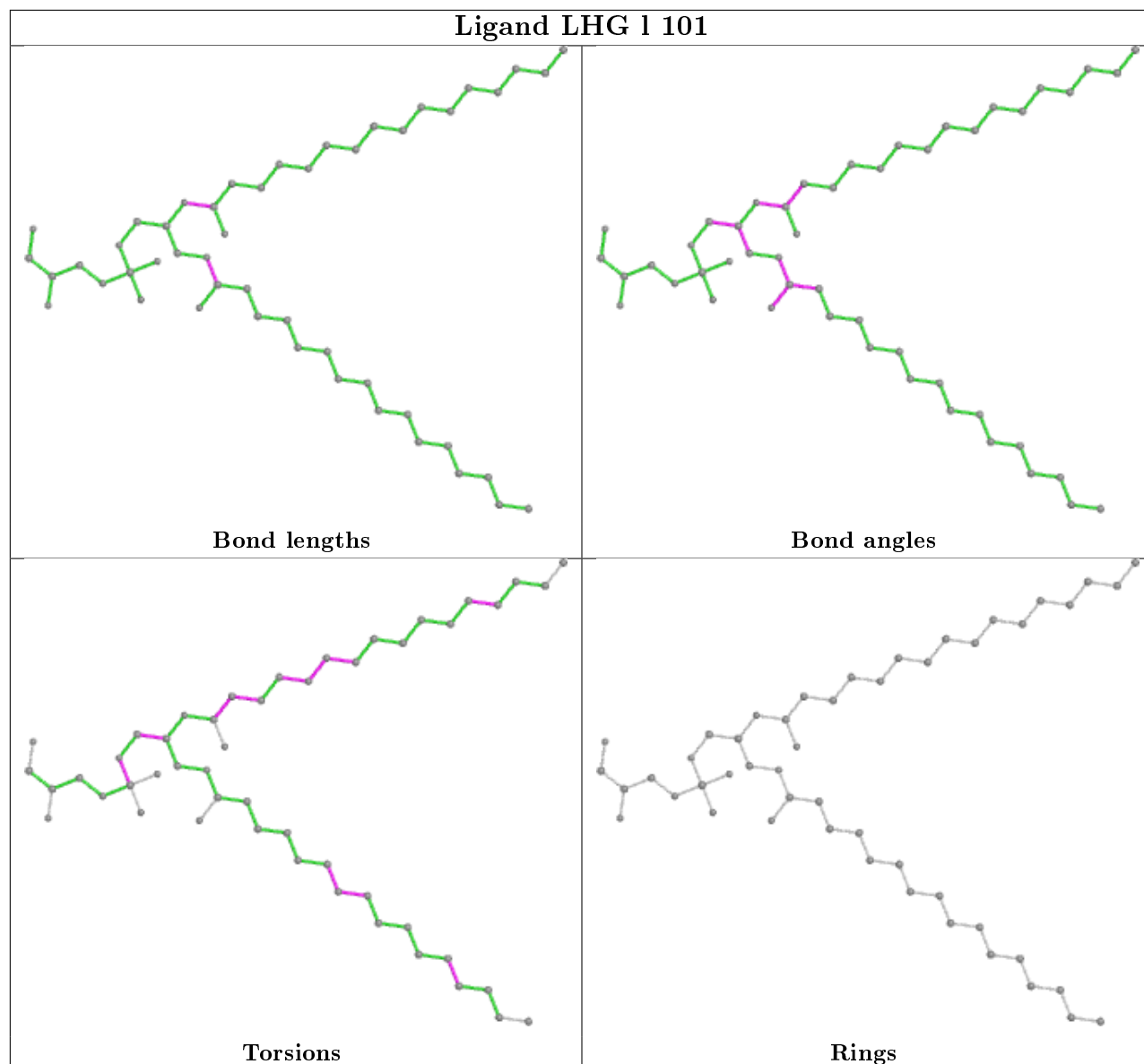
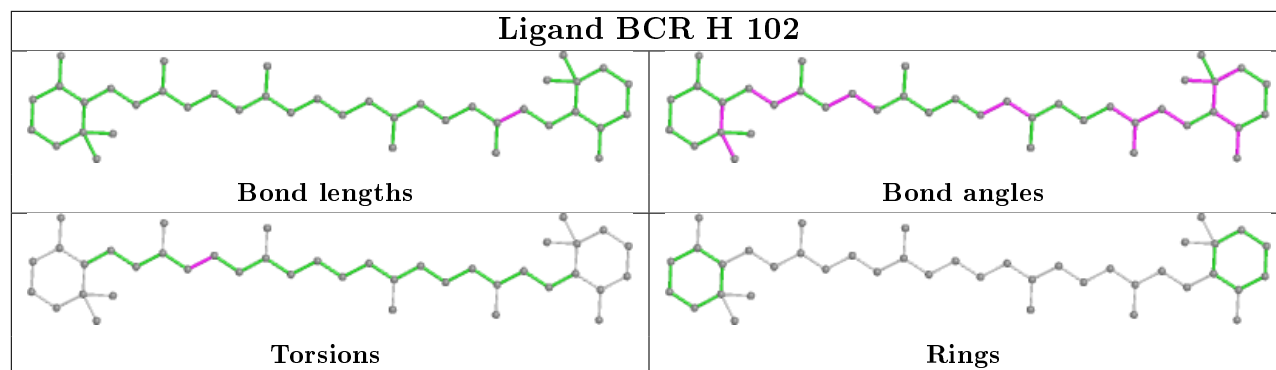


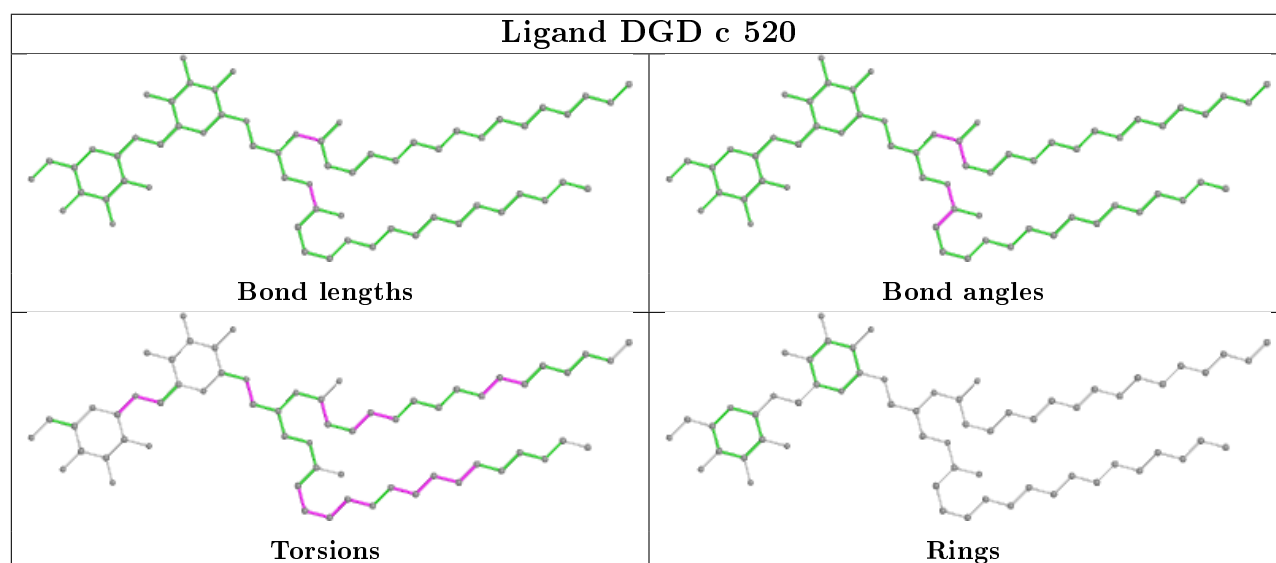
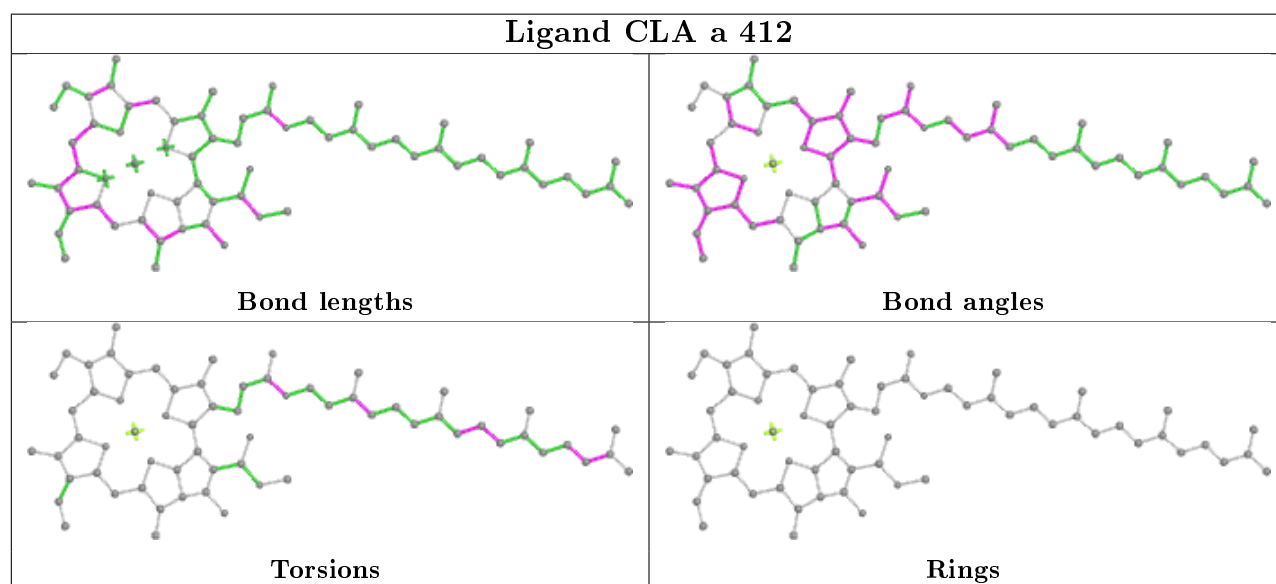
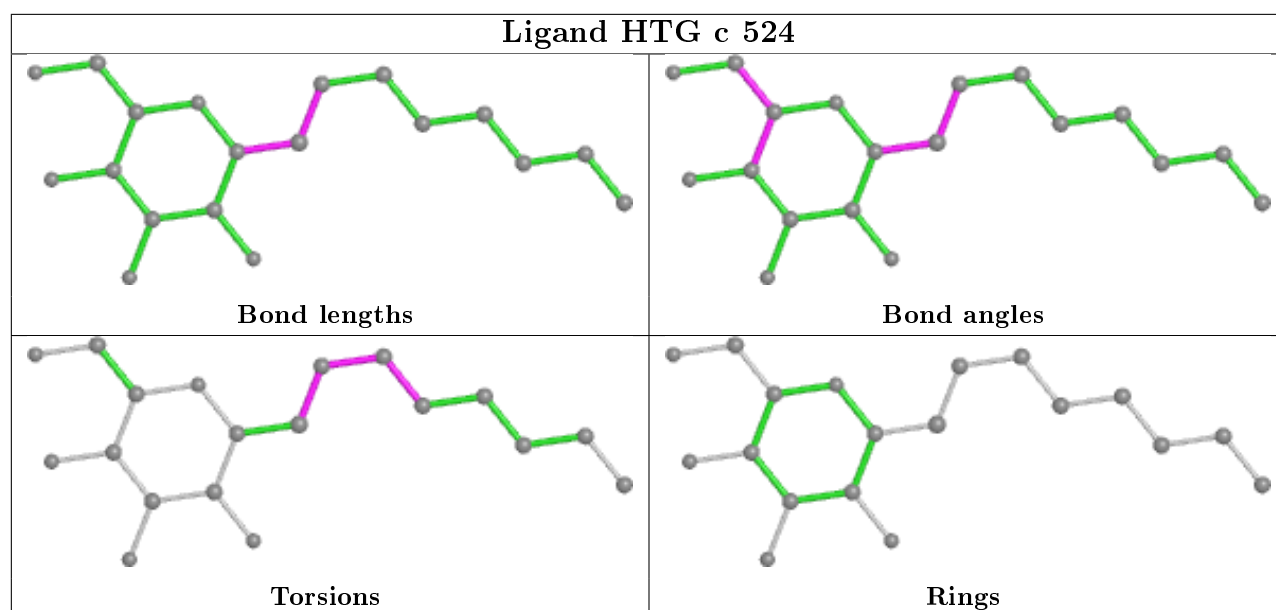


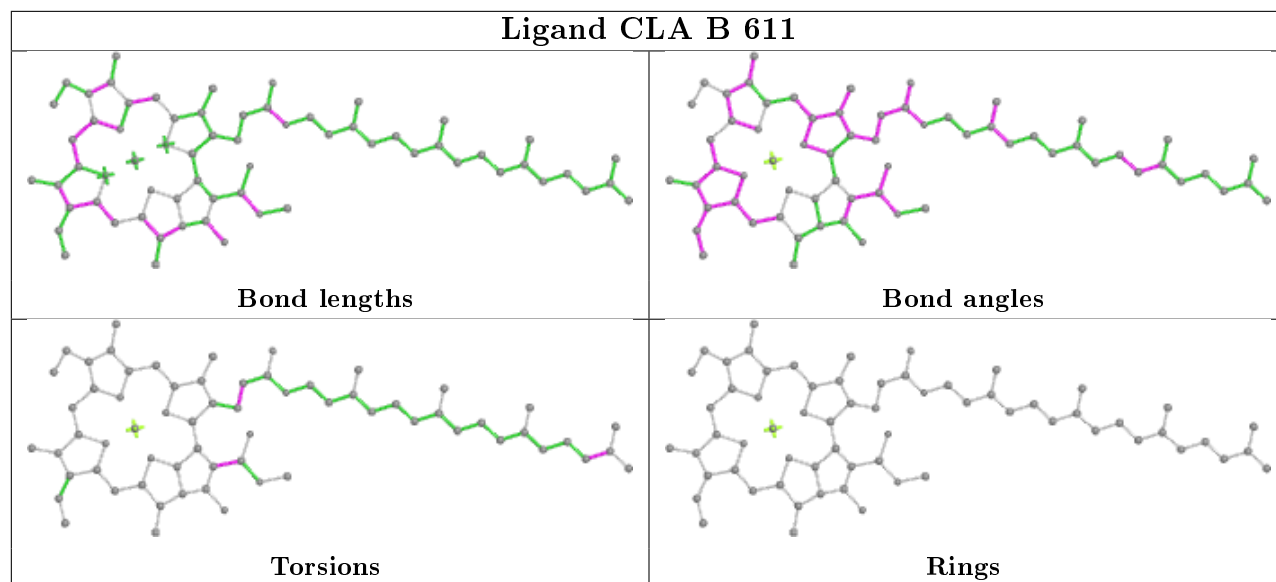
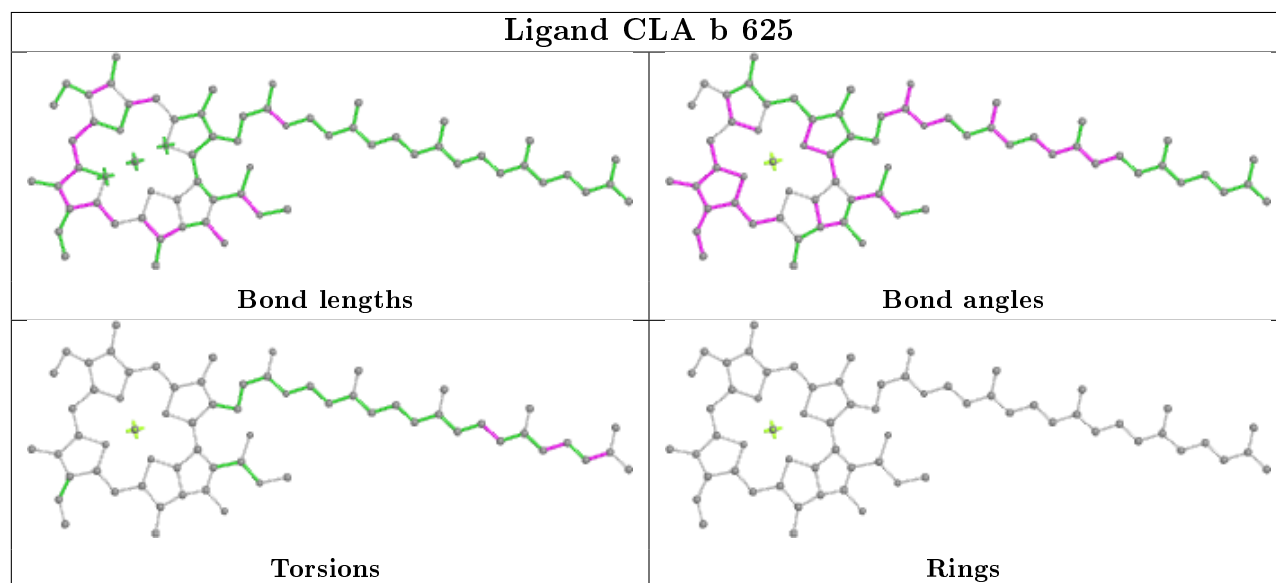


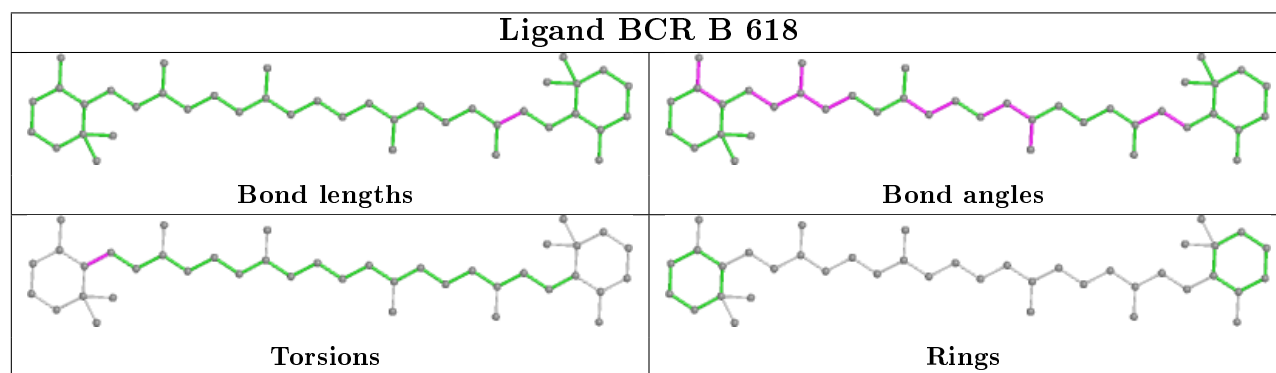
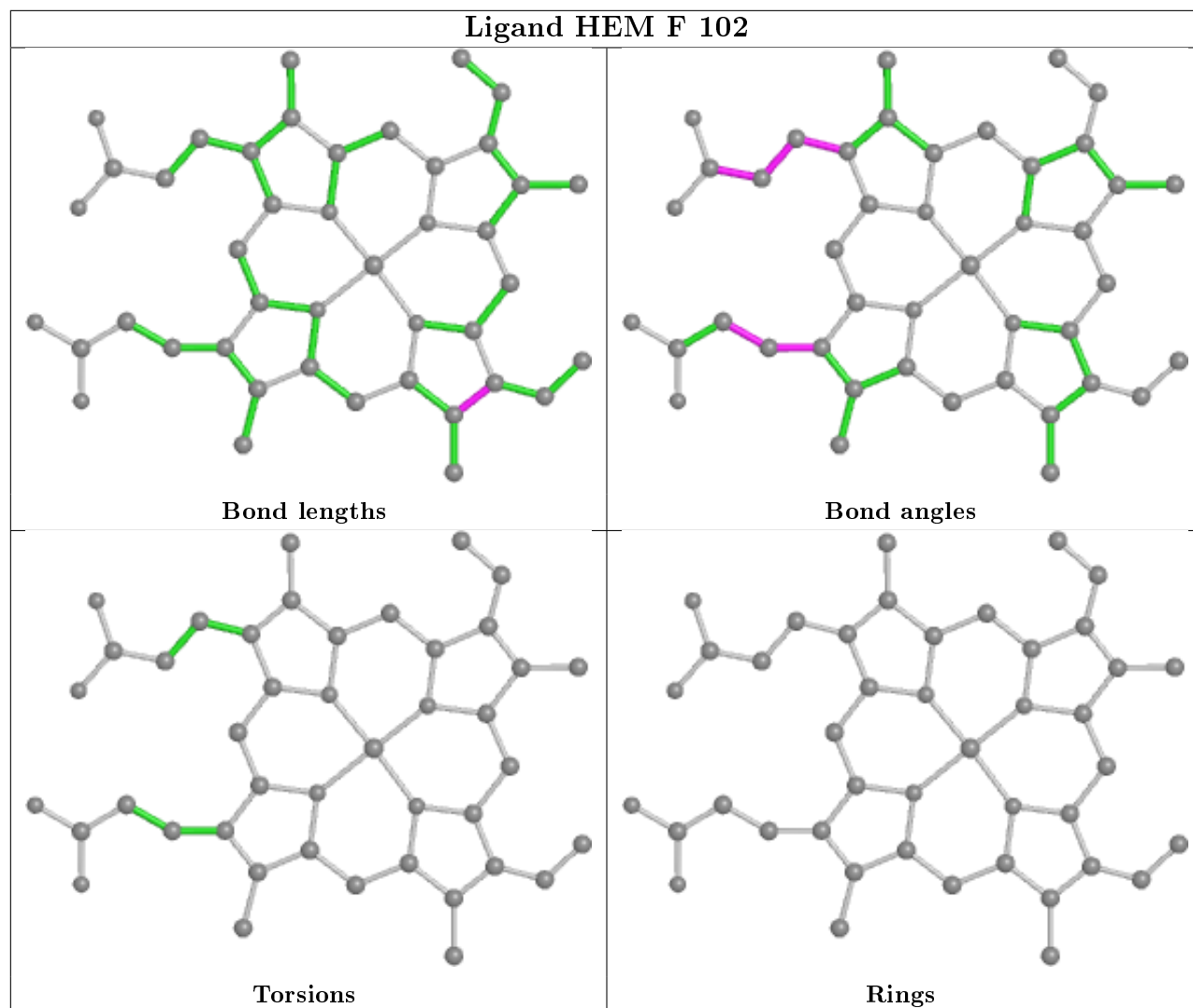
Ligand CLA B 617**Ligand CLA c 507****Ligand LMG C 520**

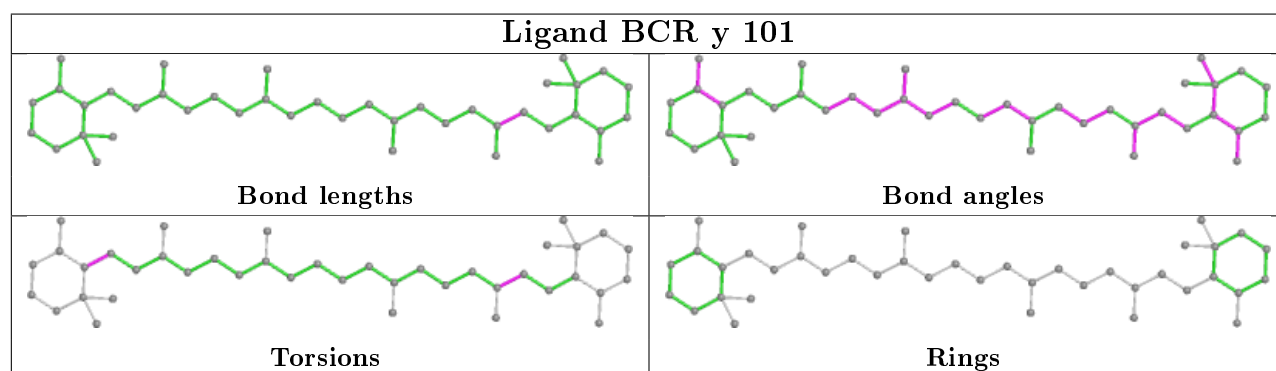
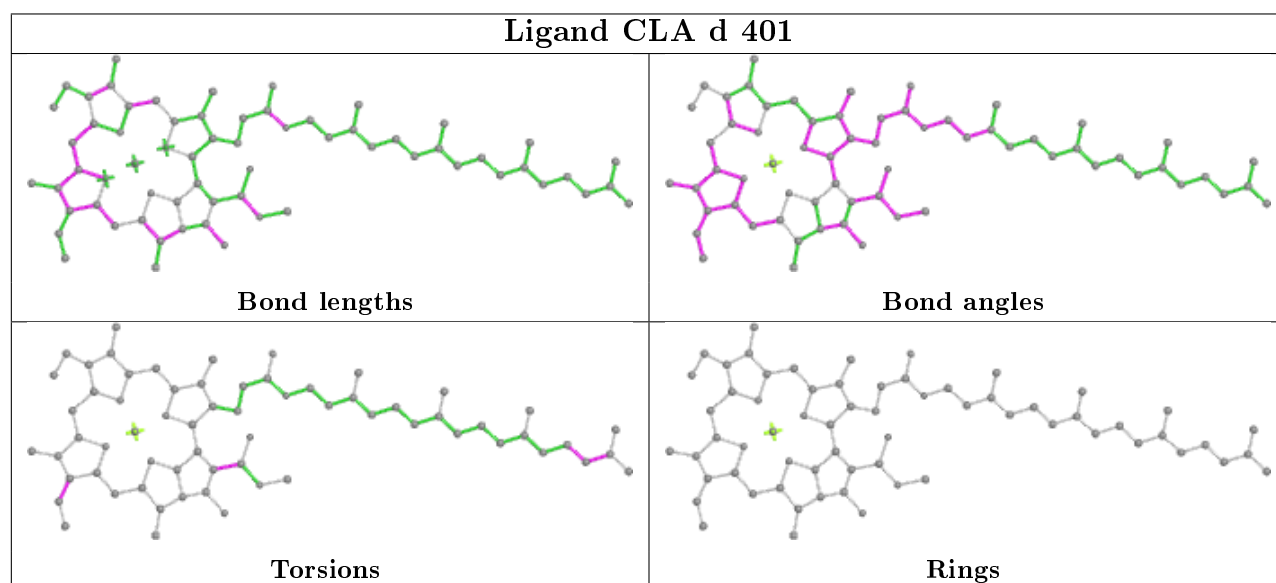
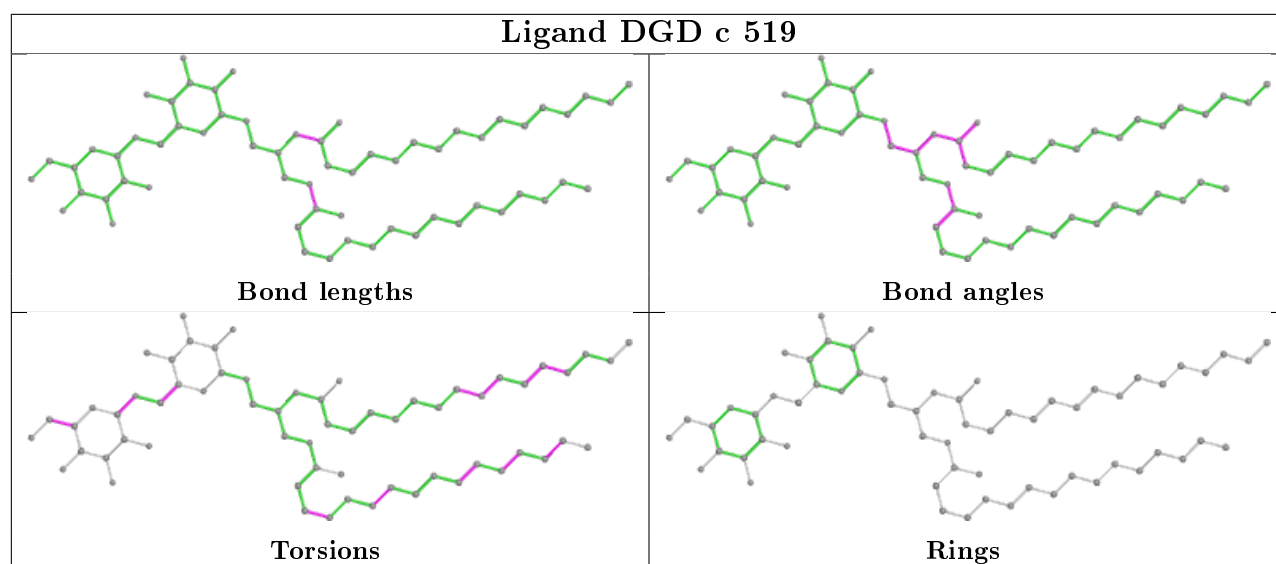


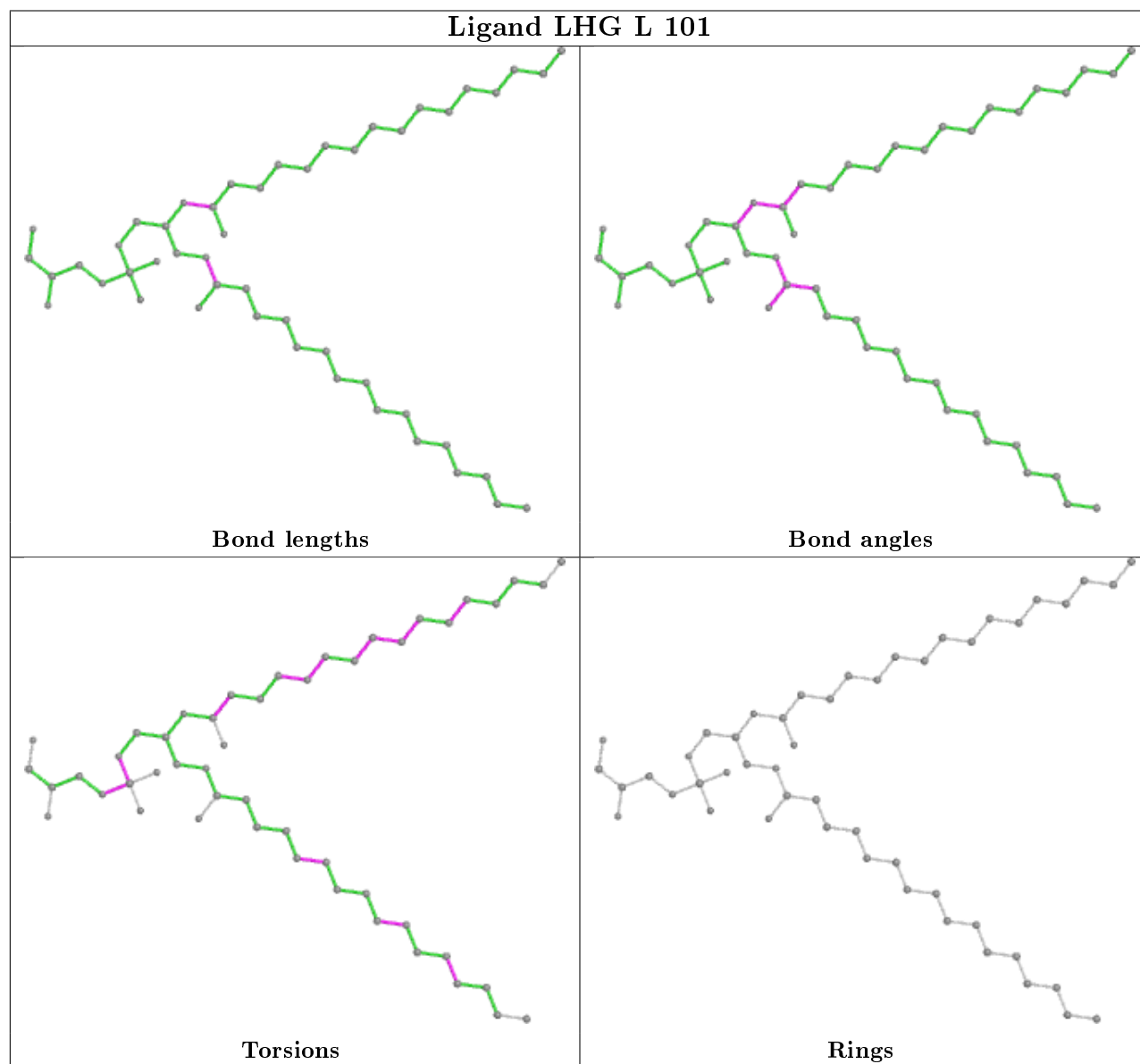
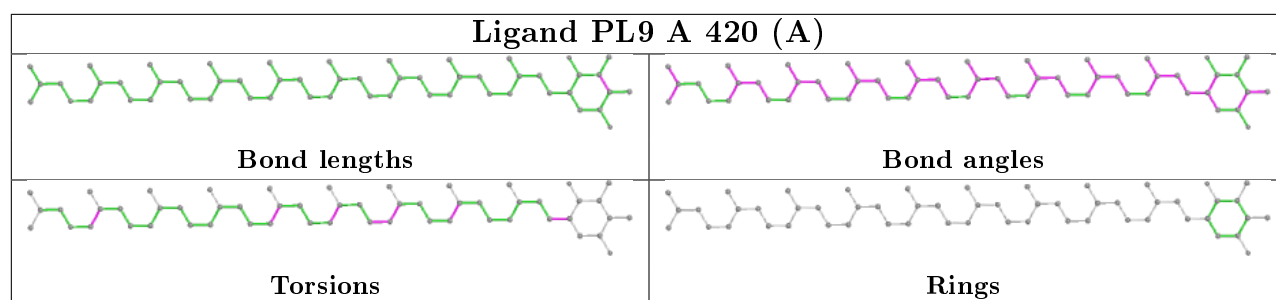


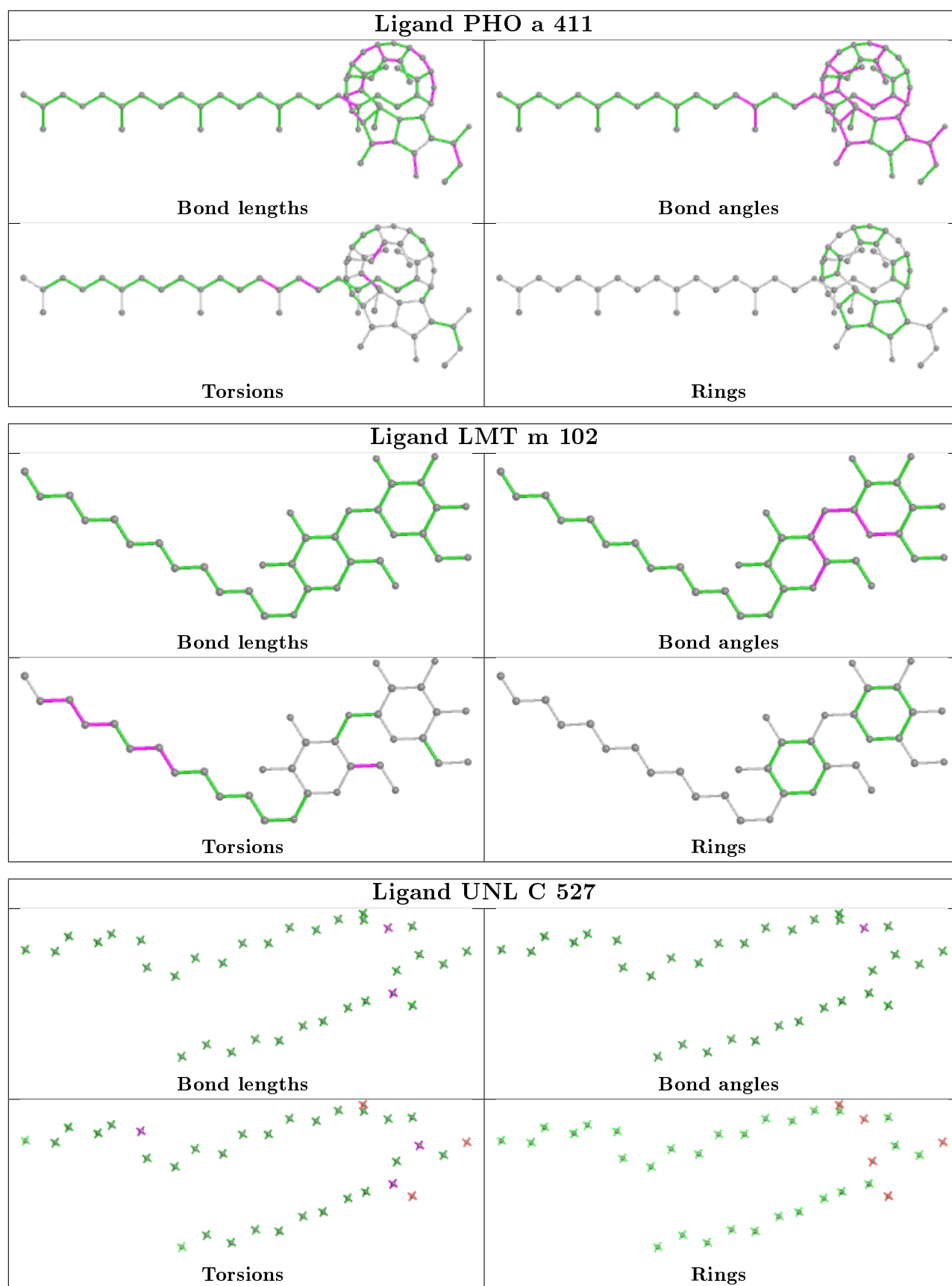


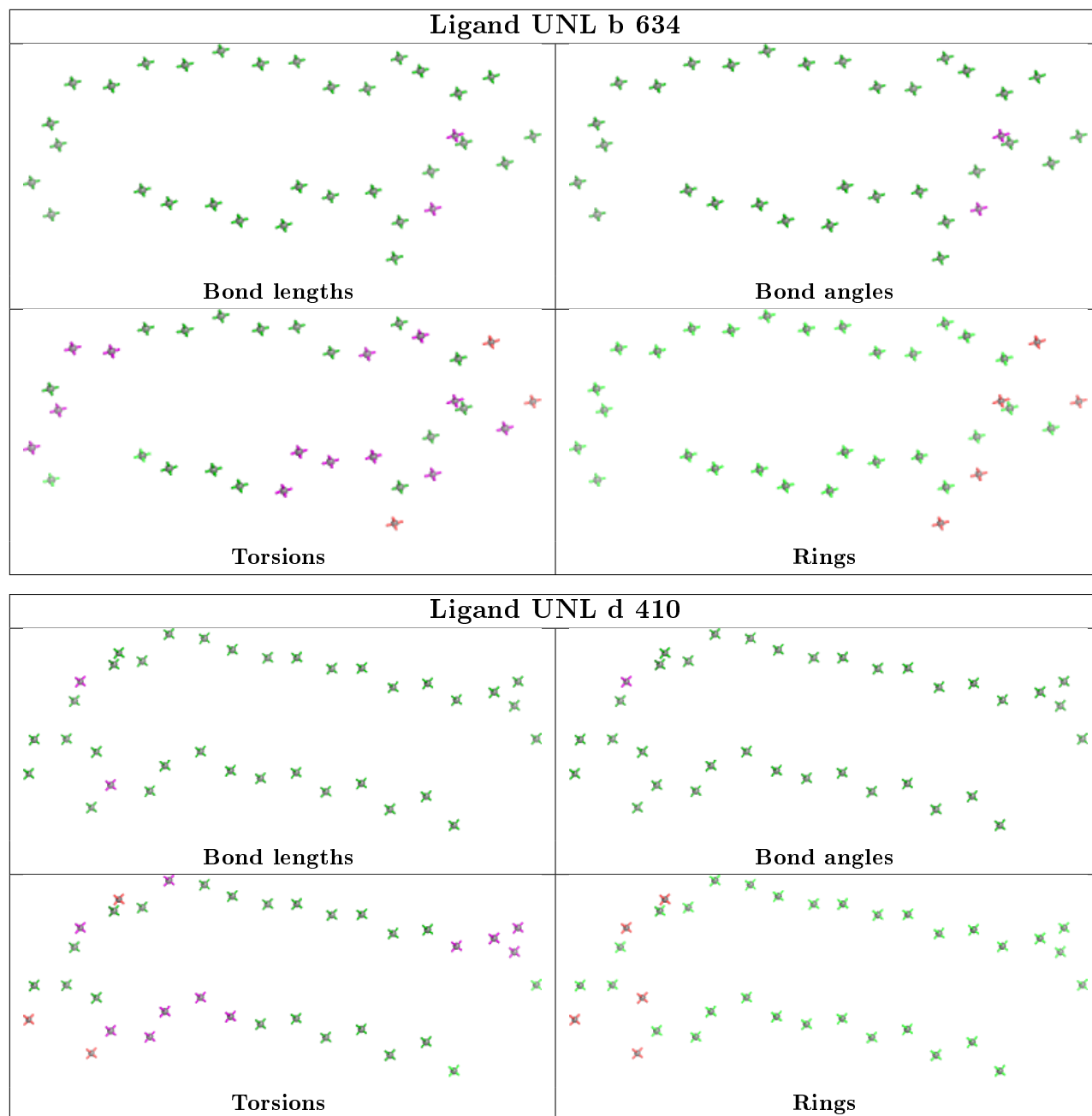
Ligand CLA B 611**Ligand CLA b 625**

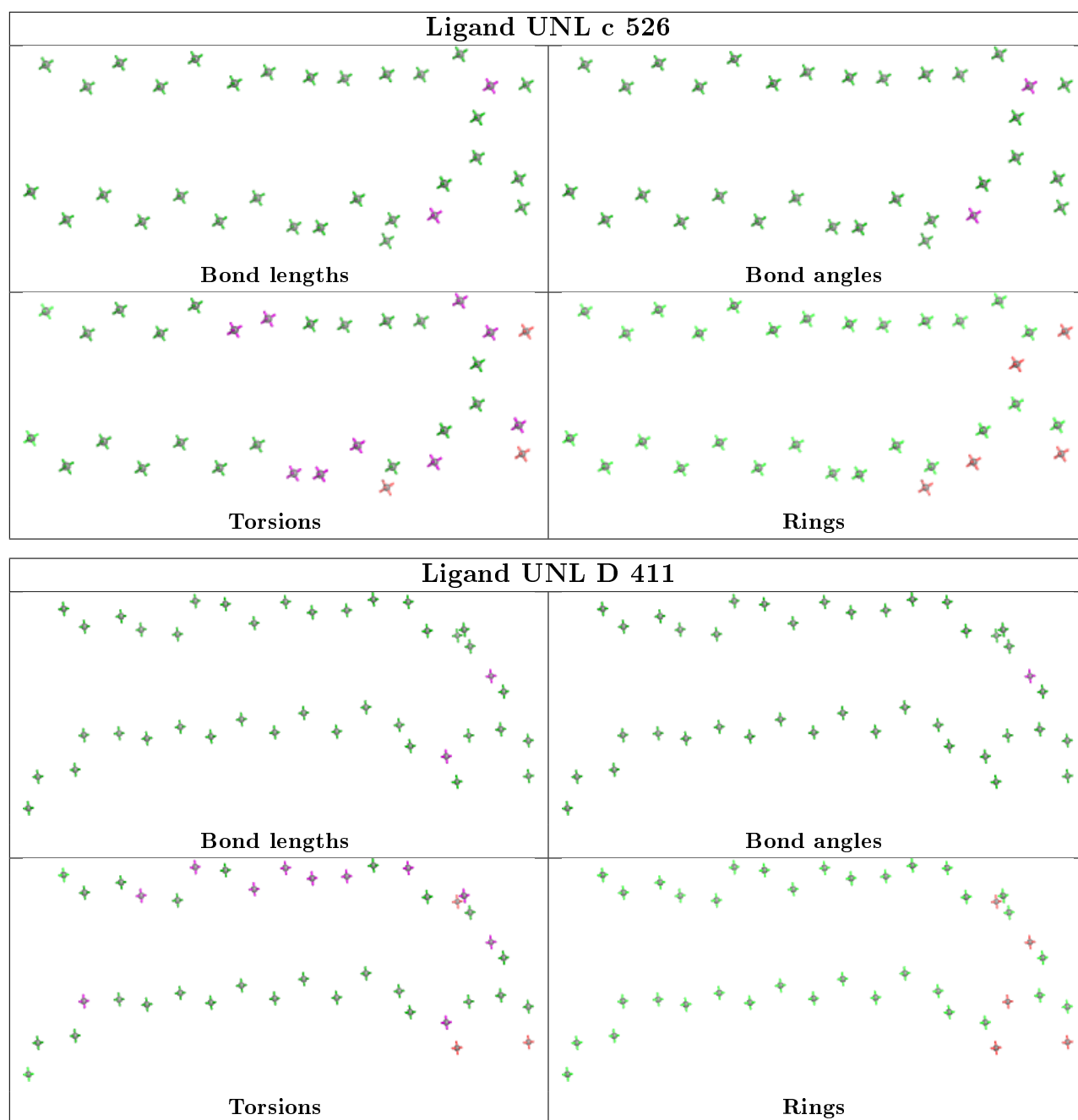


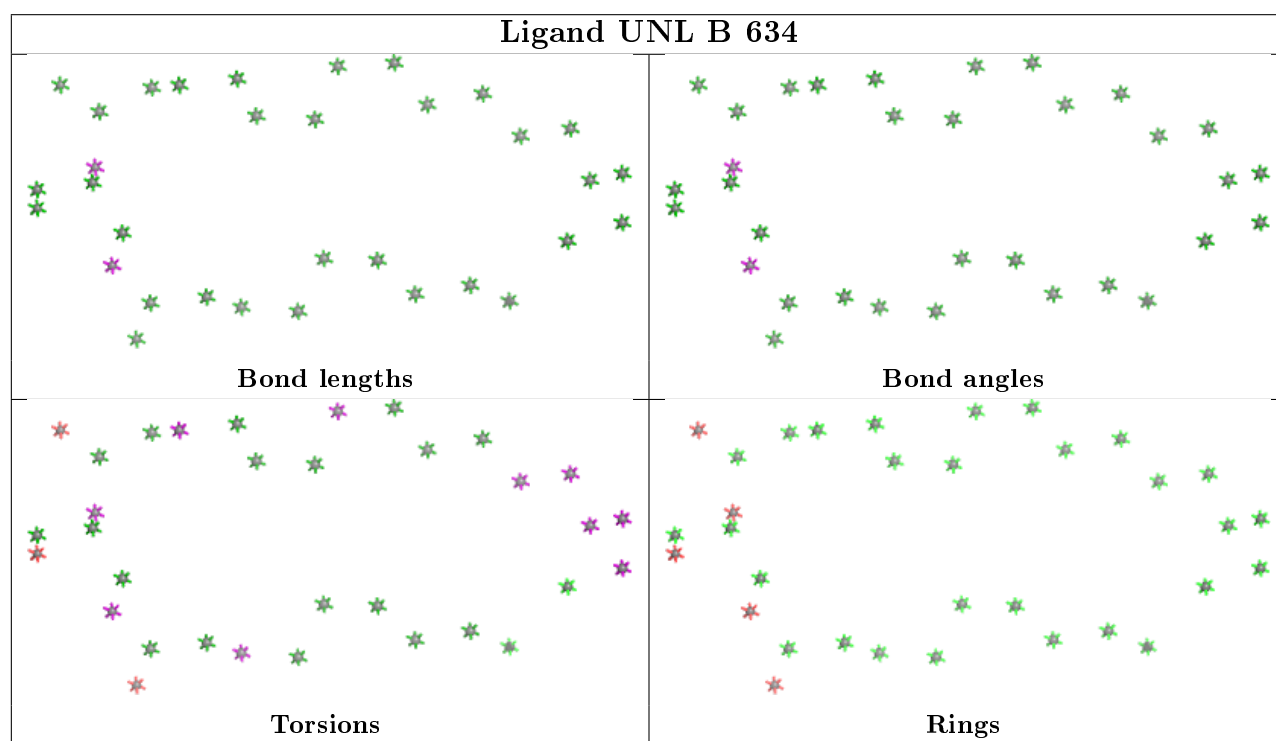
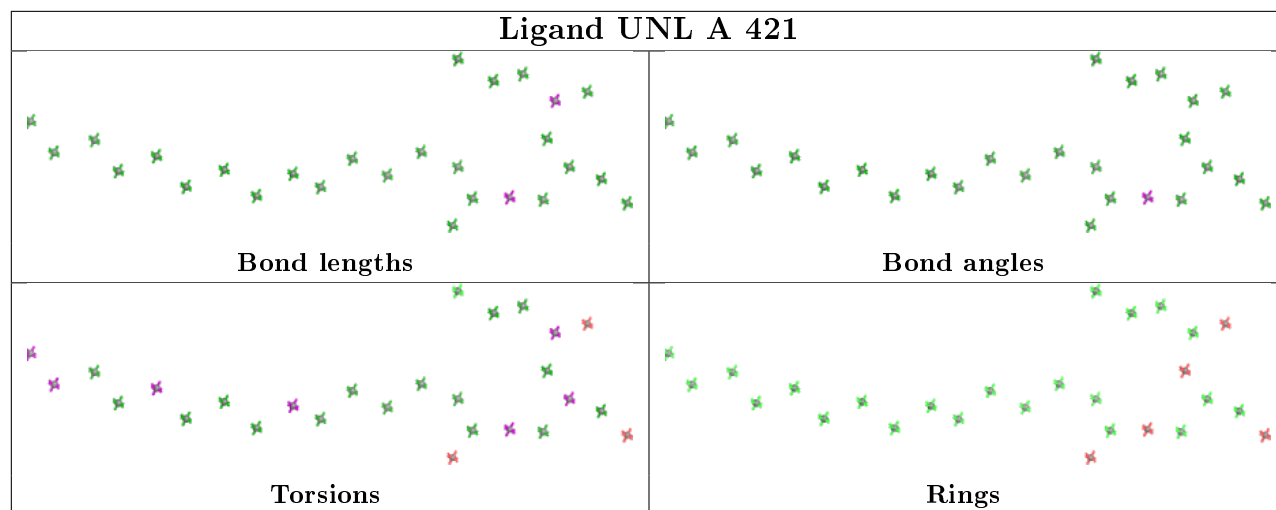


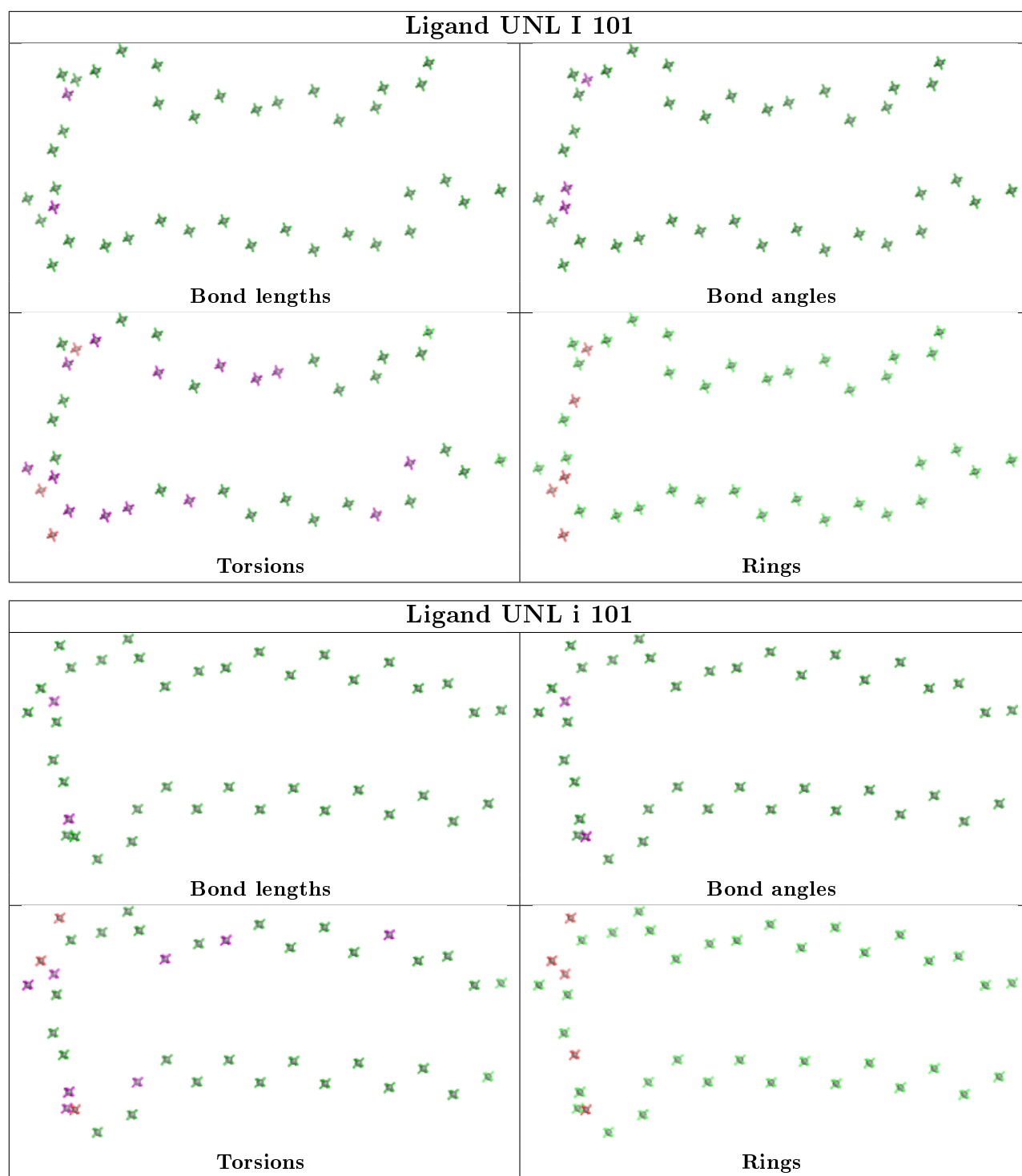


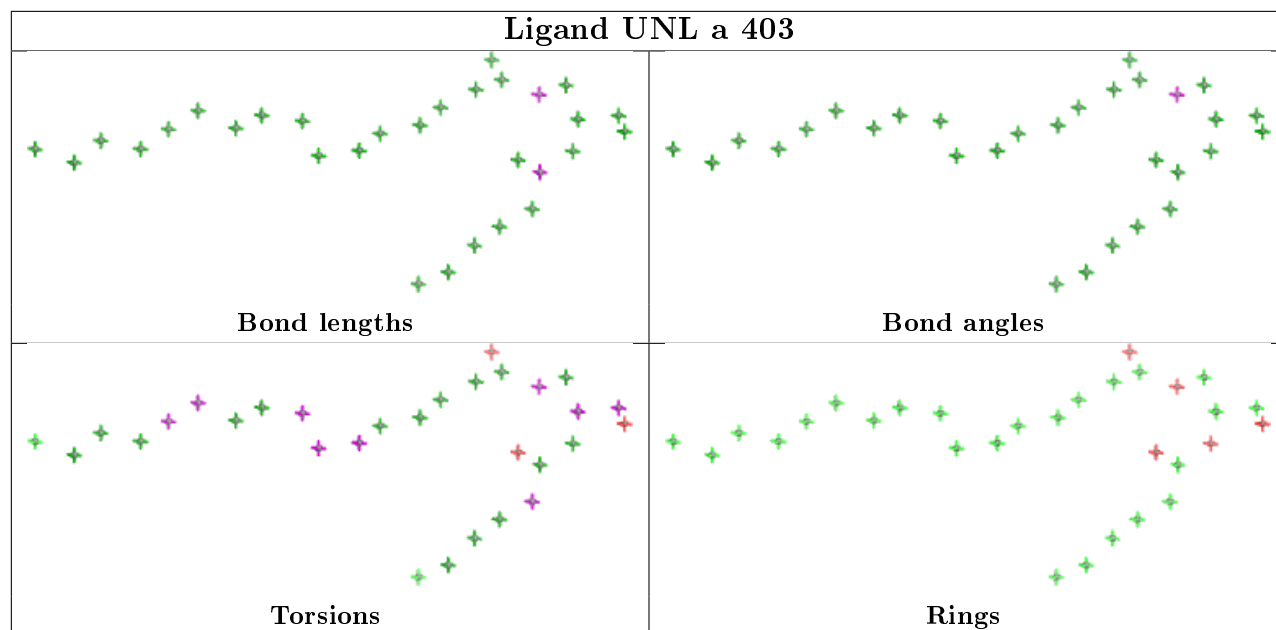












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	334/344 (97%)	0.06	2 (0%) 89 91	28, 37, 66, 107	0
1	a	334/344 (97%)	0.17	10 (2%) 50 59	29, 38, 73, 150	0
2	B	504/505 (99%)	0.08	7 (1%) 75 80	29, 42, 76, 120	0
2	b	503/505 (99%)	0.21	24 (4%) 30 39	30, 43, 83, 162	0
3	C	451/455 (99%)	0.02	3 (0%) 87 91	32, 49, 69, 110	0
3	c	455/455 (100%)	0.07	4 (0%) 84 88	36, 53, 70, 121	0
4	D	341/342 (99%)	0.02	1 (0%) 94 95	27, 38, 62, 134	0
4	d	341/342 (99%)	0.02	2 (0%) 89 91	28, 41, 65, 112	0
5	E	81/84 (96%)	0.62	8 (9%) 7 11	44, 63, 92, 139	0
5	e	81/84 (96%)	0.90	10 (12%) 4 5	47, 65, 110, 167	0
6	F	34/44 (77%)	0.31	3 (8%) 10 14	45, 54, 92, 96	0
6	f	32/44 (72%)	0.29	2 (6%) 20 27	45, 54, 112, 130	0
7	H	65/65 (100%)	0.19	3 (4%) 32 42	39, 52, 68, 144	0
7	h	65/65 (100%)	0.09	2 (3%) 49 58	40, 54, 74, 162	0
8	I	37/38 (97%)	0.21	3 (8%) 12 16	44, 52, 104, 148	0
8	i	37/38 (97%)	0.18	2 (5%) 25 34	41, 50, 97, 126	0
9	J	38/39 (97%)	0.48	3 (7%) 12 17	42, 58, 135, 165	0
9	j	39/39 (100%)	0.74	4 (10%) 6 9	46, 59, 130, 162	0
10	K	37/37 (100%)	-0.03	0 100 100	50, 58, 72, 91	0
10	k	37/37 (100%)	0.23	0 100 100	50, 63, 79, 98	0
11	L	37/37 (100%)	0.14	1 (2%) 54 63	28, 34, 94, 106	0
11	l	37/37 (100%)	0.18	1 (2%) 54 63	30, 36, 90, 121	0
12	M	33/36 (91%)	0.27	2 (6%) 21 28	28, 36, 61, 112	0
12	m	33/36 (91%)	0.27	0 100 100	30, 37, 66, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	O	243/244 (99%)	0.02	3 (1%) 79 83	29, 47, 91, 130	0
13	o	243/244 (99%)	0.10	4 (1%) 72 77	31, 49, 103, 167	0
14	T	29/32 (90%)	0.16	1 (3%) 45 53	30, 36, 62, 135	0
14	t	29/32 (90%)	0.11	0 100 100	31, 37, 64, 128	0
15	U	97/104 (93%)	-0.08	0 100 100	35, 46, 75, 109	0
15	u	97/104 (93%)	-0.03	0 100 100	37, 49, 68, 117	0
16	V	137/137 (100%)	-0.06	0 100 100	31, 45, 65, 84	0
16	v	137/137 (100%)	0.08	1 (0%) 87 91	39, 56, 82, 129	0
17	Y	29/30 (96%)	1.78	7 (24%) 0 0	60, 71, 151, 153	0
17	y	29/30 (96%)	0.80	2 (6%) 16 23	68, 80, 106, 124	0
18	X	39/40 (97%)	0.48	4 (10%) 6 9	47, 60, 112, 132	0
18	x	38/40 (95%)	0.53	4 (10%) 6 9	52, 61, 113, 134	0
19	Z	62/62 (100%)	0.54	7 (11%) 5 7	56, 72, 108, 126	0
19	z	62/62 (100%)	1.11	10 (16%) 1 2	70, 83, 128, 175	0
20	R	18/34 (52%)	7.53	18 (100%) 0 0	111, 142, 169, 174	0
All	All	5275/5384 (97%)	0.17	158 (2%) 50 59	27, 47, 89, 175	0

The worst 5 of 158 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
17	Y	18	VAL	16.6
20	R	18	TRP	14.5
20	R	15	ALA	13.8
5	e	5	THR	13.8
2	b	496	TYR	10.6

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
14	FME	T	1	10/11	0.94	0.11	37,40,54,78	0
12	FME	M	1	10/11	0.97	0.13	26,45,71,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	FME	i	1	10/11	0.97	0.13	39,48,57,57	0
12	FME	m	1	10/11	0.97	0.16	34,45,87,98	0
8	FME	I	1	10/11	0.98	0.11	36,46,51,55	0
14	FME	t	1	10/11	0.98	0.12	28,35,39,84	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
37	DGD	e	101	62/66	0.44	0.39	66,114,163,166	0
29	LMT	F	101	35/35	0.54	0.33	97,128,145,146	0
29	LMT	C	521	35/35	0.57	0.32	94,119,146,148	0
29	LMT	b	631	25/35	0.58	0.32	72,95,139,144	0
33	UNL	C	527	34/-	0.59	0.22	76,103,111,117	0
38	LHG	a	422	42/49	0.59	0.30	78,125,159,162	0
33	UNL	a	403	30/-	0.62	0.24	77,91,116,118	0
37	DGD	D	406	52/66	0.63	0.28	67,101,132,138	0
29	LMT	a	421	35/35	0.64	0.37	94,110,132,135	0
33	UNL	A	421	28/-	0.66	0.22	68,84,98,99	0
33	UNL	c	526	32/-	0.66	0.23	77,98,122,128	0
33	UNL	j	102	10/-	0.66	0.21	70,80,90,91	0
29	LMT	M	103	35/35	0.67	0.25	45,92,128,137	0
36	HTG	c	525	19/19	0.67	0.34	68,104,113,143	0
36	HTG	d	411	16/19	0.67	0.19	70,111,121,126	0
29	LMT	D	401	35/35	0.68	0.28	75,118,137,137	0
29	LMT	f	103	35/35	0.70	0.29	72,117,137,137	0
36	HTG	H	101	16/19	0.71	0.27	70,131,138,139	0
33	UNL	B	634	33/-	0.72	0.24	54,88,123,126	0
33	UNL	J	101	10/-	0.72	0.22	46,70,80,85	0
27	SQD	f	102	43/54	0.72	0.27	97,116,146,147	0
35	CA	b	610	1/1	0.73	0.17	130,130,130,130	0
29	LMT	a	404	35/35	0.73	0.24	47,86,111,123	0
34	LMG	Z	101	37/55	0.73	0.27	57,108,124,127	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
33	UNL	m	101	10/-	0.74	0.22	50,57,79,81	0
36	HTG	b	609	19/19	0.74	0.21	62,113,140,141	0
29	LMT	m	102	35/35	0.75	0.23	47,95,121,125	0
36	HTG	B	625	19/19	0.76	0.26	64,120,133,158	0
36	HTG	B	633	19/19	0.76	0.21	53,110,132,175	0
32	PL9	a	416[A]	55/55	0.76	0.25	83,102,111,114	55
32	PL9	a	416[B]	55/55	0.76	0.25	84,102,111,114	55
38	LHG	E	101	42/49	0.77	0.22	69,98,119,122	0
29	LMT	A	417	35/35	0.77	0.21	41,79,99,112	0
29	LMT	M	104	35/35	0.77	0.22	46,79,89,95	0
27	SQD	b	601	54/54	0.78	0.18	52,72,120,129	0
33	UNL	b	634	33/-	0.78	0.25	48,98,141,142	0
28	GOL	V	202	6/6	0.79	0.38	62,77,81,82	0
33	UNL	I	101	40/-	0.80	0.25	43,83,129,135	0
33	UNL	d	410	36/-	0.80	0.20	53,77,122,126	0
27	SQD	A	416	54/54	0.80	0.19	47,73,104,112	0
28	GOL	v	201	6/6	0.81	0.34	78,85,89,90	0
29	LMT	T	104	25/35	0.81	0.23	38,71,116,121	0
32	PL9	A	420[B]	55/55	0.81	0.23	71,87,101,101	55
36	HTG	b	633	19/19	0.81	0.22	70,120,135,135	0
32	PL9	A	420[A]	55/55	0.81	0.23	70,87,101,101	55
33	UNL	i	101	40/-	0.81	0.23	50,74,125,128	0
29	LMT	B	635	25/35	0.82	0.24	38,73,124,127	0
27	SQD	B	621	54/54	0.82	0.19	48,81,143,146	0
34	LMG	C	519	51/55	0.82	0.19	50,78,102,103	0
28	GOL	T	102	6/6	0.83	0.28	103,114,116,120	0
34	LMG	C	520	51/55	0.83	0.20	53,105,116,119	0
36	HTG	C	523	19/19	0.83	0.22	75,95,121,124	0
34	LMG	z	101	39/55	0.83	0.24	69,112,127,136	0
27	SQD	a	405	54/54	0.83	0.16	45,76,111,114	0
29	LMT	M	101	35/35	0.83	0.20	39,82,98,103	0
34	LMG	c	523	51/55	0.83	0.23	49,106,118,120	0
33	UNL	M	102	10/-	0.84	0.19	50,64,69,73	0
34	LMG	a	415	51/55	0.85	0.18	58,75,96,97	0
33	UNL	D	411	40/-	0.85	0.18	57,79,113,123	0
34	LMG	A	422	51/55	0.86	0.17	56,79,99,104	0
37	DGD	C	517	62/66	0.86	0.15	37,52,86,94	0
34	LMG	b	630	51/55	0.86	0.17	39,48,68,82	0
28	GOL	t	102	6/6	0.87	0.42	49,76,86,89	0
34	LMG	c	522	51/55	0.87	0.18	52,86,107,110	0
33	UNL	X	101	18/-	0.87	0.16	58,70,93,100	0
28	GOL	b	607	6/6	0.87	0.16	64,77,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
28	GOL	c	502	6/6	0.87	0.43	70,79,91,98	0
27	SQD	F	103	43/54	0.87	0.21	74,97,116,118	0
33	UNL	d	412	18/-	0.88	0.20	61,68,102,107	0
36	HTG	b	632	19/19	0.88	0.24	51,67,77,78	0
37	DGD	h	102	62/66	0.88	0.15	35,48,63,73	0
36	HTG	B	624	19/19	0.88	0.17	54,64,74,81	0
28	GOL	A	415	6/6	0.88	0.17	54,73,76,79	0
34	LMG	B	622	51/55	0.89	0.16	32,49,69,85	0
37	DGD	c	520	62/66	0.89	0.16	38,51,100,112	0
28	GOL	O	301	6/6	0.89	0.10	68,76,77,77	0
24	CLA	C	513	65/65	0.89	0.17	50,64,93,98	0
28	GOL	a	402	6/6	0.89	0.22	76,90,92,92	0
28	GOL	C	524	6/6	0.89	0.28	63,65,79,82	0
37	DGD	H	103	62/66	0.90	0.16	32,47,70,74	0
28	GOL	A	414	6/6	0.90	0.25	52,54,57,60	0
36	HTG	c	524	19/19	0.90	0.14	81,89,96,118	0
27	SQD	A	412	54/54	0.90	0.17	43,76,91,94	0
36	HTG	b	608	19/19	0.90	0.13	48,68,78,79	0
28	GOL	A	413	6/6	0.90	0.12	43,44,56,59	0
28	GOL	B	636	6/6	0.90	0.12	48,51,55,55	0
36	HTG	B	632	19/19	0.91	0.13	41,75,91,92	0
24	CLA	c	511	65/65	0.91	0.14	43,54,62,67	0
38	LHG	D	407	49/49	0.91	0.17	35,47,59,64	0
36	HTG	V	207	19/19	0.91	0.24	63,87,104,205	0
37	DGD	c	521	62/66	0.91	0.15	39,51,82,89	0
24	CLA	c	517	65/65	0.91	0.15	61,77,92,94	0
28	GOL	T	101	6/6	0.91	0.34	55,69,88,96	0
27	SQD	a	414	54/54	0.91	0.15	54,77,98,101	0
28	GOL	v	202	6/6	0.91	0.19	72,79,89,99	0
28	GOL	B	630	6/6	0.91	0.24	50,66,68,71	0
36	HTG	C	522	19/19	0.91	0.15	72,80,91,95	0
24	CLA	c	515	65/65	0.92	0.15	43,55,73,80	0
38	LHG	D	409	49/49	0.92	0.19	37,54,105,113	0
28	GOL	f	101	6/6	0.92	0.20	74,84,86,89	0
35	CA	f	104	1/1	0.92	0.09	97,97,97,97	0
37	DGD	C	518	62/66	0.92	0.14	37,47,75,87	0
24	CLA	C	506	65/65	0.92	0.14	44,60,101,105	0
34	LMG	j	101	51/55	0.92	0.15	46,56,92,106	0
24	CLA	b	619	65/65	0.92	0.15	35,49,56,65	0
28	GOL	b	606	6/6	0.92	0.19	75,79,94,95	0
24	CLA	C	501	65/65	0.93	0.14	38,47,69,78	0
36	HTG	B	623	19/19	0.93	0.14	37,51,65,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
24	CLA	B	602	65/65	0.93	0.16	44,61,94,111	0
24	CLA	b	616	65/65	0.93	0.14	30,43,84,96	0
36	HTG	b	602	19/19	0.93	0.12	35,49,65,66	0
24	CLA	b	612	65/65	0.93	0.15	33,44,51,57	0
28	GOL	B	628	6/6	0.93	0.16	52,70,78,85	0
24	CLA	c	507	65/65	0.93	0.13	41,51,60,77	0
34	LMG	D	412	51/55	0.93	0.16	35,55,100,106	0
24	CLA	b	617	65/65	0.93	0.14	26,34,42,50	0
28	GOL	v	203	6/6	0.93	0.17	46,50,57,61	0
24	CLA	b	626	65/65	0.93	0.13	35,50,97,100	0
33	UNL	d	409	17/-	0.93	0.18	46,63,91,92	0
24	CLA	C	504	65/65	0.93	0.15	35,46,77,83	0
28	GOL	a	401	6/6	0.93	0.27	50,61,66,76	0
24	CLA	B	614	65/65	0.93	0.14	25,35,63,75	0
22	CL	v	204	1/1	0.93	0.11	88,88,88,88	0
24	CLA	C	507	65/65	0.93	0.14	40,52,67,72	0
24	CLA	C	511	65/65	0.93	0.12	42,56,67,78	0
24	CLA	b	611	65/65	0.93	0.15	46,69,101,116	0
28	GOL	V	203	6/6	0.93	0.15	39,50,64,67	0
24	CLA	C	512	65/65	0.94	0.12	46,64,76,80	0
24	CLA	C	509	65/65	0.94	0.14	41,52,73,76	0
24	CLA	C	508	65/65	0.94	0.13	35,48,107,117	0
28	GOL	V	201	6/6	0.94	0.21	68,75,76,79	0
26	BCR	h	101	40/40	0.94	0.12	39,54,64,66	0
38	LHG	d	406	49/49	0.94	0.16	41,49,58,63	0
28	GOL	B	626	6/6	0.94	0.14	39,52,57,71	0
24	CLA	c	512	65/65	0.94	0.13	36,46,109,121	0
38	LHG	d	407	49/49	0.94	0.16	30,39,57,75	0
26	BCR	c	527	40/40	0.94	0.12	56,72,78,81	0
26	BCR	y	101	40/40	0.94	0.14	43,60,68,76	0
24	CLA	c	509	65/65	0.94	0.12	34,45,64,72	0
35	CA	F	104	1/1	0.94	0.07	82,82,82,82	0
24	CLA	c	510	65/65	0.94	0.12	44,62,87,95	0
28	GOL	o	301	6/6	0.94	0.17	64,70,80,88	0
24	CLA	c	505	65/65	0.94	0.13	40,54,62,66	0
26	BCR	b	628	40/40	0.94	0.14	31,43,54,61	0
24	CLA	c	514	65/65	0.94	0.12	38,50,60,68	0
38	LHG	l	101	49/49	0.94	0.16	33,44,53,59	0
24	CLA	B	603	65/65	0.94	0.13	33,42,47,53	0
24	CLA	c	516	65/65	0.94	0.13	51,62,77,83	0
37	DGD	c	519	62/66	0.94	0.13	37,46,91,95	0
35	CA	B	601	1/1	0.94	0.07	118,118,118,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
24	CLA	c	508	65/65	0.94	0.12	38,50,71,75	0
28	GOL	V	205	6/6	0.94	0.20	71,75,81,91	0
24	CLA	B	607	65/65	0.94	0.14	31,43,85,91	0
33	UNL	D	410	17/-	0.94	0.16	39,67,83,87	0
26	BCR	k	101	40/40	0.94	0.14	44,60,70,74	0
24	CLA	b	621	65/65	0.94	0.13	26,38,48,55	0
28	GOL	B	627	6/6	0.95	0.22	56,65,80,92	0
38	LHG	d	408	49/49	0.95	0.17	34,52,103,105	0
26	BCR	T	103	40/40	0.95	0.12	28,45,55,58	0
24	CLA	b	613	65/65	0.95	0.13	34,43,52,58	0
26	BCR	Y	101	40/40	0.95	0.11	48,59,67,72	0
26	BCR	d	404	40/40	0.95	0.14	38,50,73,79	0
24	CLA	b	622	65/65	0.95	0.13	29,39,47,49	0
24	CLA	B	616	65/65	0.95	0.13	33,44,60,68	0
32	PL9	D	405[A]	55/55	0.95	0.15	28,35,45,49	55
24	CLA	B	608	65/65	0.95	0.13	24,33,44,53	0
26	BCR	D	404	40/40	0.95	0.14	36,49,79,88	0
24	CLA	B	604	65/65	0.95	0.13	33,43,50,53	0
24	CLA	C	503	65/65	0.95	0.13	39,50,59,65	0
24	CLA	B	610	65/65	0.95	0.13	35,46,55,71	0
25	PHO	a	420[B]	64/64	0.95	0.14	31,40,46,50	64
26	BCR	B	620	40/40	0.95	0.14	31,43,57,59	0
24	CLA	B	617	65/65	0.95	0.15	31,50,107,110	0
24	CLA	b	624	65/65	0.95	0.14	27,39,83,97	0
32	PL9	D	405[B]	55/55	0.95	0.15	27,35,43,47	55
24	CLA	B	615	65/65	0.95	0.14	27,38,82,86	0
38	LHG	D	408	49/49	0.95	0.16	30,41,62,74	0
24	CLA	D	403	65/65	0.95	0.13	39,49,99,104	0
37	DGD	C	516	62/66	0.95	0.14	33,44,85,86	0
24	CLA	a	409	65/65	0.95	0.14	27,32,48,57	0
26	BCR	H	102	40/40	0.95	0.13	36,52,65,68	0
25	PHO	a	420[A]	64/64	0.95	0.14	31,41,46,49	64
24	CLA	b	618	65/65	0.95	0.12	32,42,51,56	0
24	CLA	d	403	65/65	0.95	0.13	39,49,98,106	0
24	CLA	b	625	65/65	0.95	0.12	34,44,62,67	0
24	CLA	C	510	65/65	0.95	0.12	39,51,60,69	0
24	CLA	d	401	65/65	0.95	0.13	26,32,41,51	0
24	CLA	c	513	65/65	0.95	0.13	43,54,67,82	0
26	BCR	c	518	40/40	0.95	0.14	39,55,64,64	0
38	LHG	L	101	49/49	0.95	0.15	31,43,54,61	0
28	GOL	B	631	6/6	0.95	0.32	48,62,69,70	0
28	GOL	b	603	6/6	0.95	0.20	53,57,64,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
24	CLA	C	505	65/65	0.95	0.13	32,47,66,74	0
26	BCR	C	514	40/40	0.95	0.13	49,65,73,78	0
26	BCR	K	101	40/40	0.95	0.14	43,55,62,63	0
23	BCT	a	419[B]	4/4	0.96	0.13	53,53,57,64	4
25	PHO	A	409[B]	64/64	0.96	0.14	30,39,44,49	64
24	CLA	b	614	65/65	0.96	0.13	26,39,70,74	0
24	CLA	a	410	65/65	0.96	0.14	29,40,99,105	0
24	CLA	b	623	65/65	0.96	0.14	28,39,55,57	0
24	CLA	b	615	65/65	0.96	0.13	28,38,50,52	0
26	BCR	C	515	40/40	0.96	0.15	39,53,60,63	0
26	BCR	t	101	40/40	0.96	0.13	30,43,60,68	0
24	CLA	B	612	65/65	0.96	0.14	26,35,47,53	0
24	CLA	D	402	65/65	0.96	0.14	24,33,52,57	0
24	CLA	A	410	65/65	0.96	0.13	29,47,108,113	0
24	CLA	b	620	65/65	0.96	0.13	33,44,51,57	0
24	CLA	B	609	65/65	0.96	0.14	32,42,52,54	0
32	PL9	d	405[A]	55/55	0.96	0.16	25,35,44,49	55
26	BCR	B	619	40/40	0.96	0.14	26,36,55,58	0
25	PHO	A	408	64/64	0.96	0.13	26,32,38,43	0
24	CLA	A	406	65/65	0.96	0.14	24,32,38,45	0
24	CLA	c	506	65/65	0.96	0.13	38,50,63,69	0
24	CLA	d	402	65/65	0.96	0.13	26,35,54,64	0
28	GOL	b	604	6/6	0.96	0.16	41,56,70,75	0
24	CLA	A	405	65/65	0.96	0.14	25,32,41,57	0
24	CLA	a	412	65/65	0.96	0.15	32,45,111,115	0
28	GOL	V	204	6/6	0.96	0.12	55,61,65,65	0
24	CLA	B	611	65/65	0.96	0.13	35,44,50,57	0
26	BCR	A	411	40/40	0.96	0.15	29,37,44,45	0
28	GOL	B	629	6/6	0.96	0.13	43,47,50,52	0
32	PL9	d	405[B]	55/55	0.96	0.16	25,35,43,49	55
24	CLA	B	605	65/65	0.96	0.13	25,35,67,69	0
24	CLA	B	606	65/65	0.96	0.13	28,37,50,52	0
39	HEM	e	102	43/43	0.96	0.17	53,76,114,130	0
40	MG	j	103	1/1	0.96	0.17	55,55,55,55	0
28	GOL	C	525	6/6	0.96	0.12	39,48,50,51	0
23	BCT	a	419[A]	4/4	0.96	0.13	53,54,57,63	4
28	GOL	b	605	6/6	0.96	0.21	53,64,74,84	0
25	PHO	A	409[A]	64/64	0.96	0.14	29,40,44,47	64
26	BCR	a	413	40/40	0.97	0.12	28,38,46,47	0
26	BCR	b	627	40/40	0.97	0.14	30,39,47,47	0
24	CLA	A	407	65/65	0.97	0.12	27,37,90,96	0
25	PHO	a	411	64/64	0.97	0.14	26,34,40,45	0

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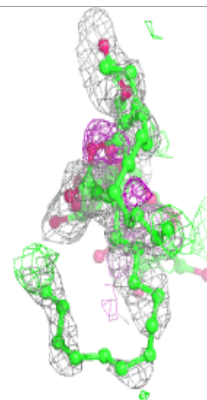
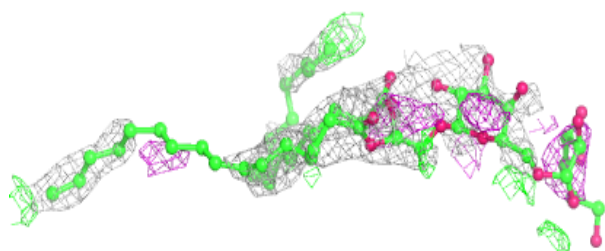
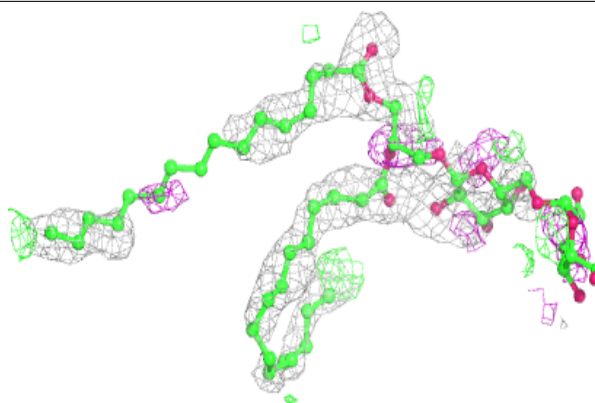
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
40	MG	J	102	1/1	0.97	0.09	50,50,50,50	0
26	BCR	b	629	40/40	0.97	0.14	37,48,60,64	0
26	BCR	B	618	40/40	0.97	0.14	28,37,45,45	0
24	CLA	B	613	65/65	0.97	0.12	27,36,45,47	0
24	CLA	C	502	65/65	0.97	0.12	36,44,55,70	0
39	HEM	v	205	43/43	0.98	0.11	41,49,55,57	0
28	GOL	c	501	6/6	0.98	0.14	43,46,52,53	0
35	CA	c	504	1/1	0.98	0.06	73,73,73,73	0
35	CA	o	302	1/1	0.98	0.06	86,86,86,86	0
23	BCT	A	404[A]	4/4	0.98	0.12	51,52,57,63	4
23	BCT	A	404[B]	4/4	0.98	0.12	51,52,57,63	4
22	CL	A	403[A]	1/1	0.98	0.12	33,33,33,33	1
35	CA	C	526	1/1	0.98	0.07	67,67,67,67	0
22	CL	U	201	1/1	0.98	0.17	93,93,93,93	0
22	CL	A	403[B]	1/1	0.98	0.12	33,33,33,33	1
39	HEM	V	206	43/43	0.98	0.12	34,39,47,50	0
35	CA	c	503	1/1	0.98	0.08	63,63,63,63	0
39	HEM	F	102	43/43	0.98	0.13	46,64,75,83	0
22	CL	A	402[A]	1/1	0.99	0.12	30,30,30,30	1
30	OEX	A	418[A]	10/10	0.99	0.13	31,35,38,46	10
22	CL	a	407[A]	1/1	0.99	0.09	34,34,34,34	1
22	CL	A	402[B]	1/1	0.99	0.12	31,31,31,31	1
35	CA	O	302	1/1	0.99	0.05	80,80,80,80	0
22	CL	a	408[A]	1/1	0.99	0.10	40,40,40,40	1
22	CL	a	407[B]	1/1	0.99	0.09	33,33,33,33	1
22	CL	a	408[B]	1/1	0.99	0.10	38,38,38,38	1
21	FE2	a	406[B]	1/1	0.99	0.13	46,46,46,46	0
31	OXY	A	419[B]	11/11	0.99	0.14	31,36,42,47	11
30	OEX	a	417[A]	10/10	0.99	0.12	31,37,39,45	10
31	OXY	a	418[B]	11/11	0.99	0.13	32,37,44,57	11
21	FE2	A	401[B]	1/1	1.00	0.11	47,47,47,47	1
21	FE2	A	401[A]	1/1	1.00	0.11	45,45,45,45	1

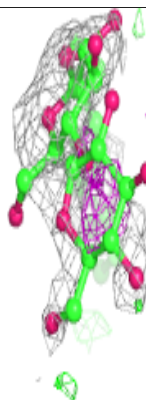
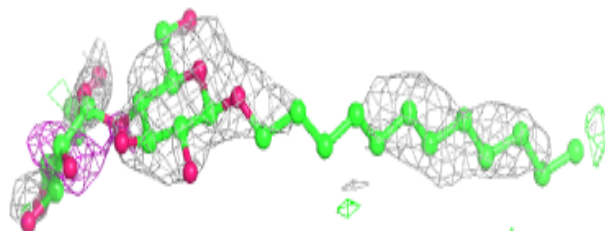
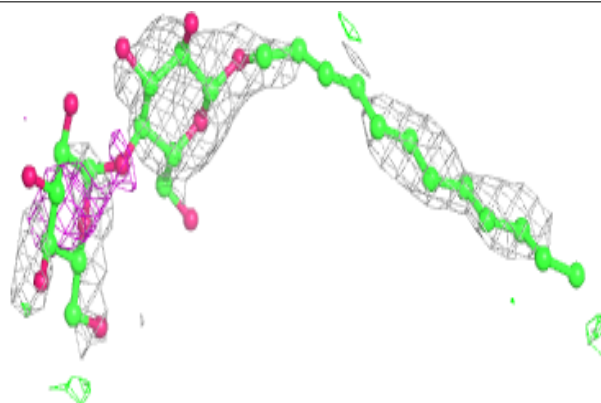
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around DGD e 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

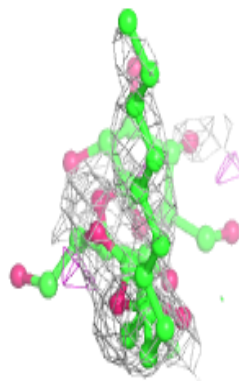
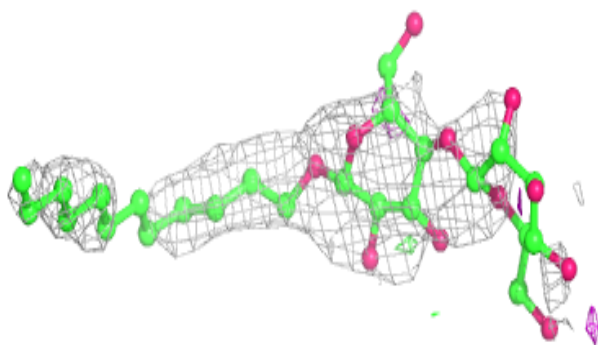
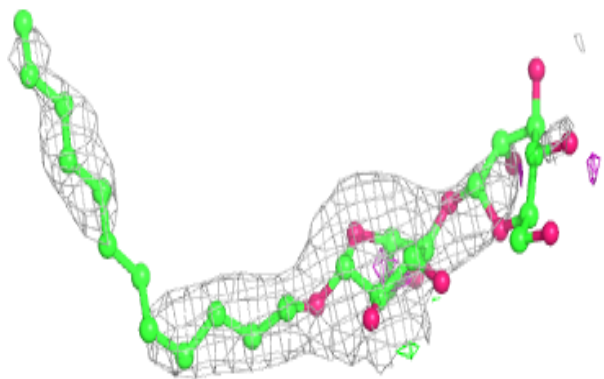
**Electron density around LMT F 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

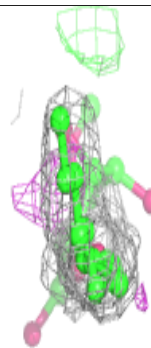
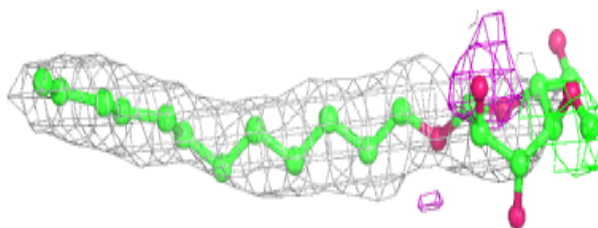
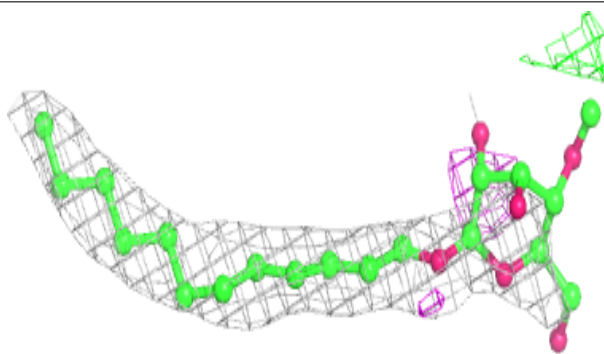


Electron density around LMT C 521:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

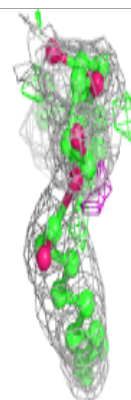
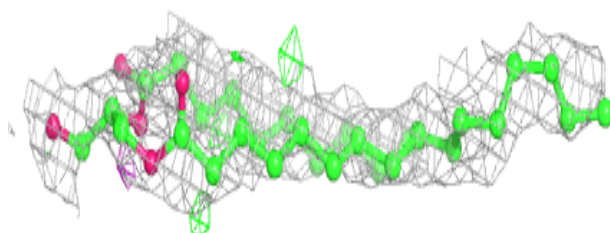
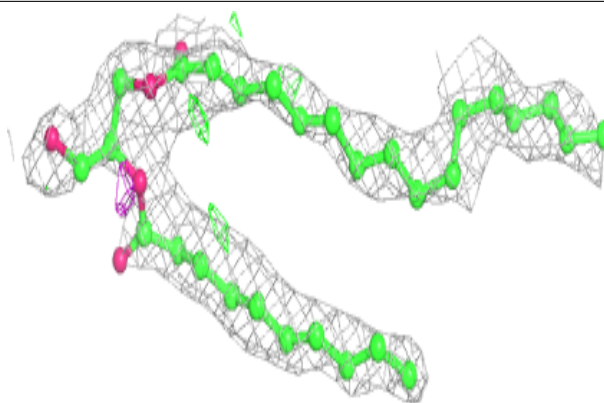
**Electron density around LMT b 631:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

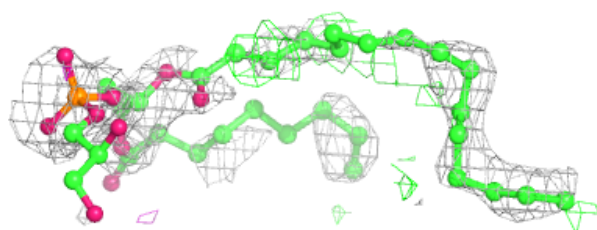
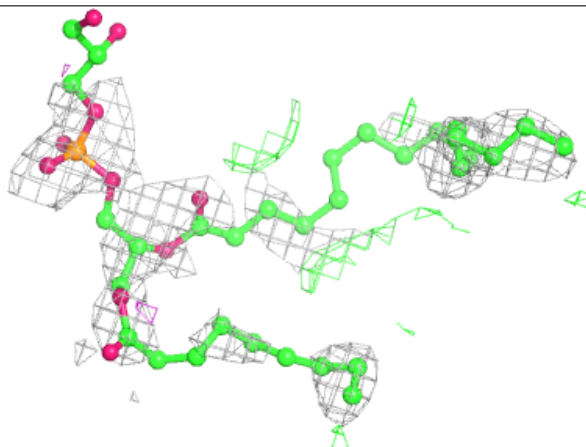


Electron density around UNL C 527:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

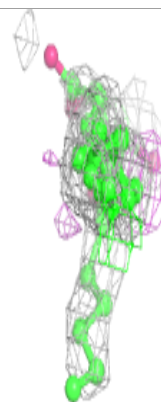
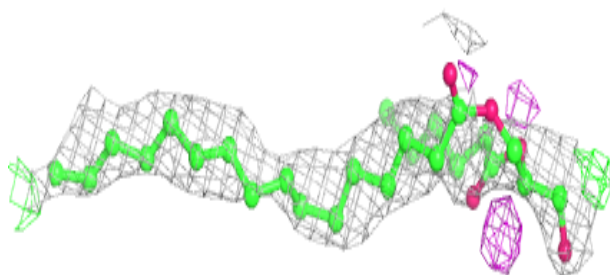
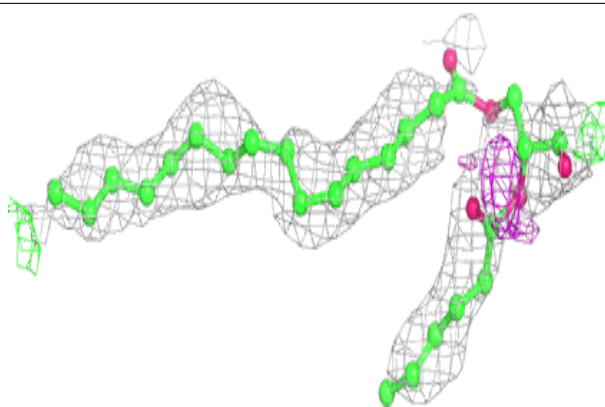
**Electron density around LHG a 422:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

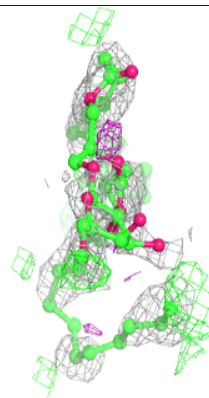
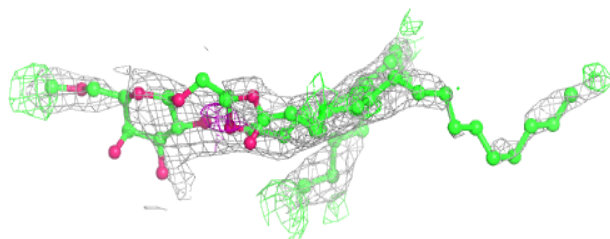
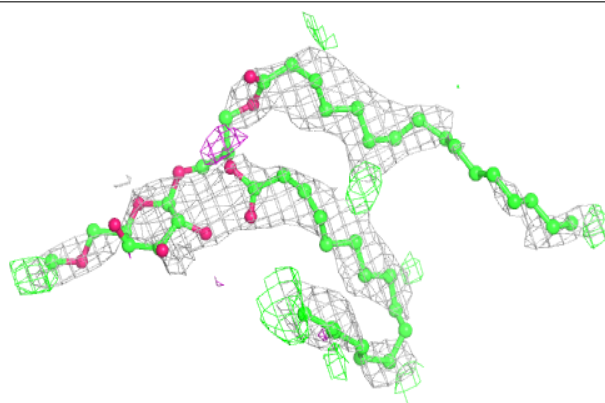


Electron density around UNL a 403:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

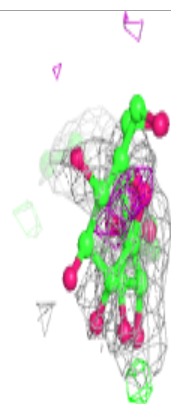
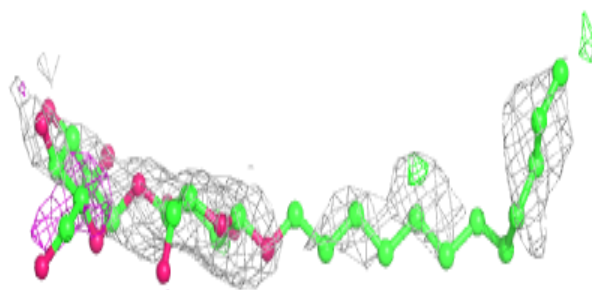
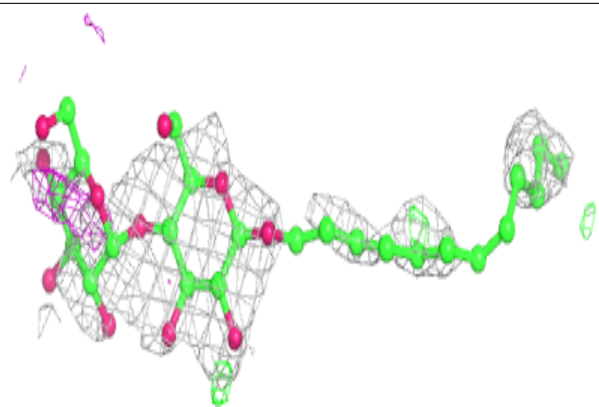
**Electron density around DGD D 406:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

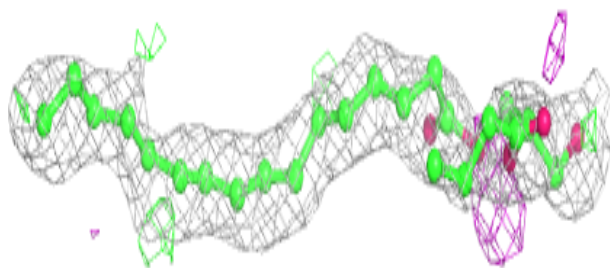
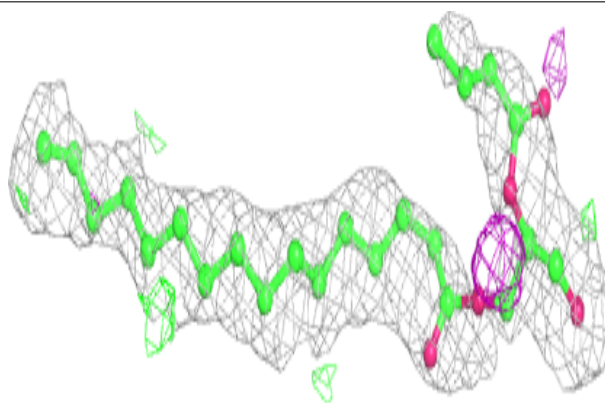


Electron density around LMT a 421:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

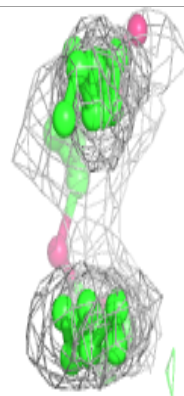
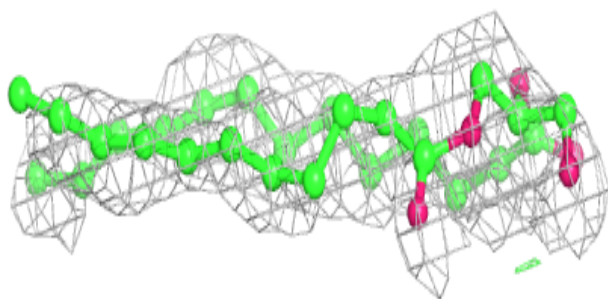
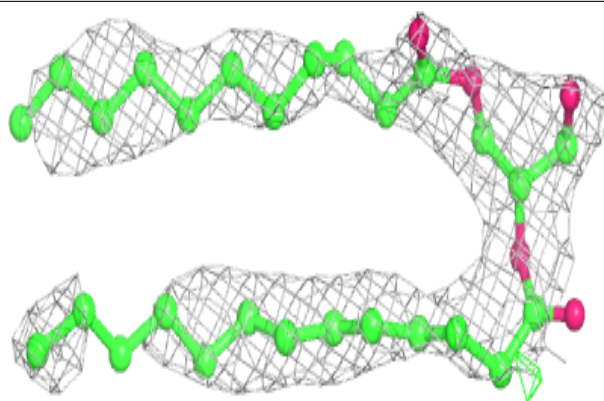
**Electron density around UNL A 421:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

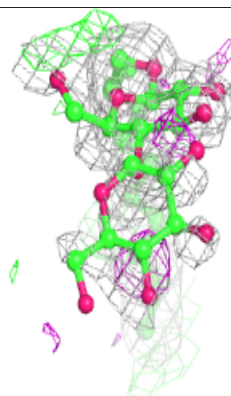
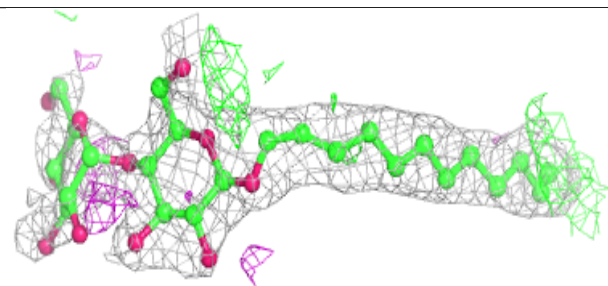
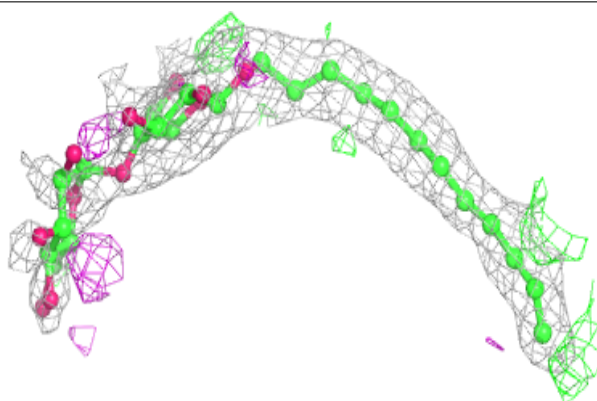


Electron density around UNL c 526:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

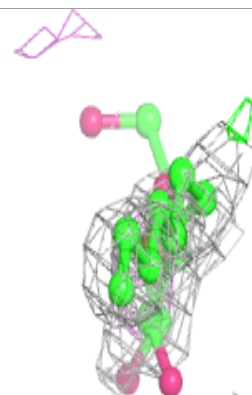
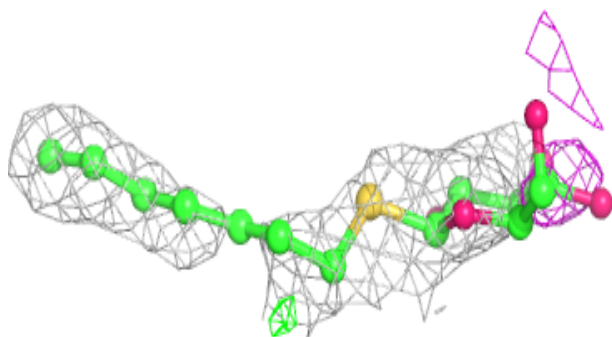
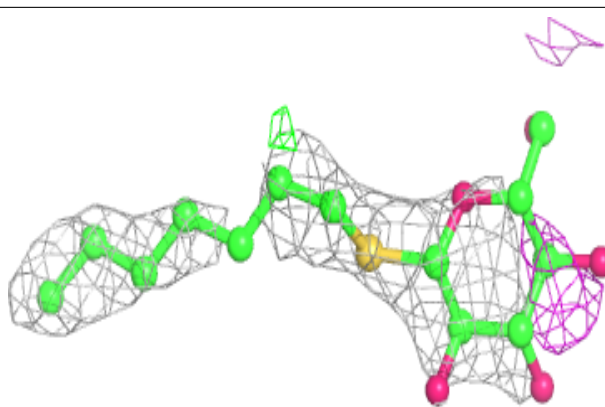
**Electron density around LMT M 103:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

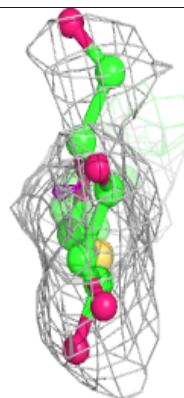
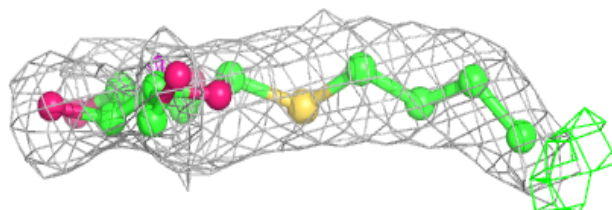
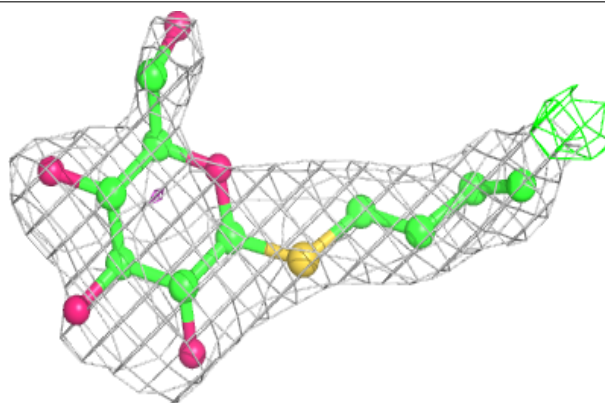


Electron density around HTG c 525:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

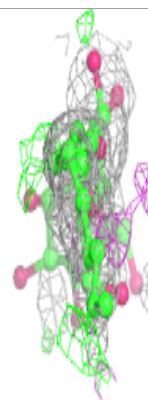
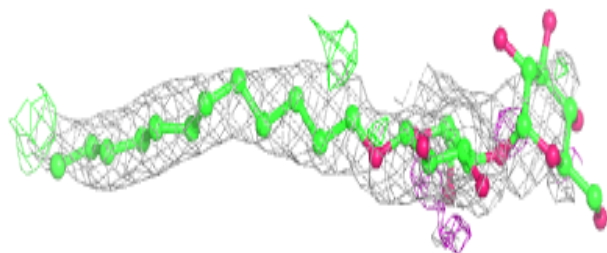
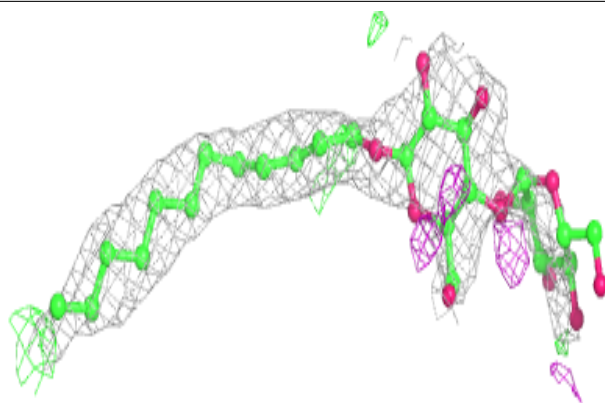
**Electron density around HTG d 411:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

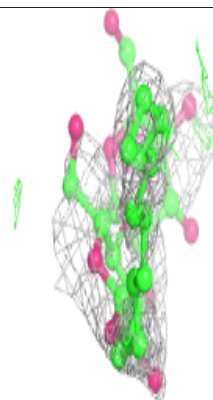
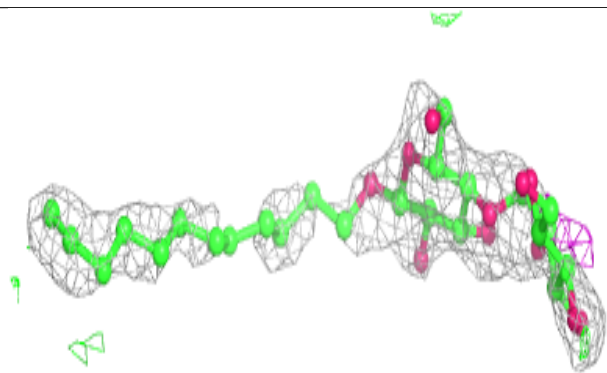
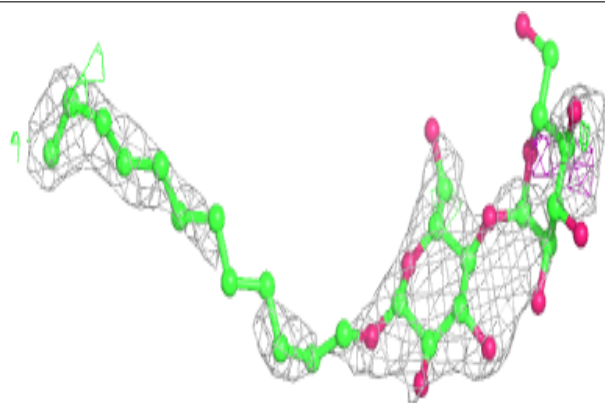


Electron density around LMT D 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

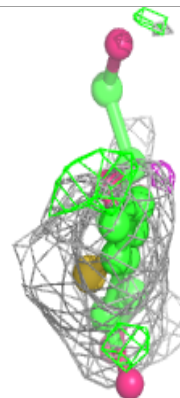
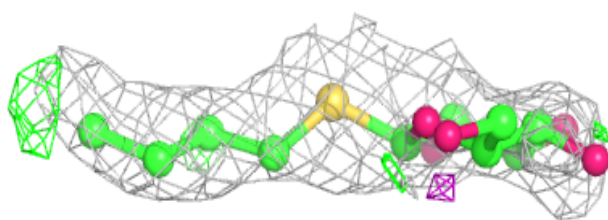
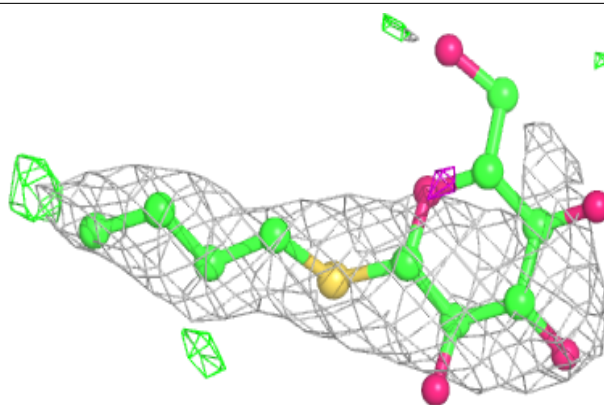
**Electron density around LMT f 103:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

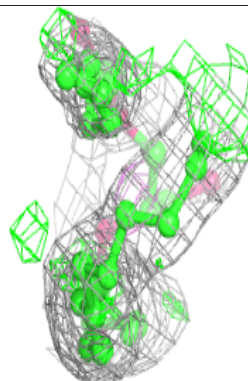
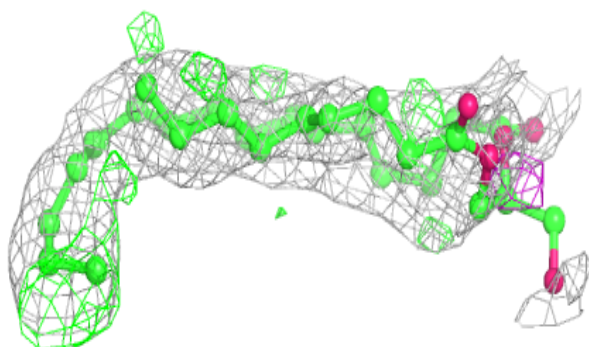
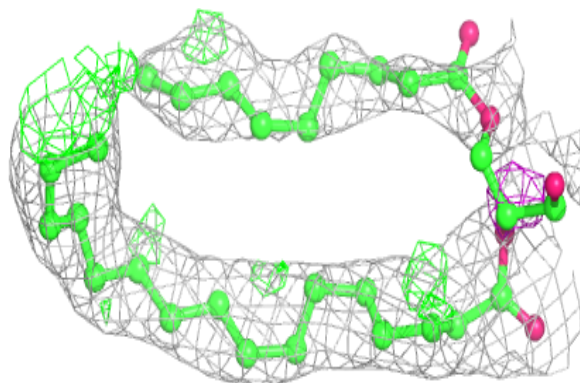


Electron density around HTG H 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

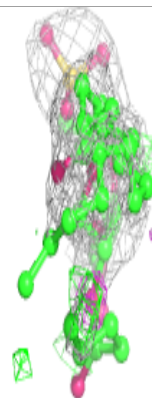
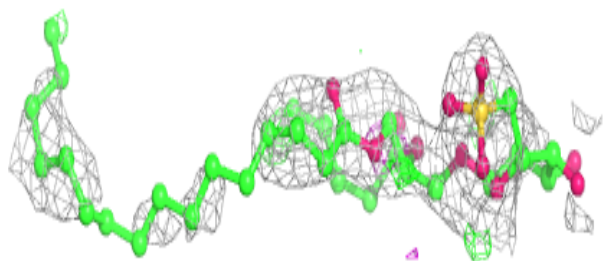
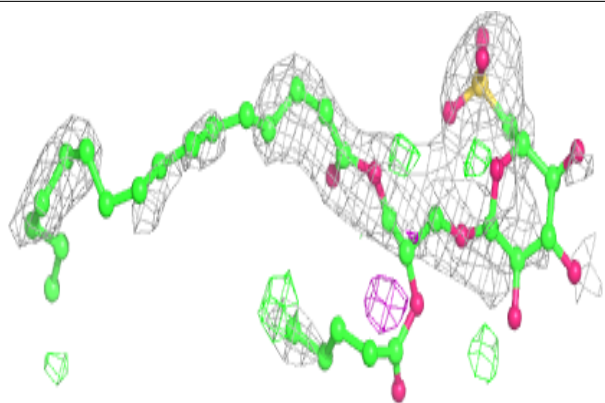
**Electron density around UNL B 634:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

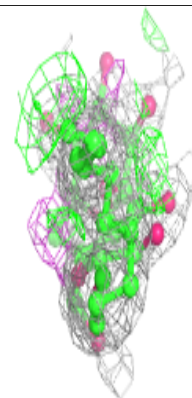
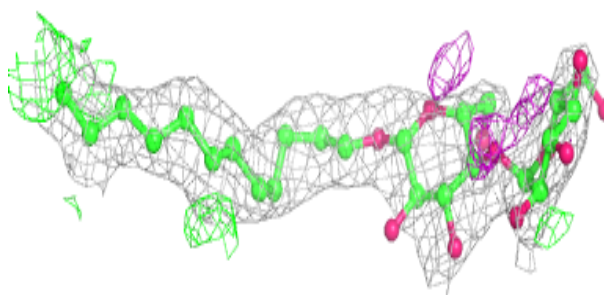
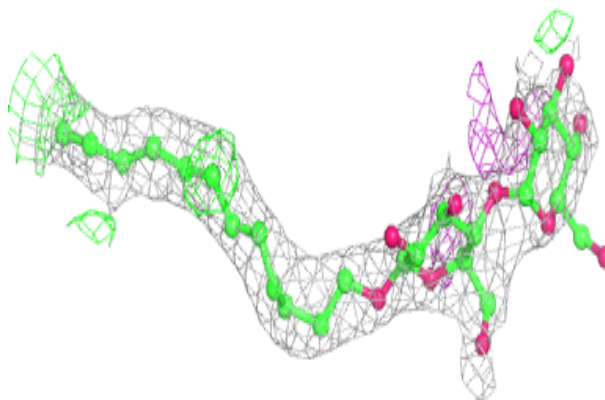


Electron density around SQD f 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

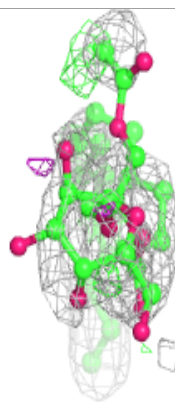
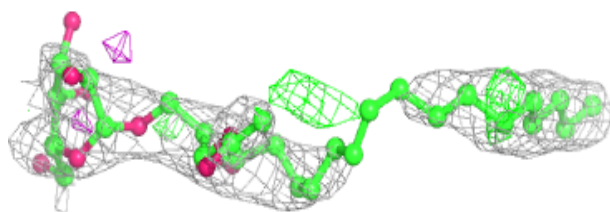
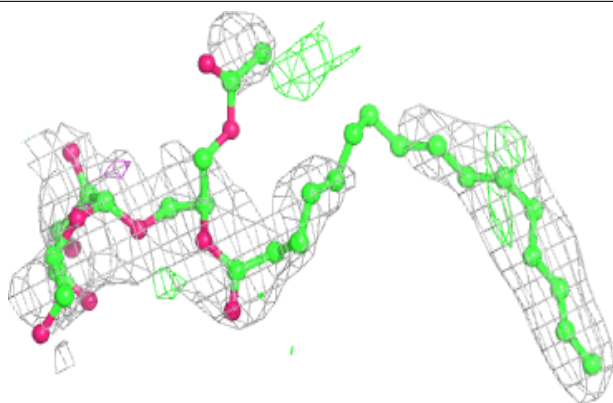
**Electron density around LMT a 404:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

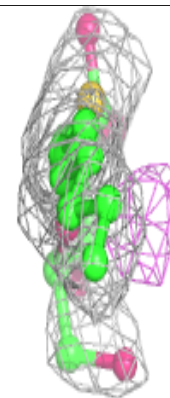
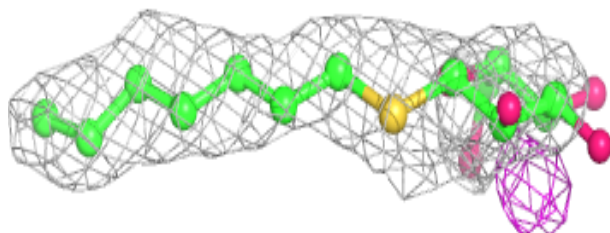
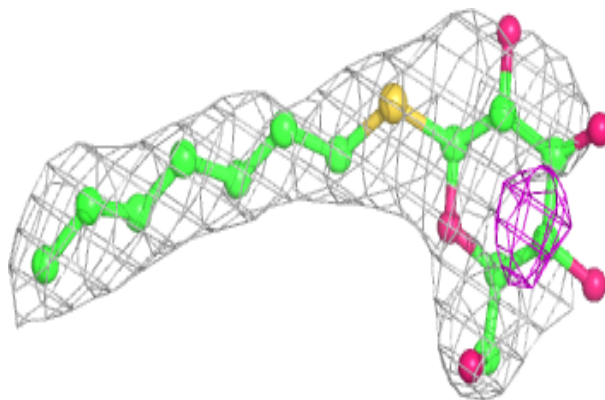


Electron density around LMG Z 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

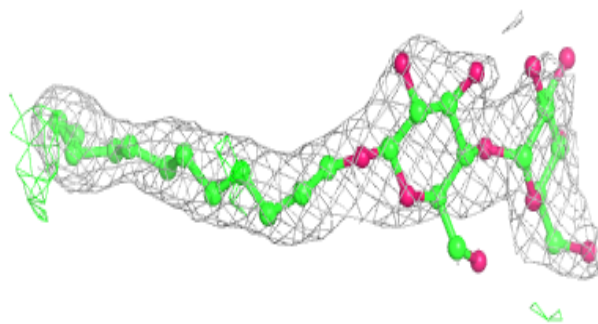
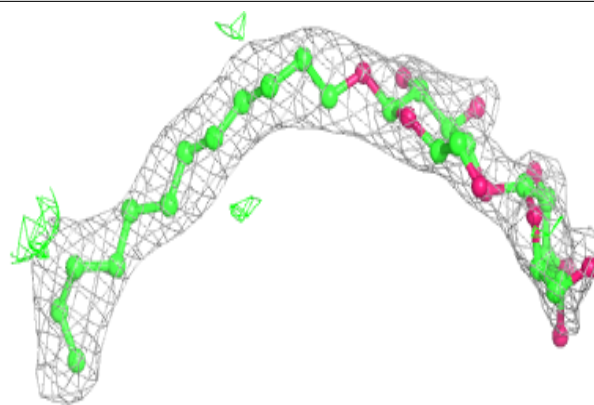
**Electron density around HTG b 609:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

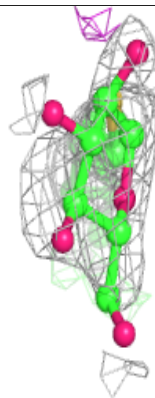
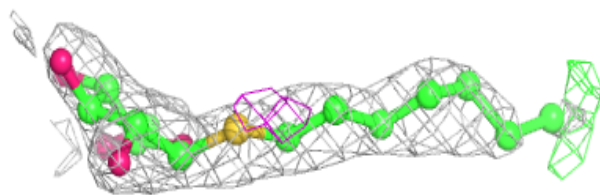
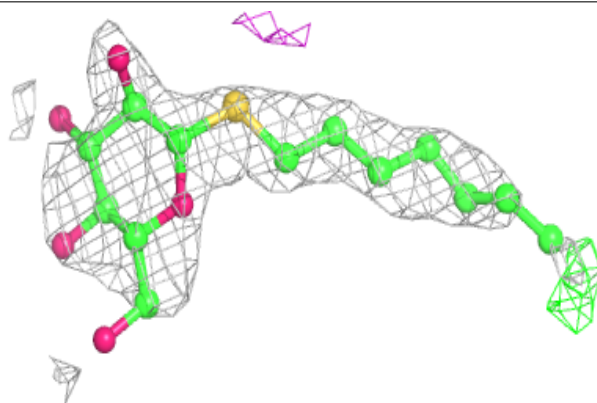


Electron density around LMT m 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

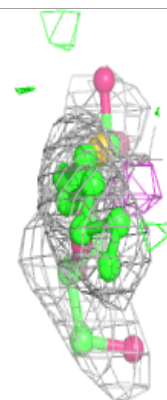
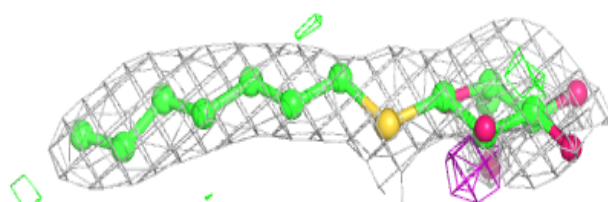
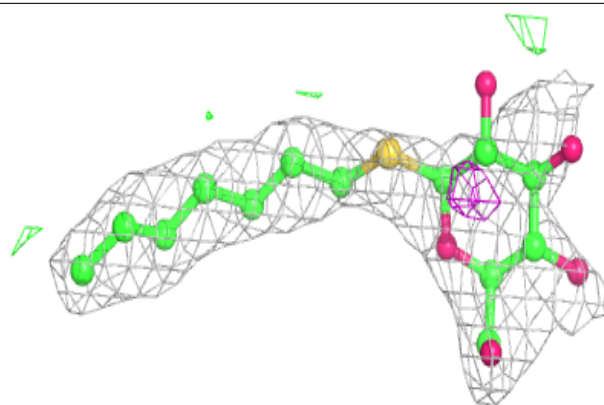
**Electron density around HTG B 625:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

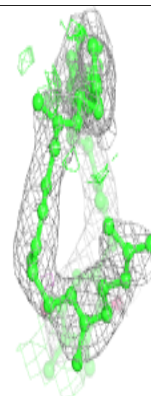
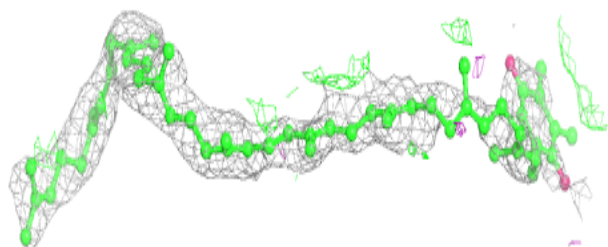
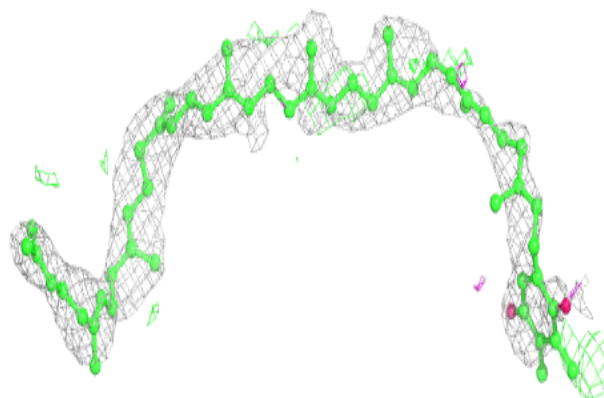


Electron density around HTG B 633:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

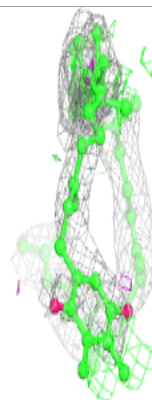
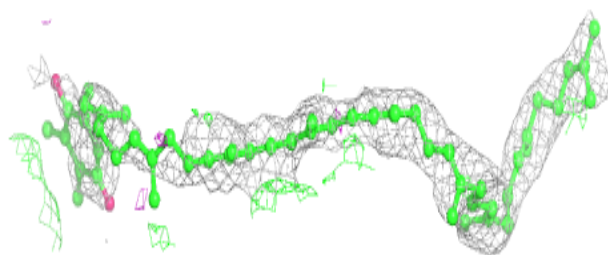
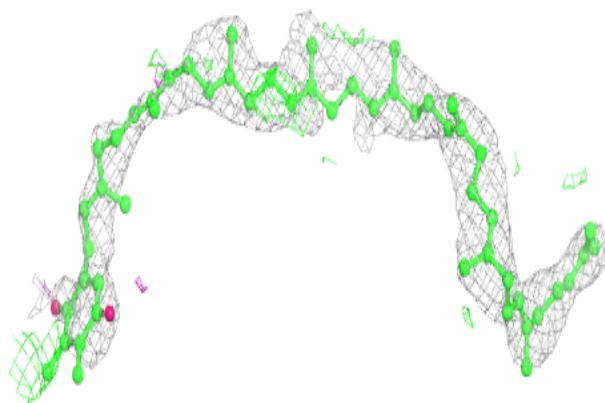
**Electron density around PL9 a 416 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



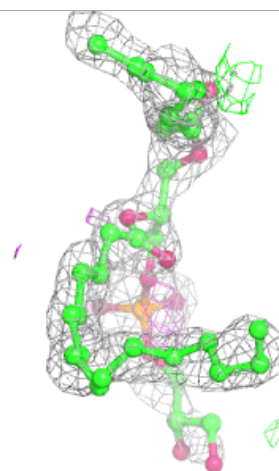
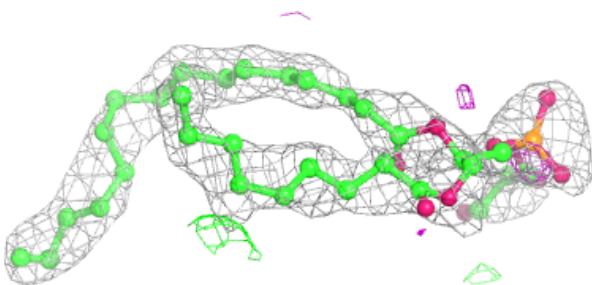
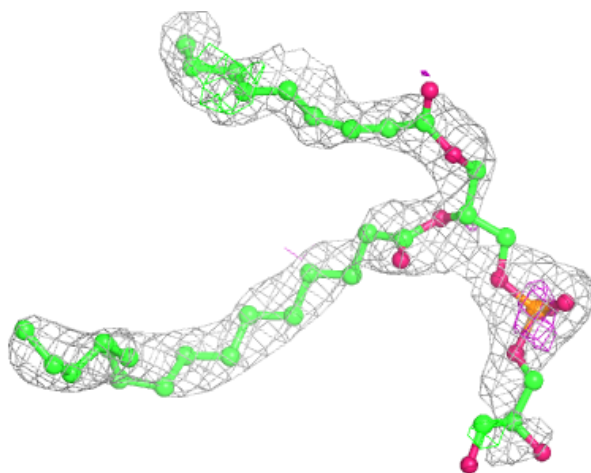
Electron density around PL9 a 416 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



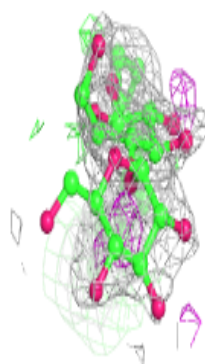
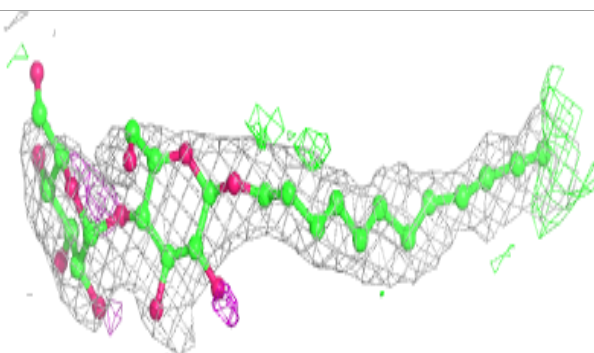
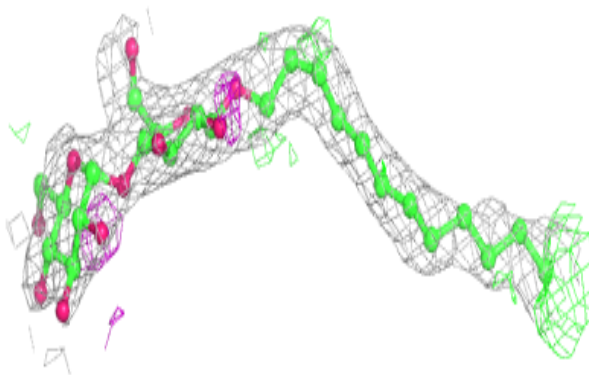
Electron density around LHG E 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

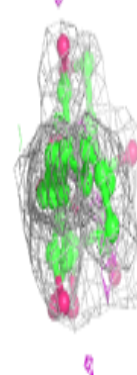
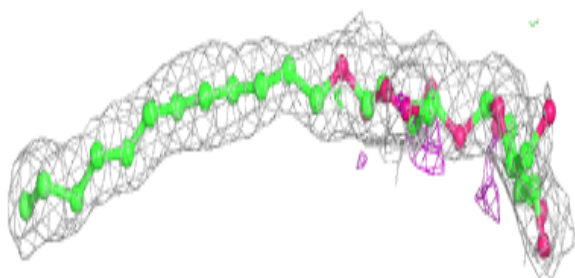
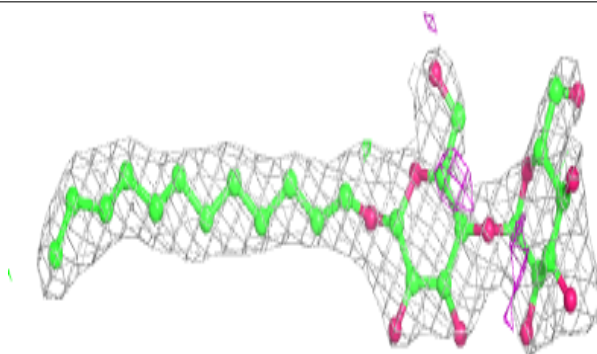


Electron density around LMT A 417:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

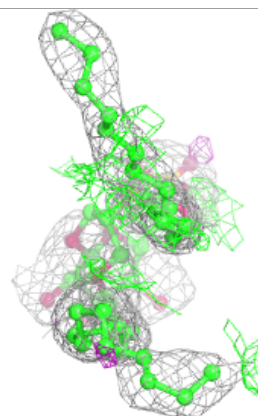
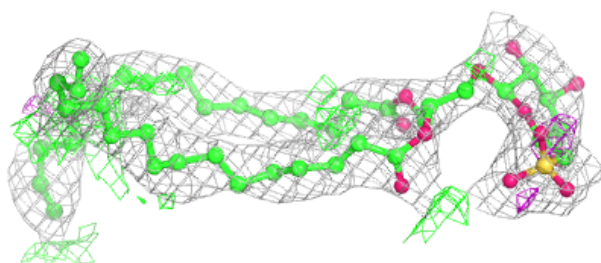
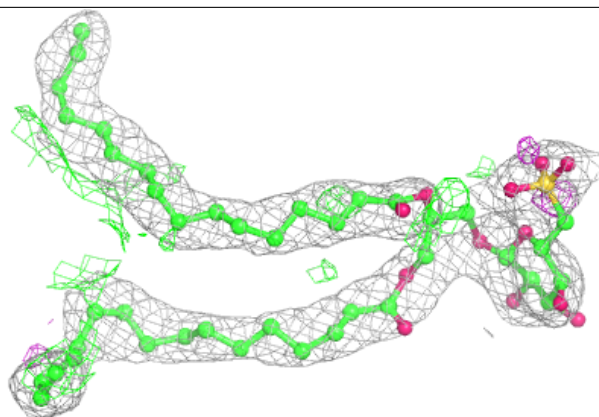
**Electron density around LMT M 104:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

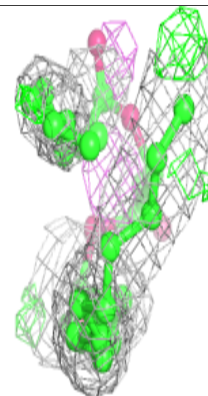
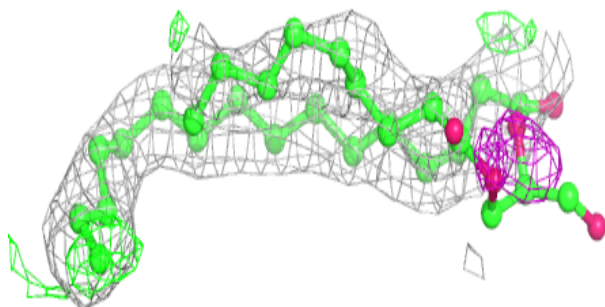
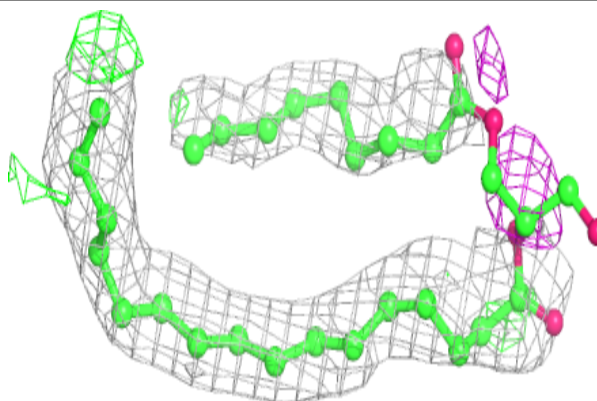


Electron density around SQD b 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

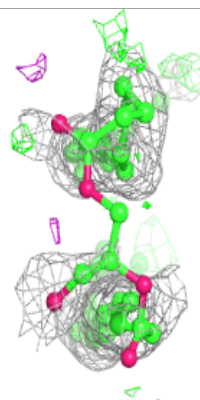
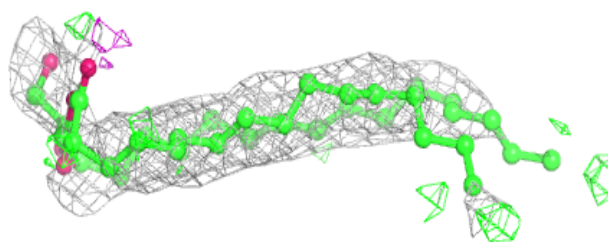
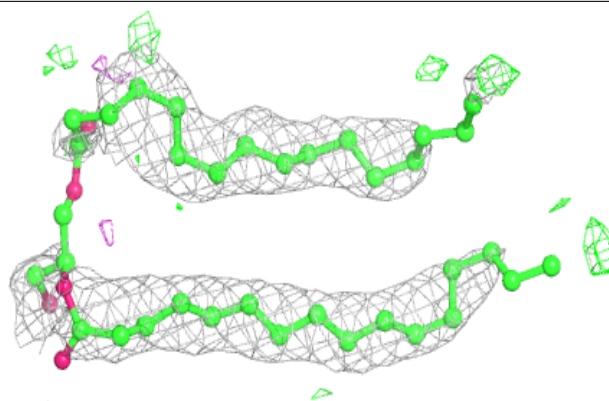
**Electron density around UNL b 634:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

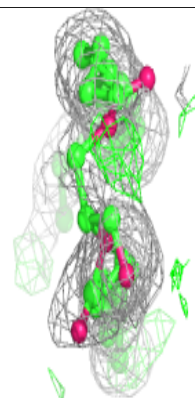
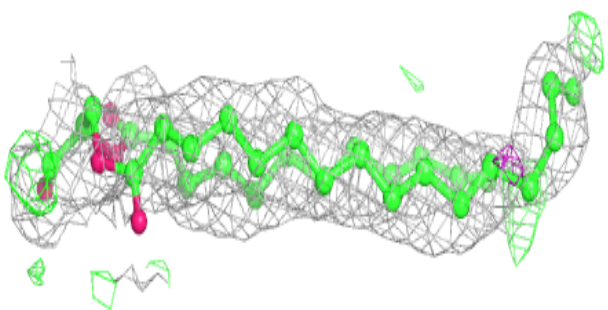
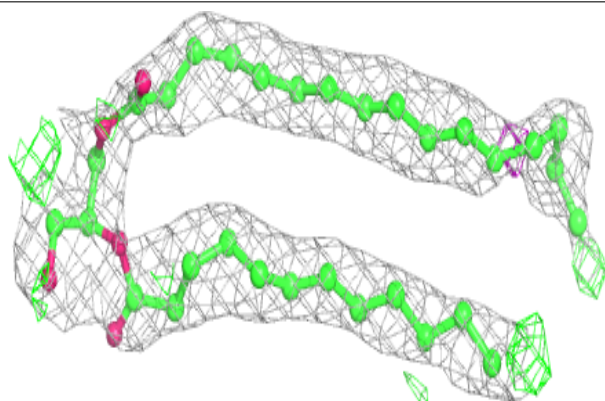


Electron density around UNL I 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

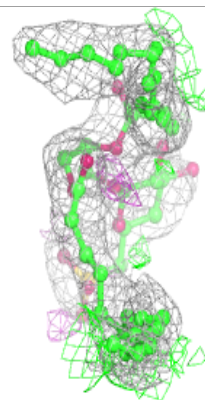
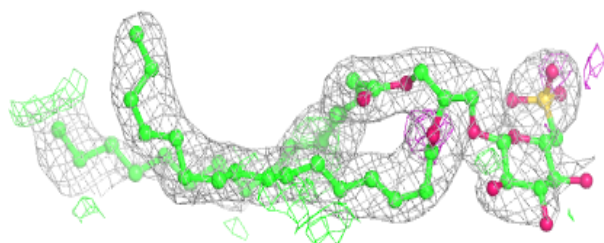
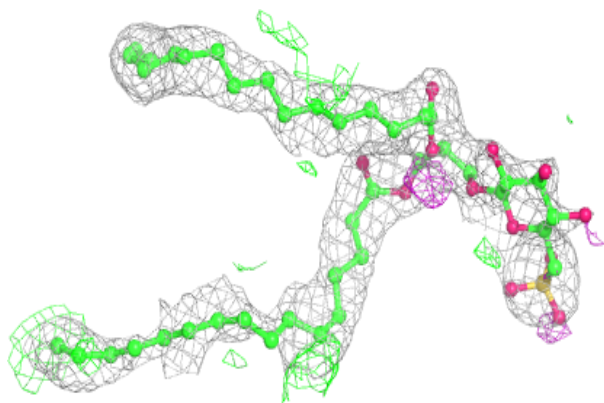
**Electron density around UNL d 410:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

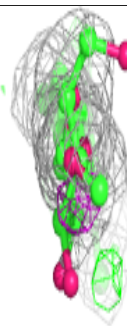
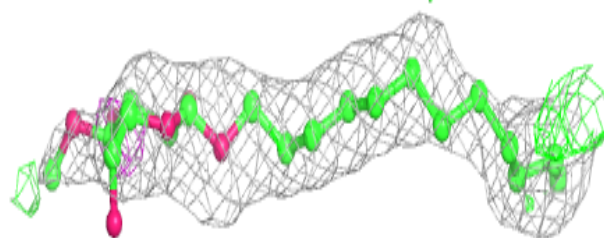
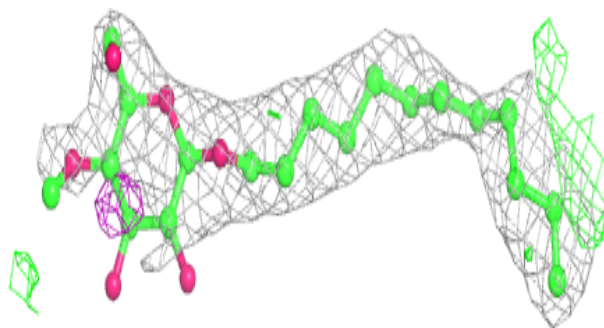


Electron density around SQD A 416:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

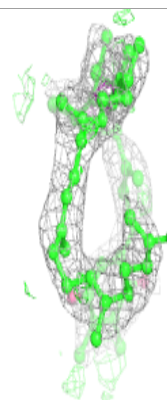
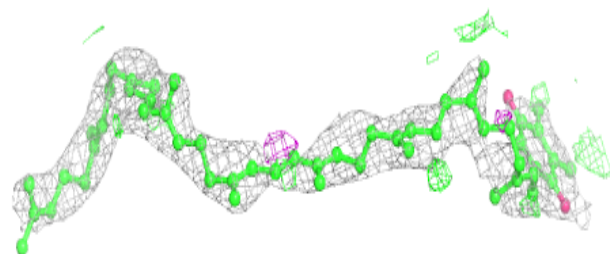
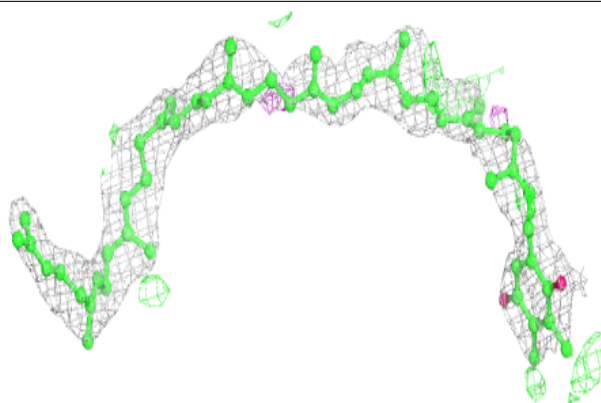
**Electron density around LMT T 104:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

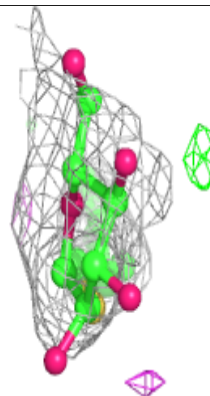
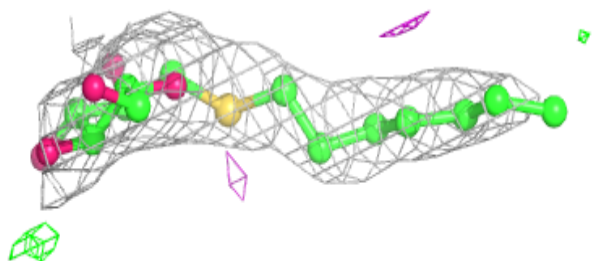
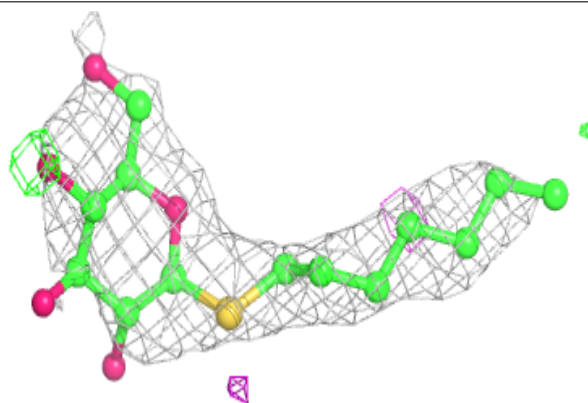


Electron density around PL9 A 420 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

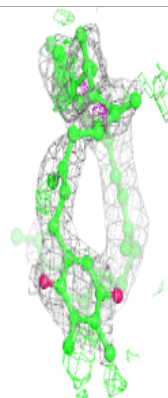
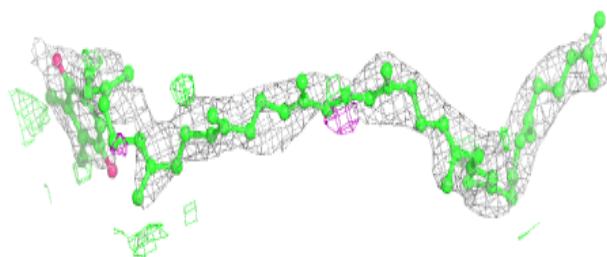
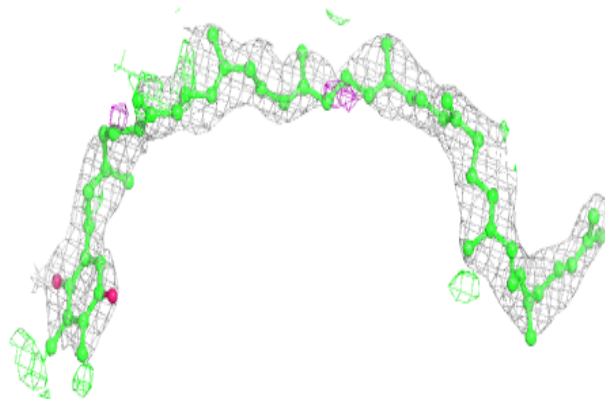
**Electron density around HTG b 633:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

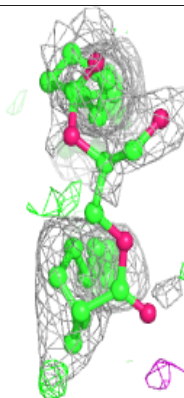
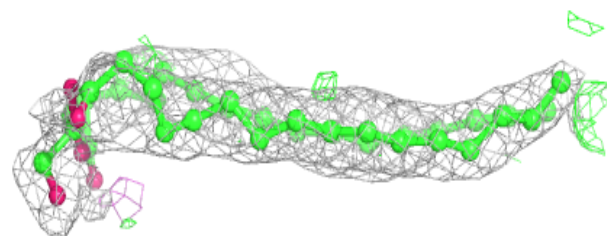
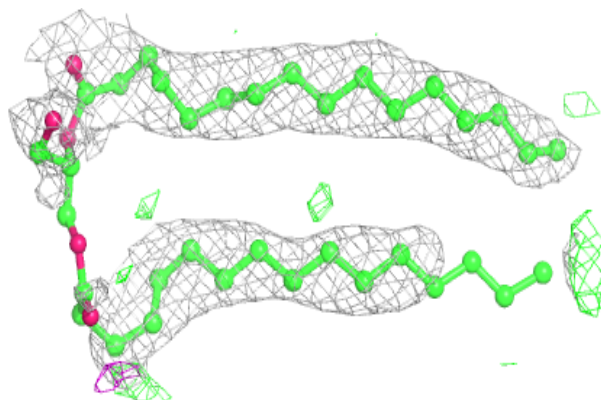


Electron density around PL9 A 420 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

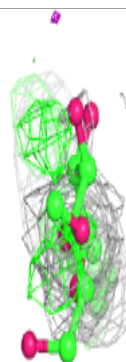
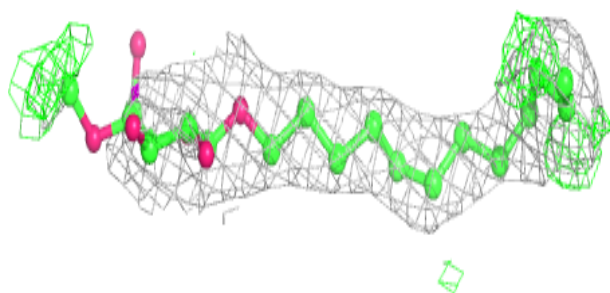
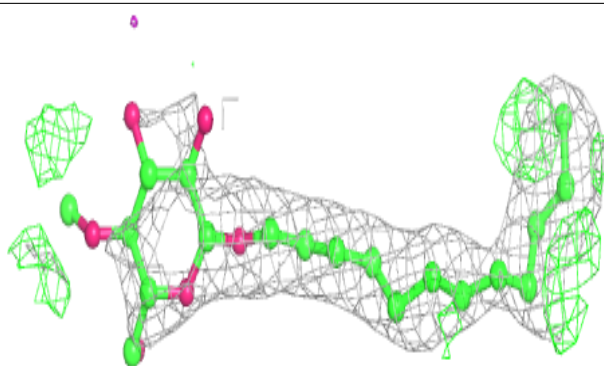
**Electron density around UNL i 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

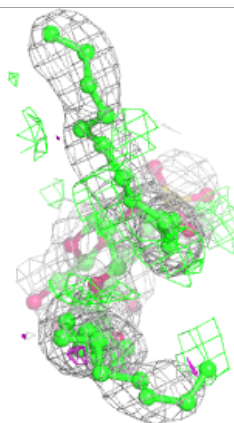
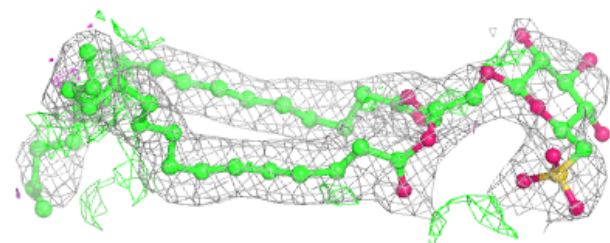
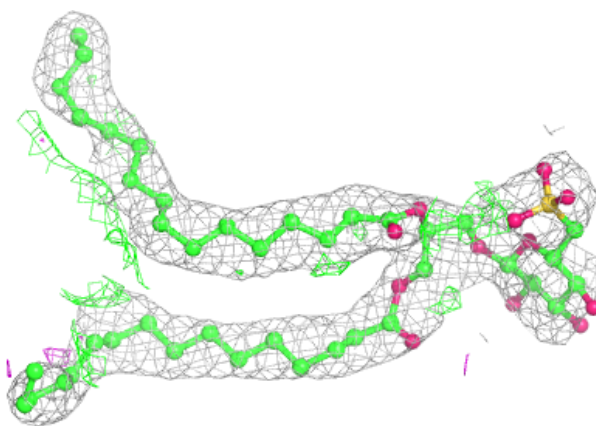


Electron density around LMT B 635:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

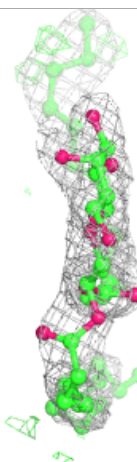
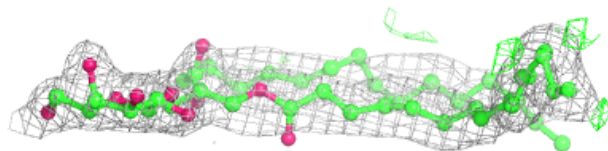
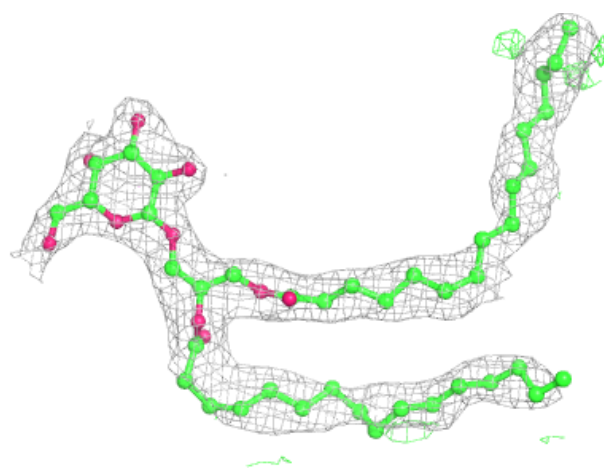
**Electron density around SQD B 621:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



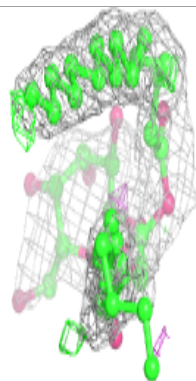
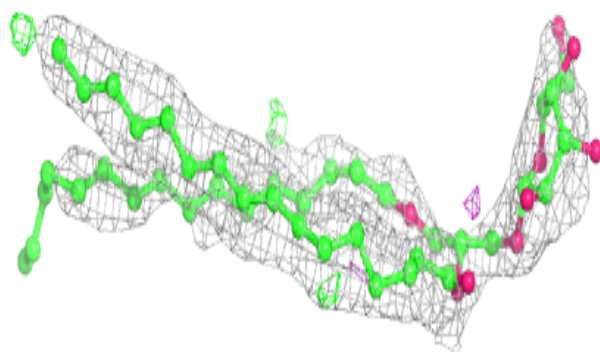
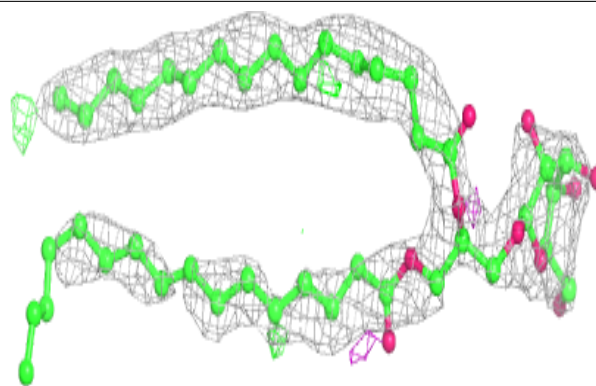
Electron density around LMG C 519:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

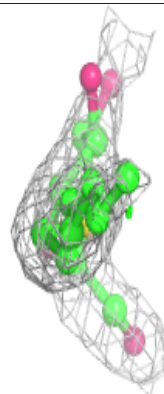
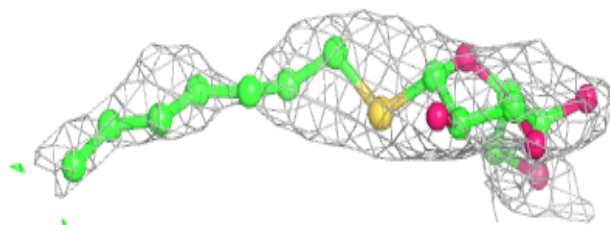
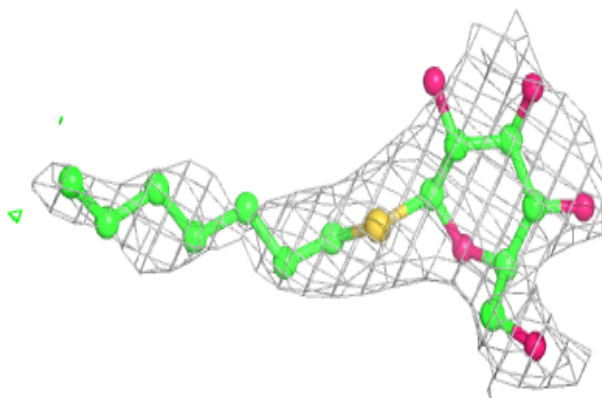


Electron density around LMG C 520:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

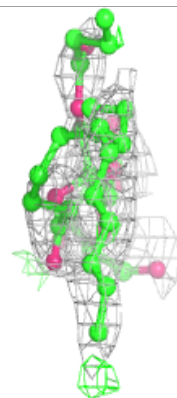
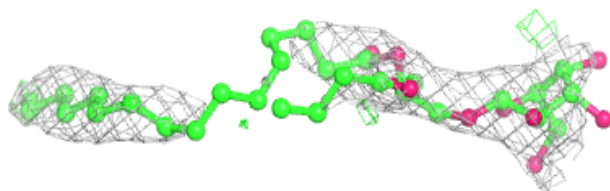
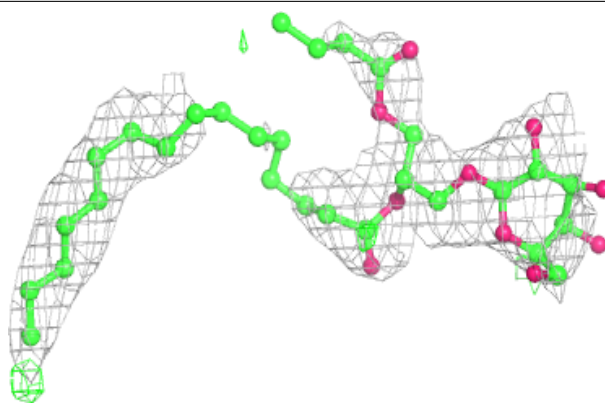
**Electron density around HTG C 523:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

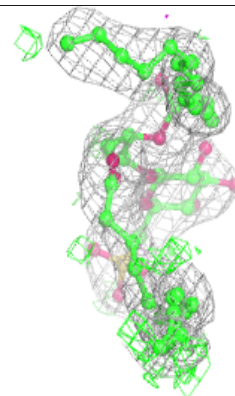
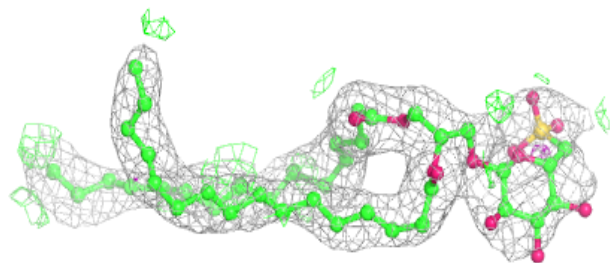
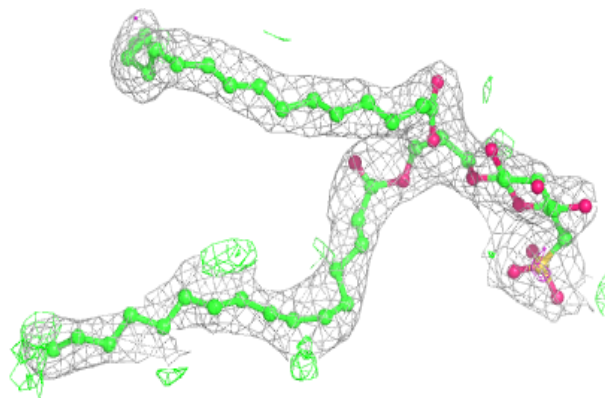


Electron density around LMG z 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

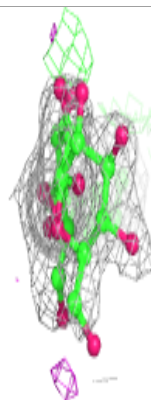
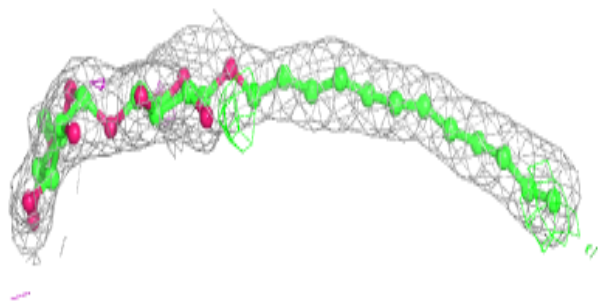
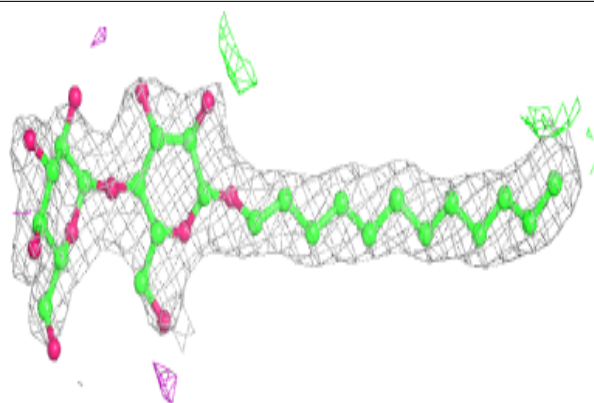
**Electron density around SQD a 405:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

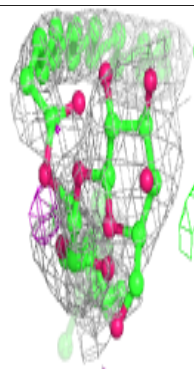
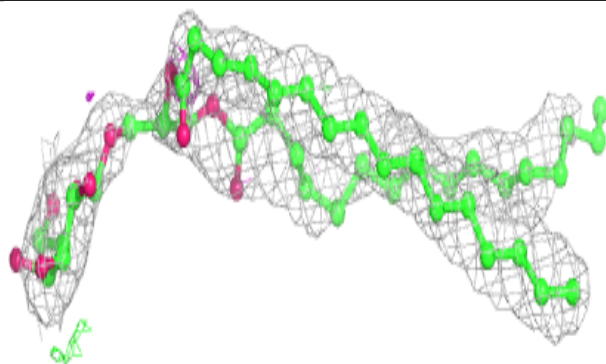
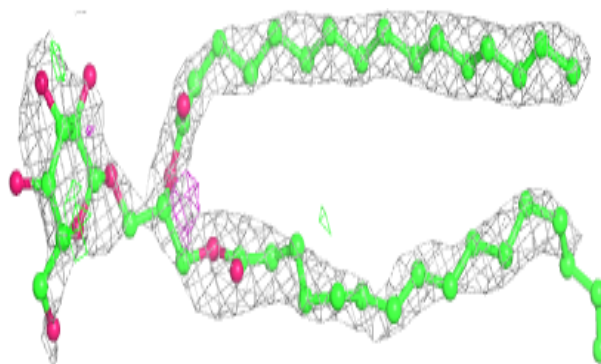


Electron density around LMT M 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

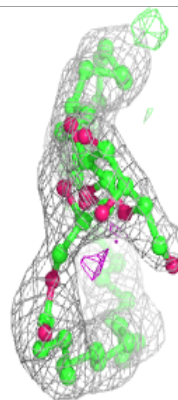
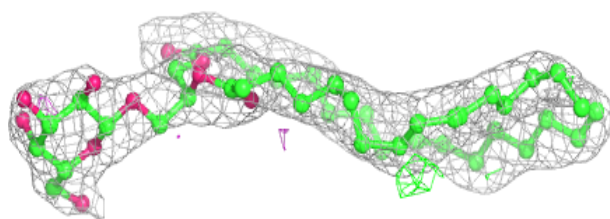
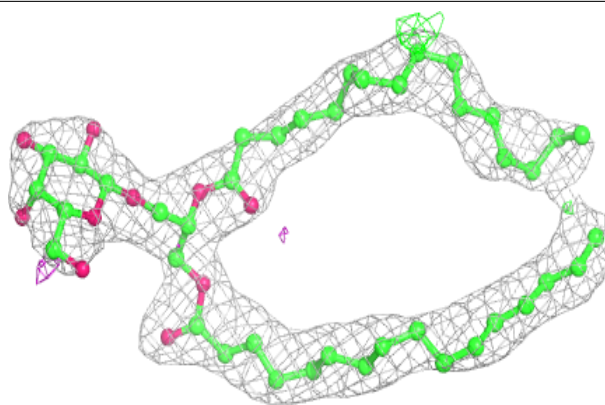
**Electron density around LMG c 523:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

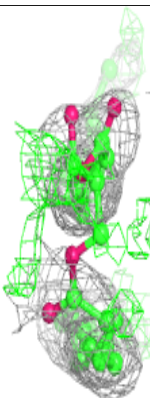
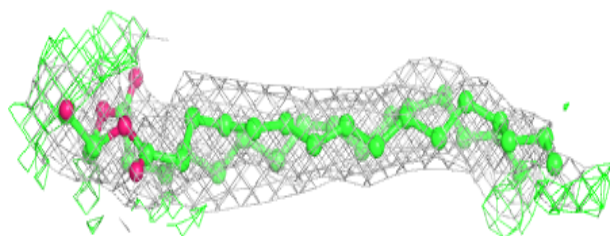
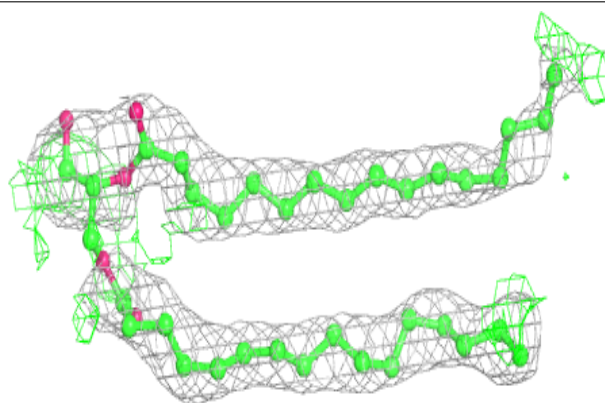


Electron density around LMG a 415:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

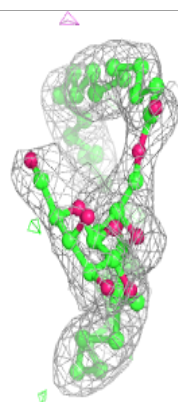
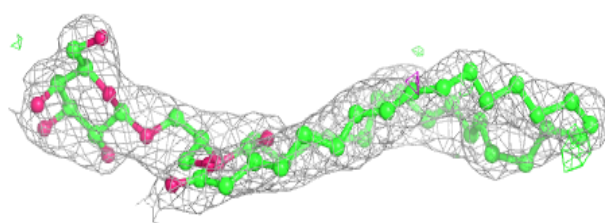
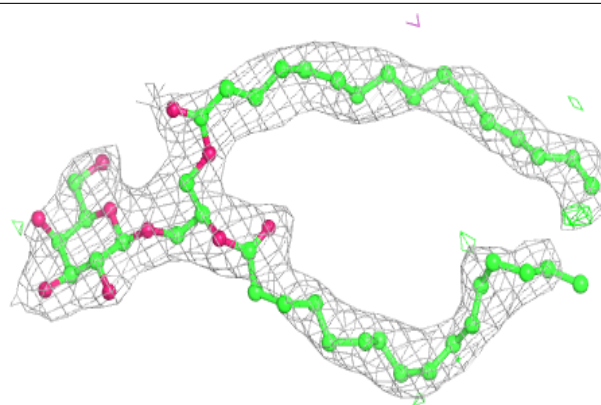
**Electron density around UNL D 411:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

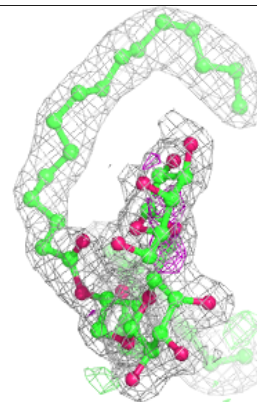
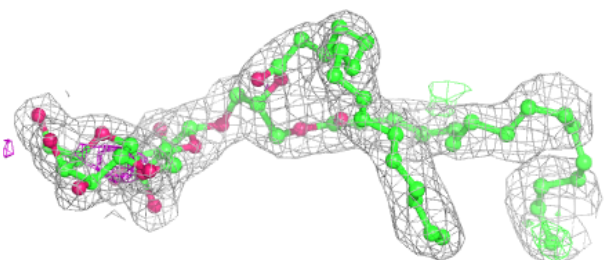
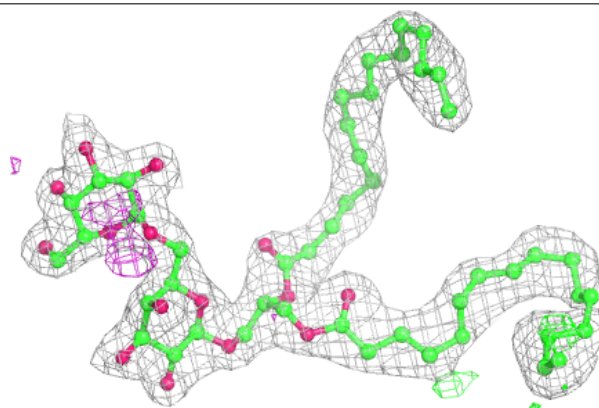


Electron density around LMG A 422:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

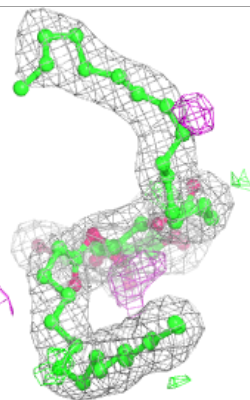
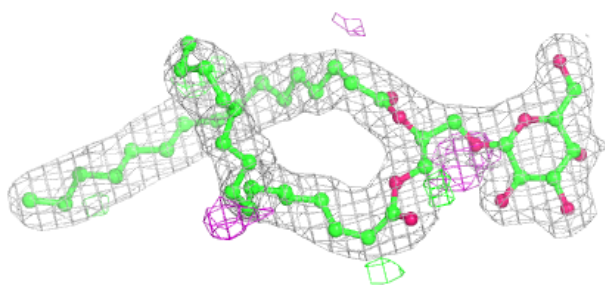
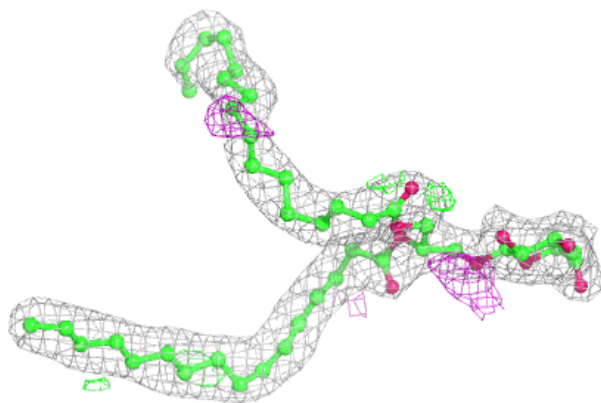
**Electron density around DGD C 517:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



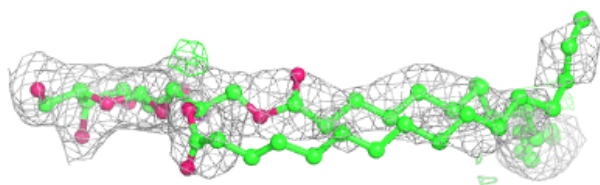
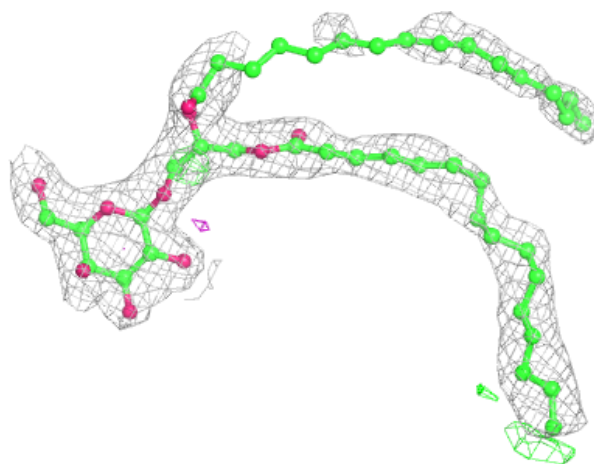
Electron density around LMG b 630:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



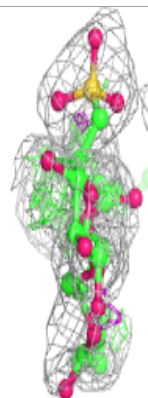
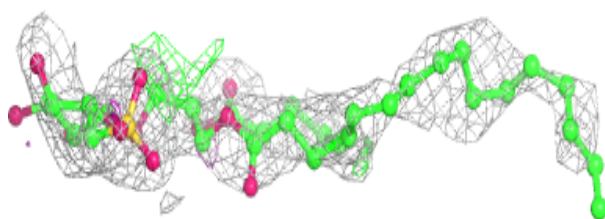
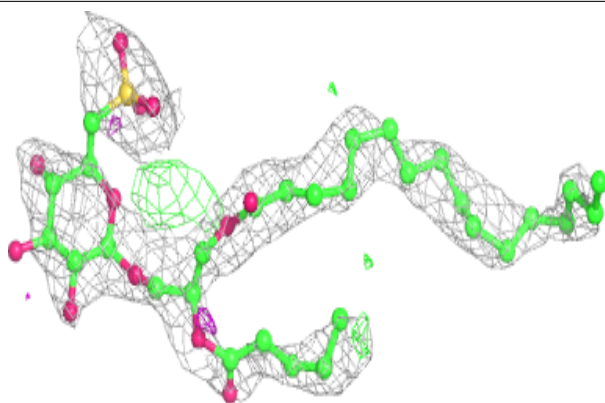
Electron density around LMG c 522:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

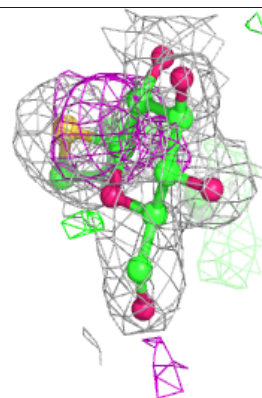
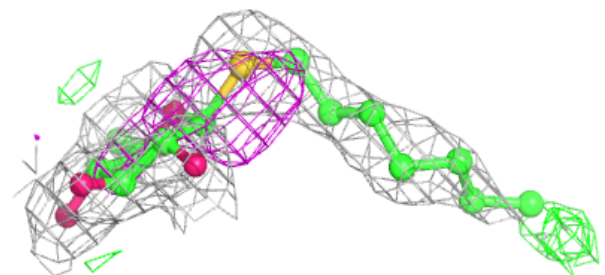
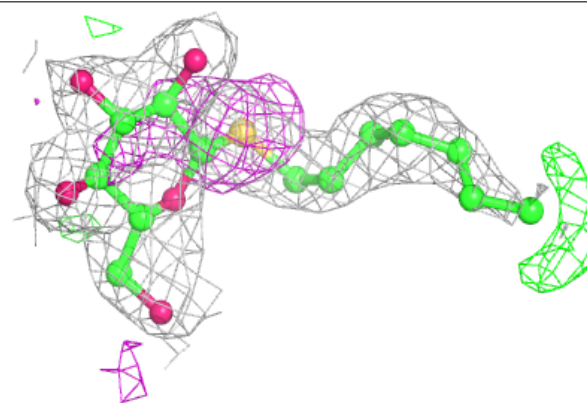


Electron density around SQD F 103:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

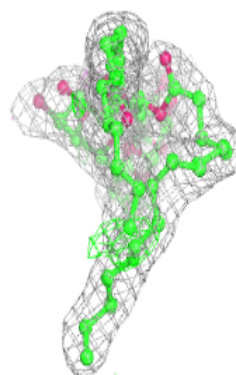
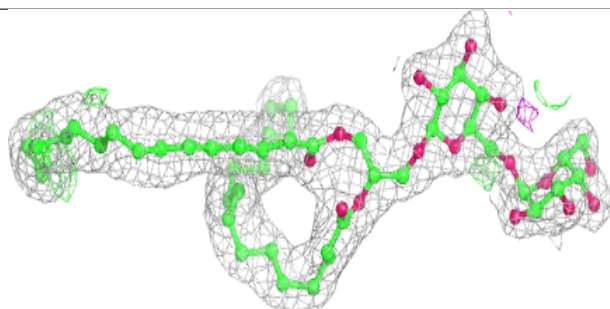
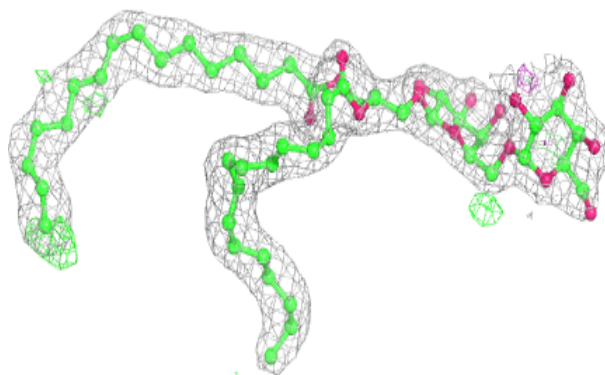
**Electron density around HTG b 632:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

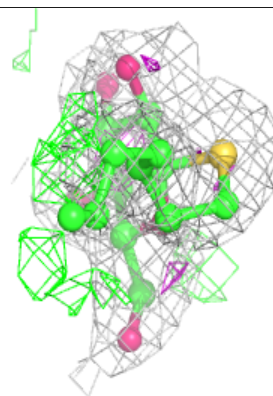
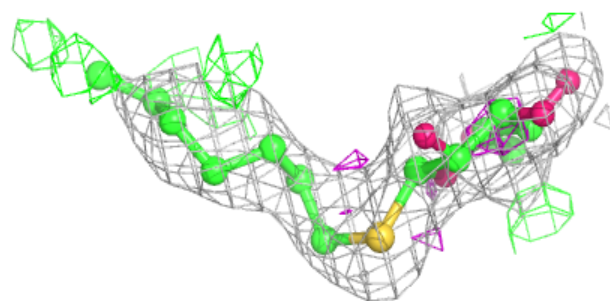
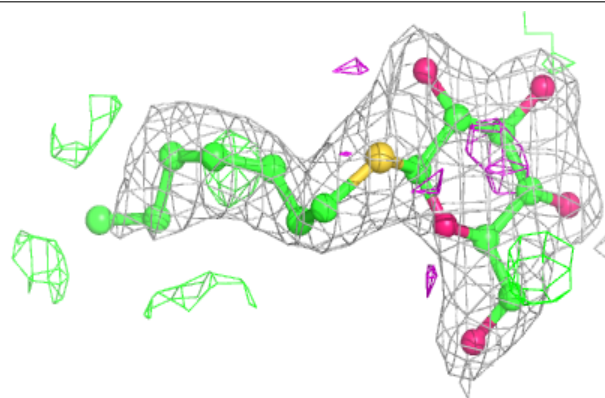


Electron density around DGD h 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

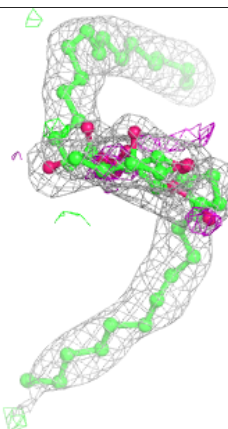
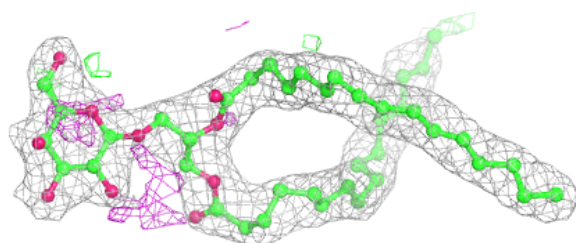
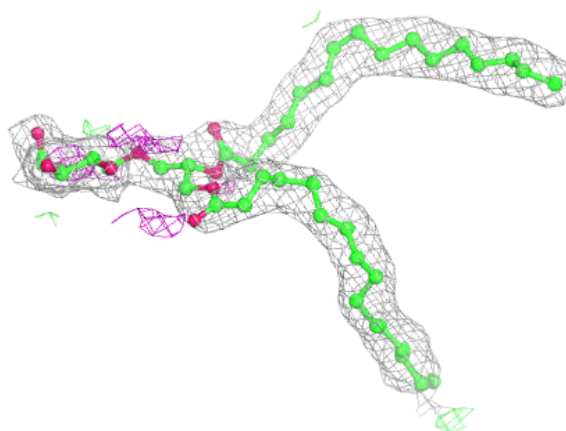
**Electron density around HTG B 624:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

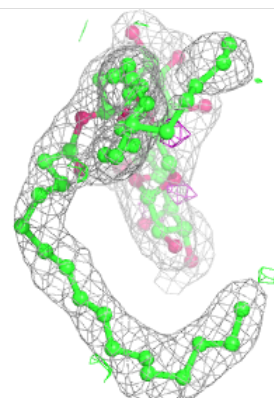
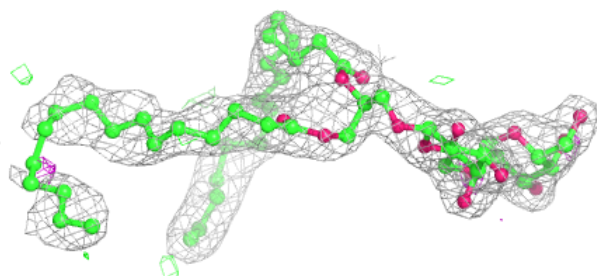
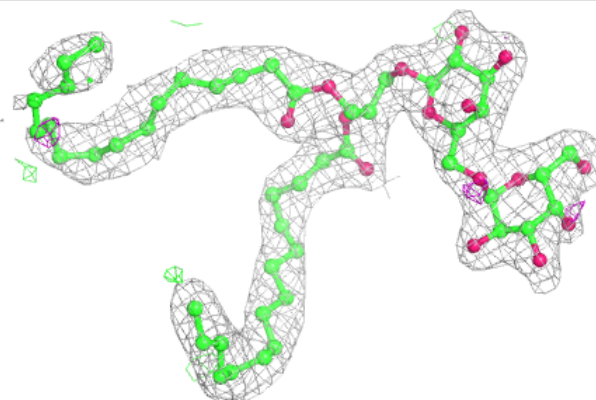


Electron density around LMG B 622:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

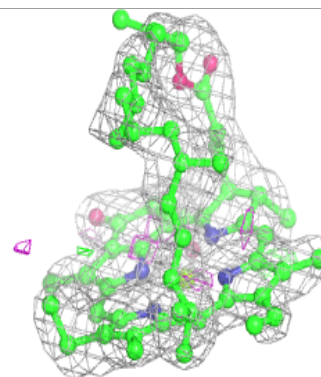
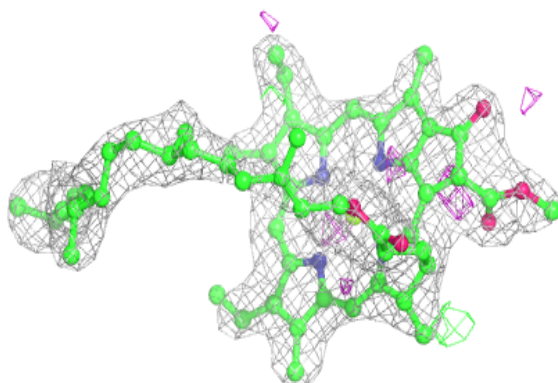
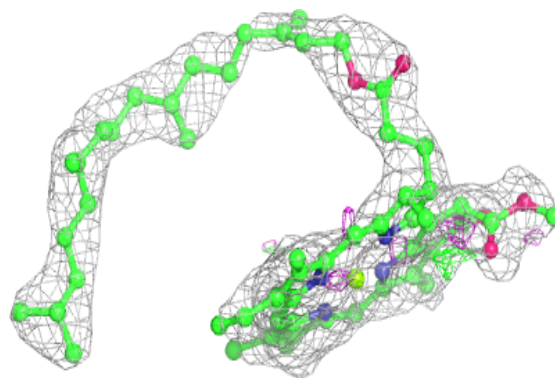
**Electron density around DGD c 520:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

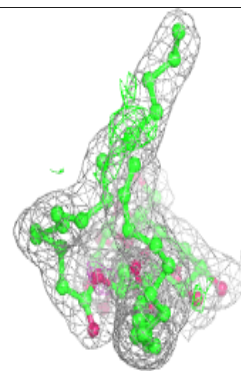
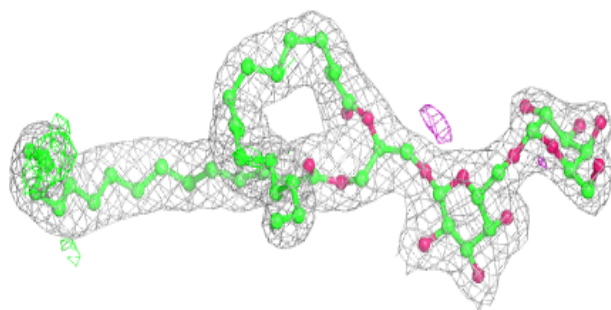
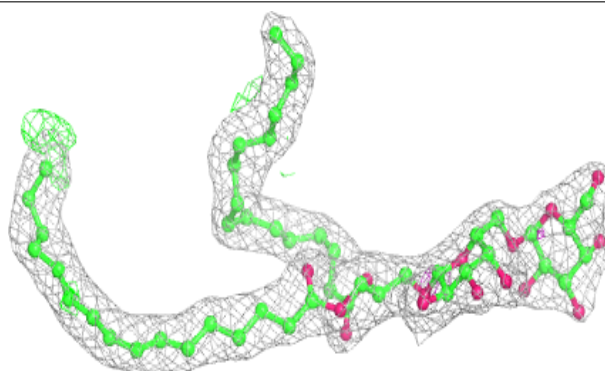


Electron density around CLA C 513:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

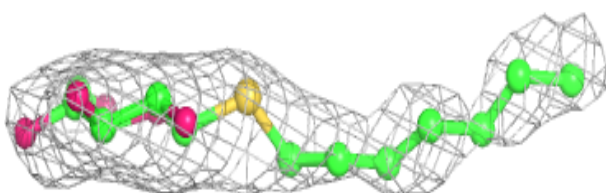
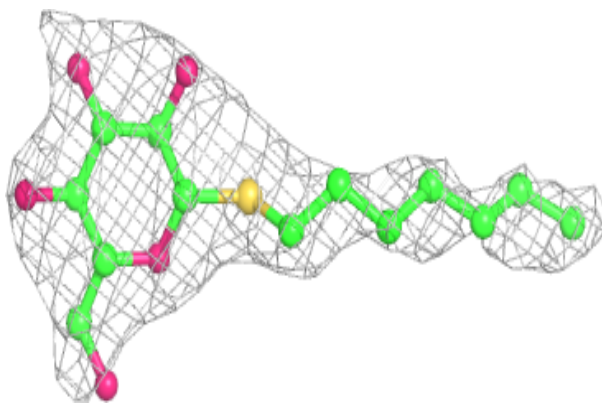
**Electron density around DGD H 103:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



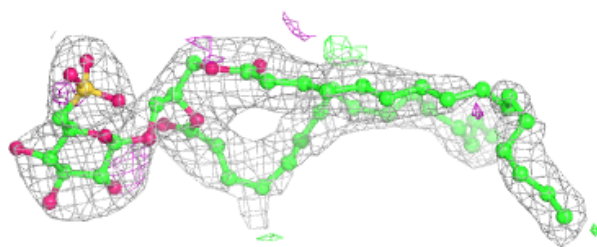
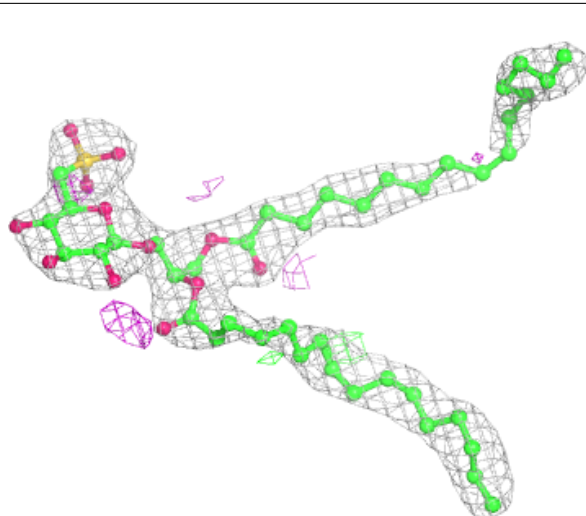
Electron density around HTG c 524:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



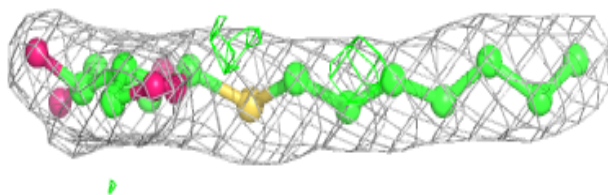
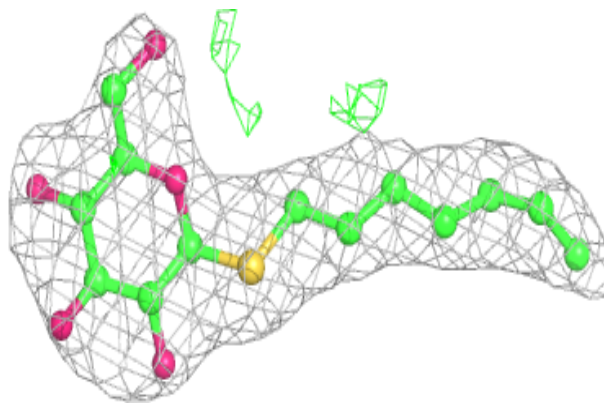
Electron density around SQD A 412:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

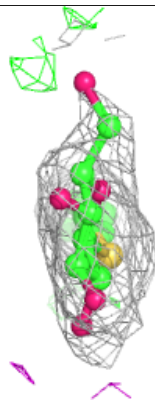
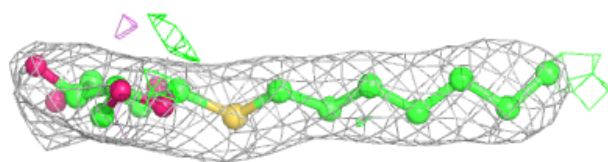
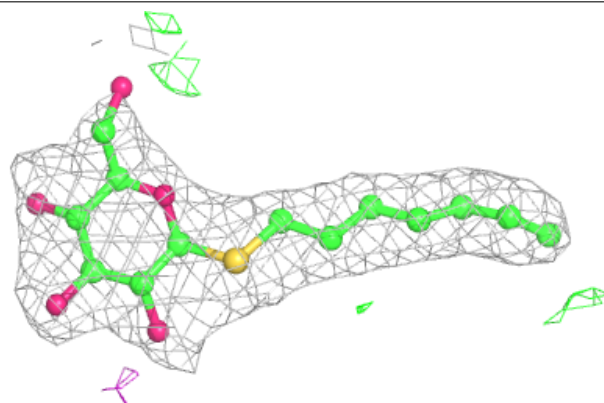


Electron density around HTG b 608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

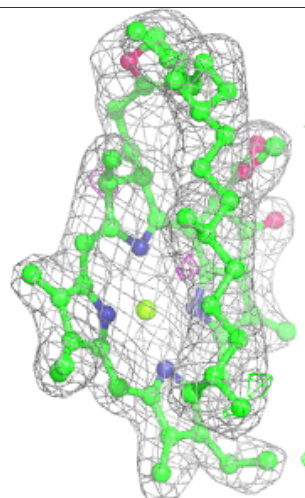
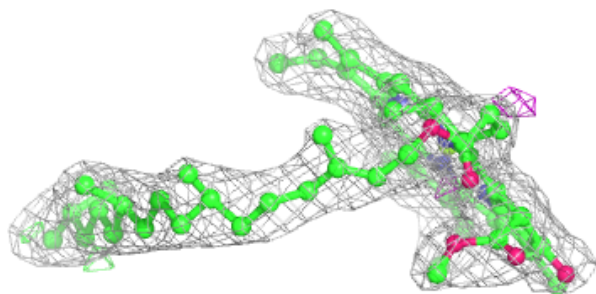
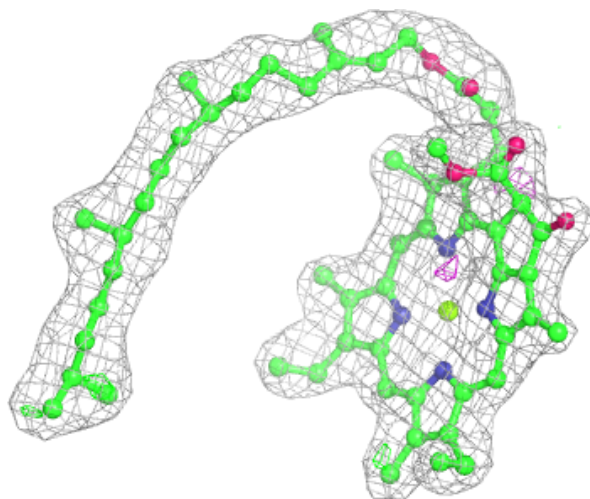
**Electron density around HTG B 632:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



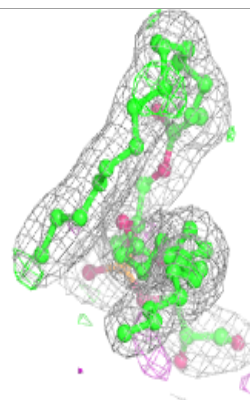
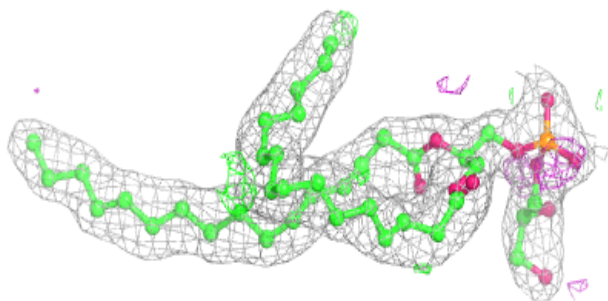
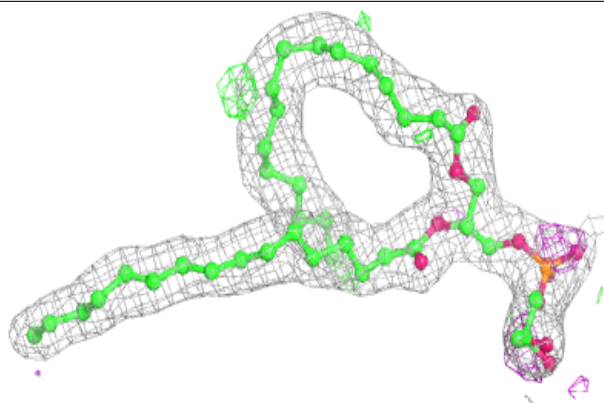
Electron density around CLA c 511:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

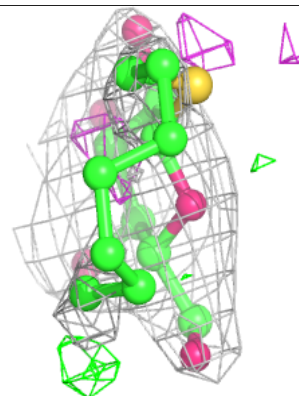
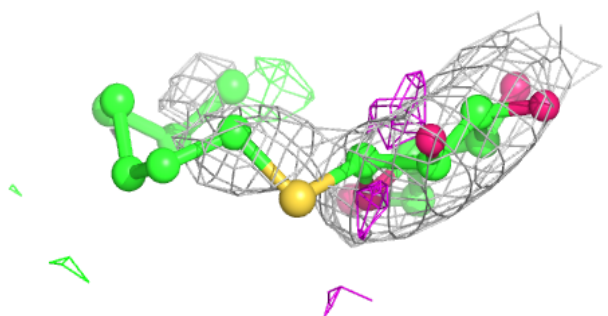
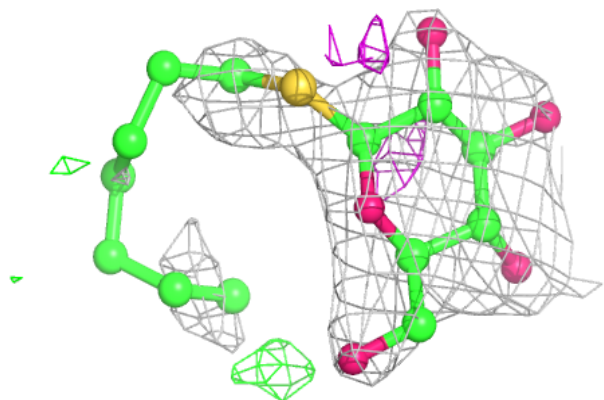


Electron density around LHG D 407:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

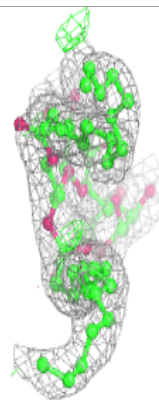
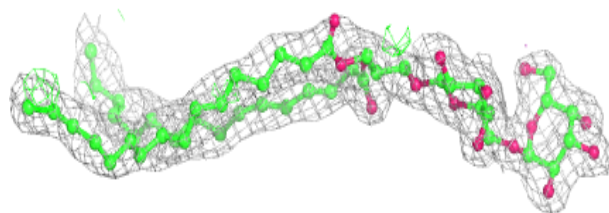
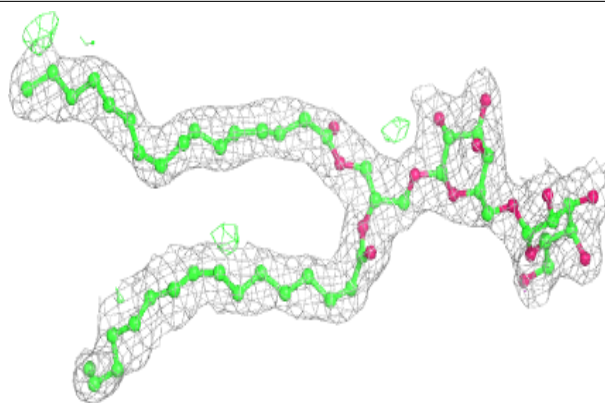
**Electron density around HTG V 207:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

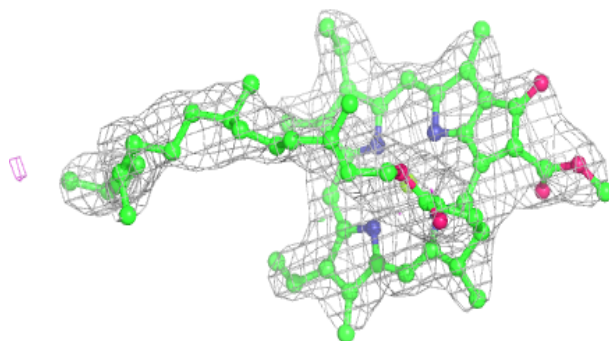
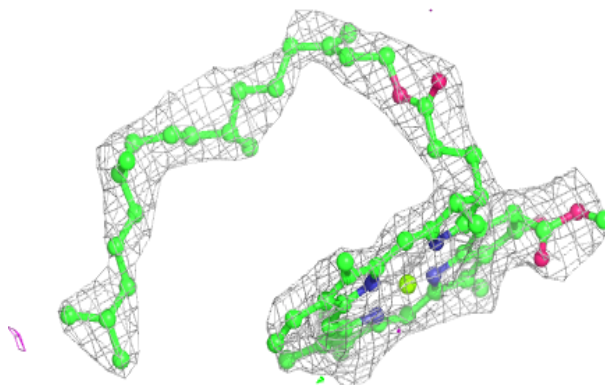


Electron density around DGD c 521:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

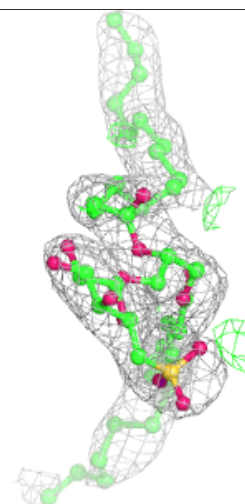
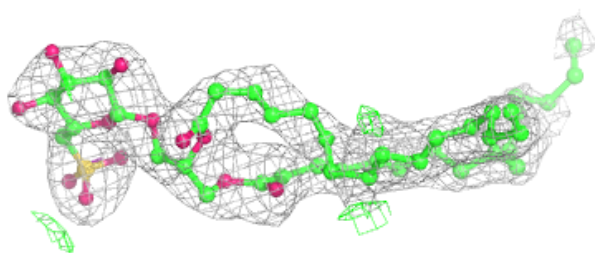
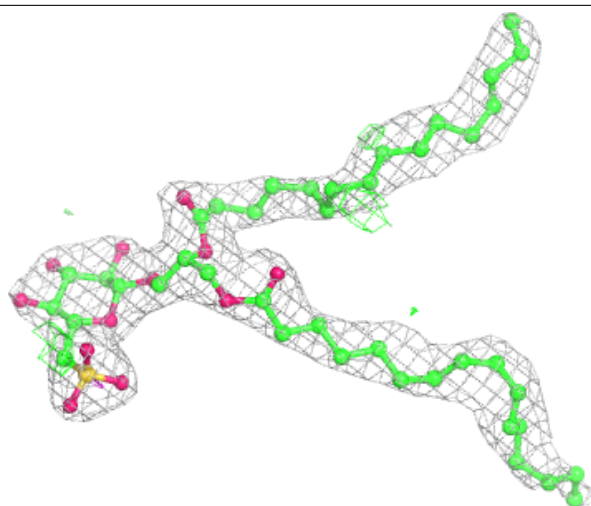
**Electron density around CLA c 517:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



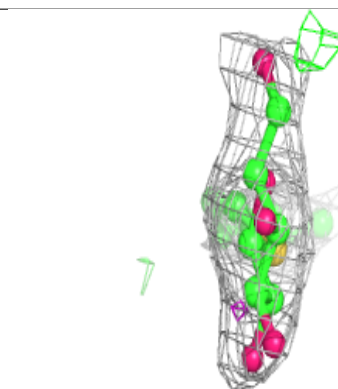
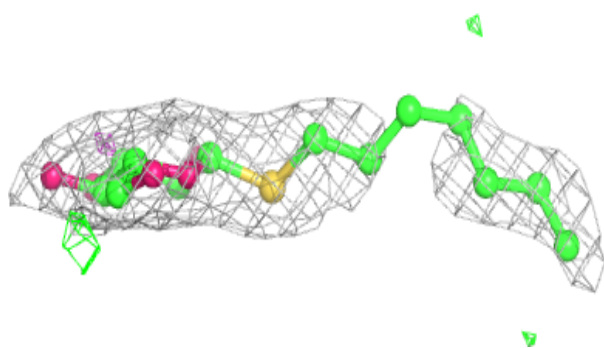
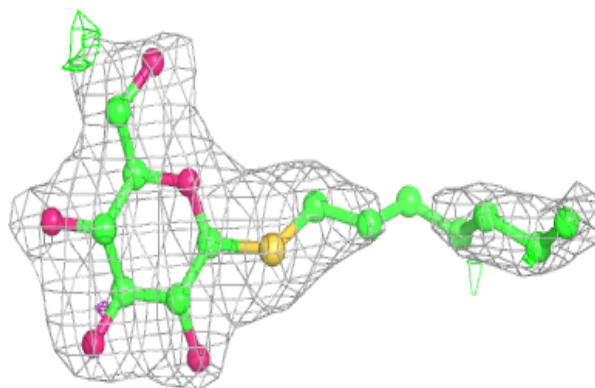
Electron density around SQD a 414:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

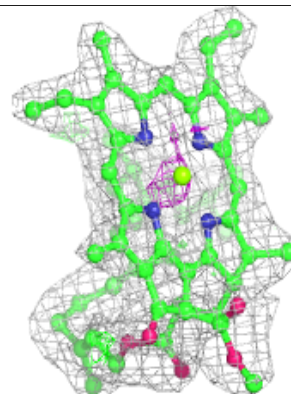
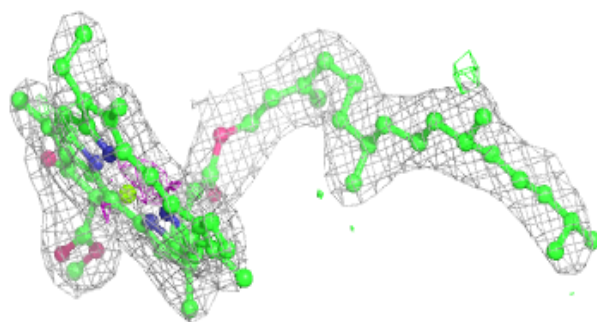
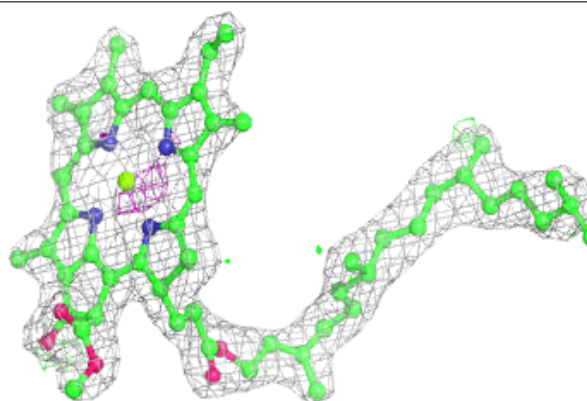


Electron density around HTG C 522:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

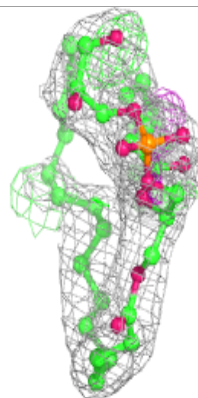
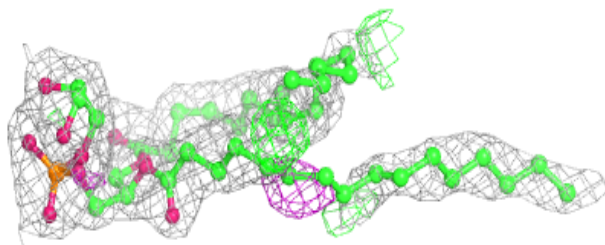
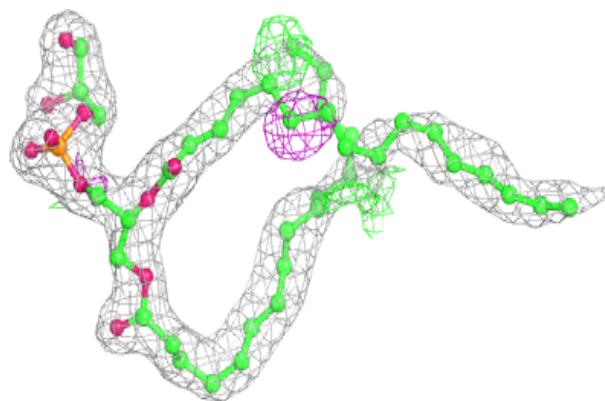
**Electron density around CLA c 515:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

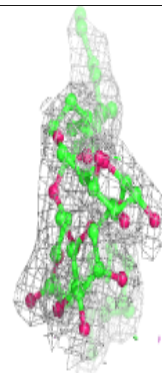
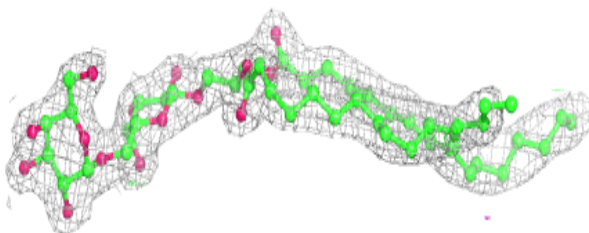
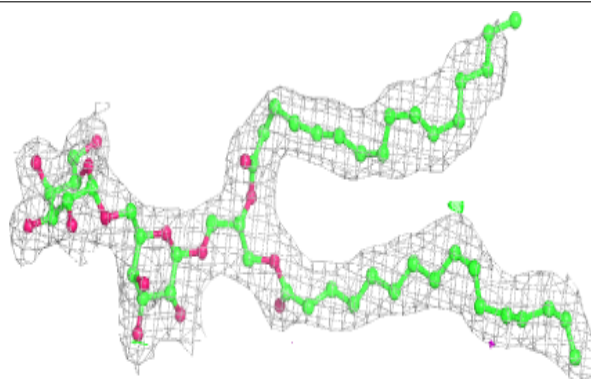


Electron density around LHG D 409:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

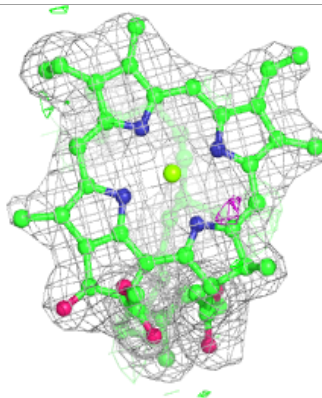
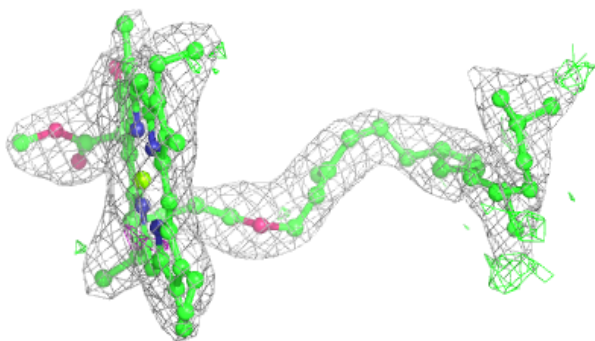
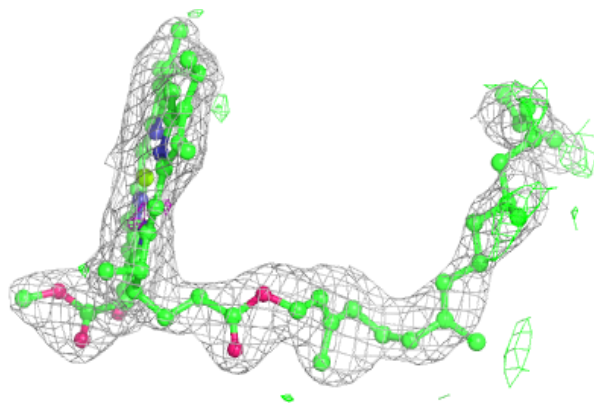
**Electron density around DGD C 518:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

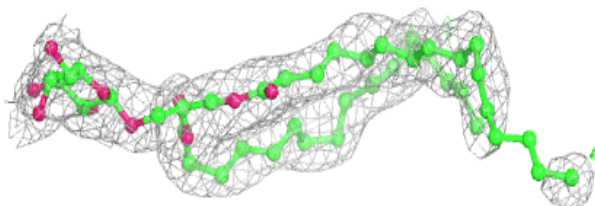
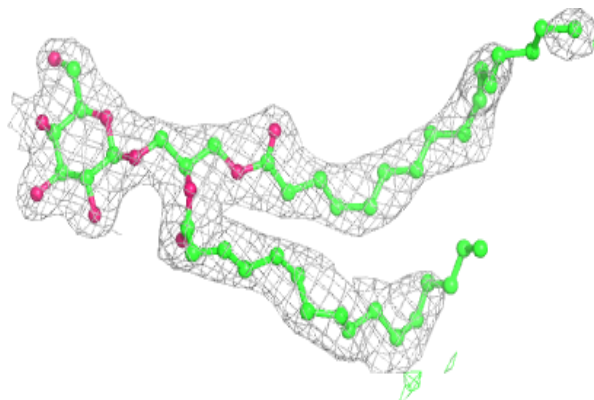


Electron density around CLA C 506:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

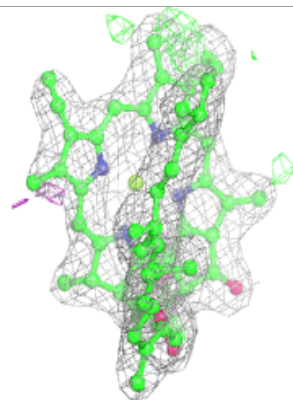
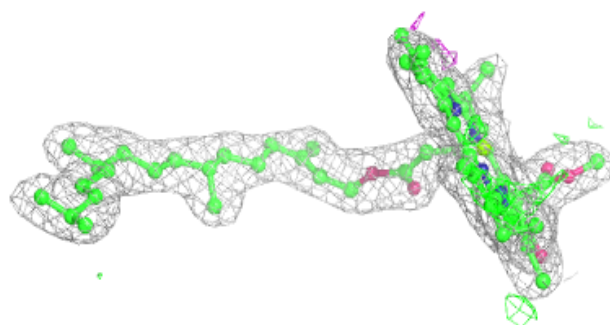
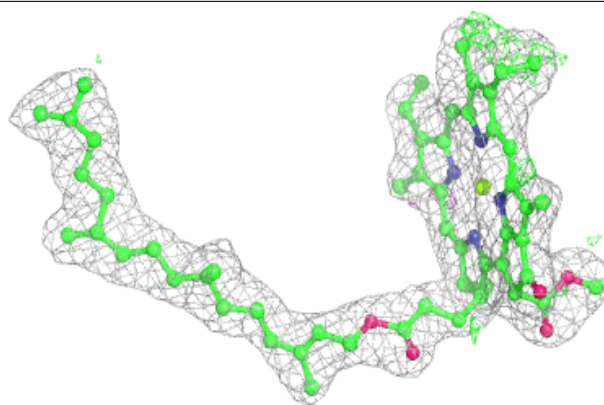
**Electron density around LMG j 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

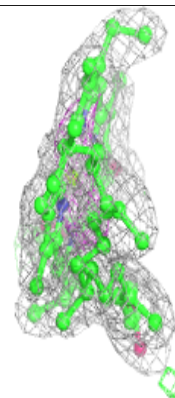
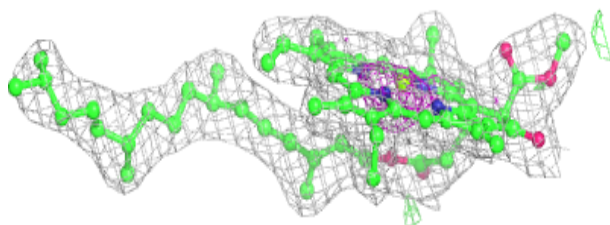
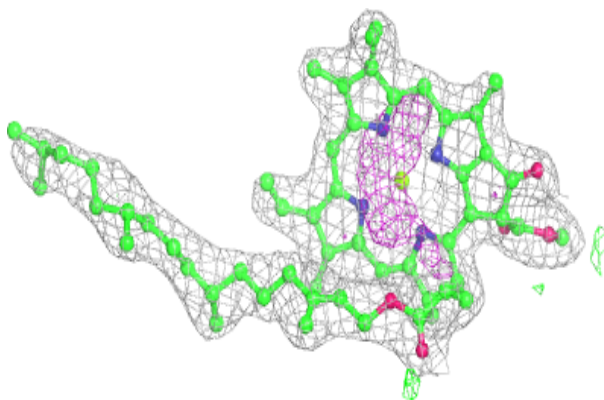


Electron density around CLA b 619:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

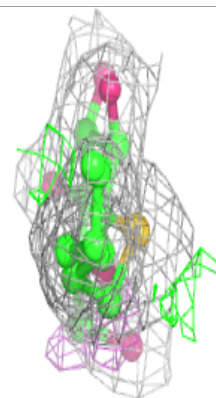
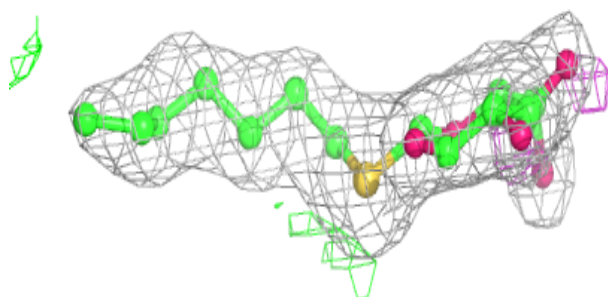
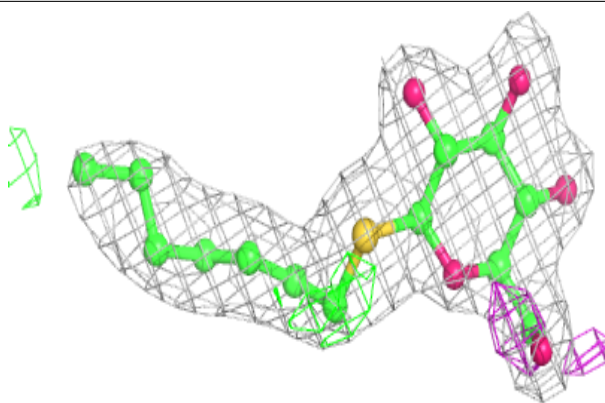
**Electron density around CLA C 501:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

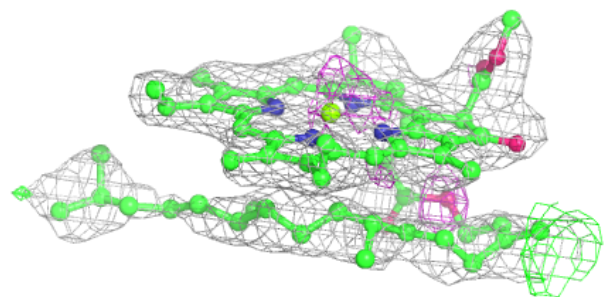
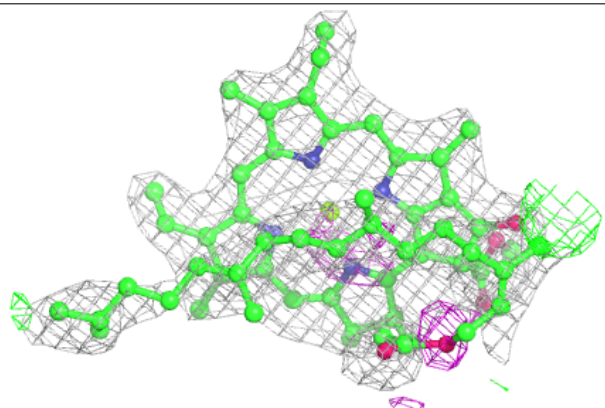


Electron density around HTG B 623:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

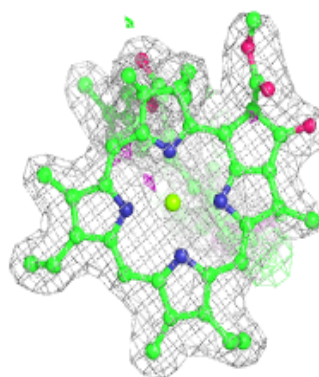
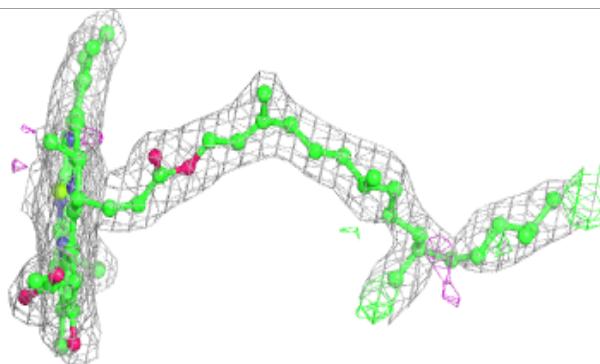
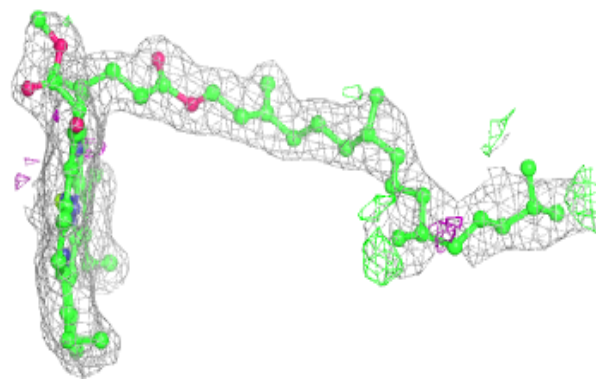
**Electron density around CLA B 602:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

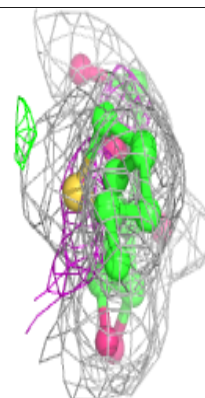
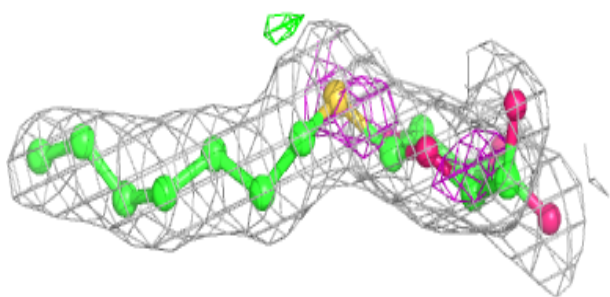
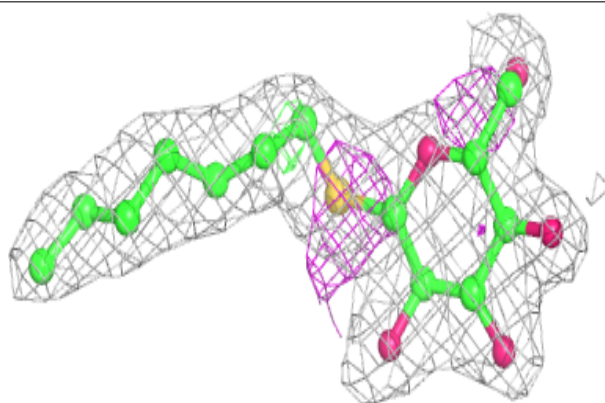


Electron density around CLA b 616:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

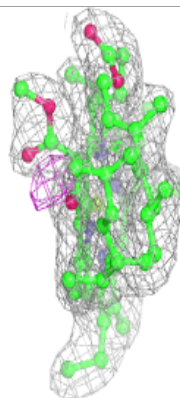
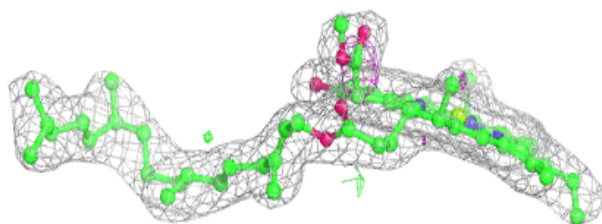
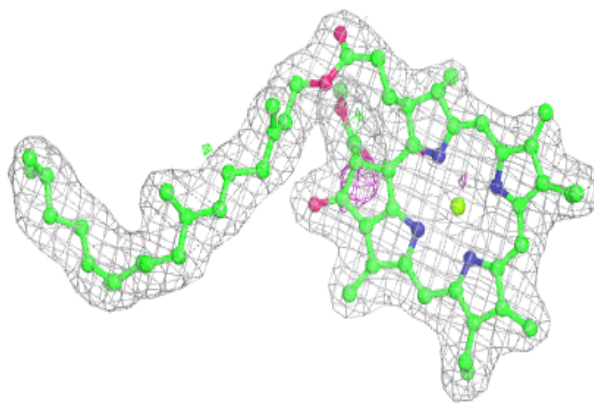
**Electron density around HTG b 602:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



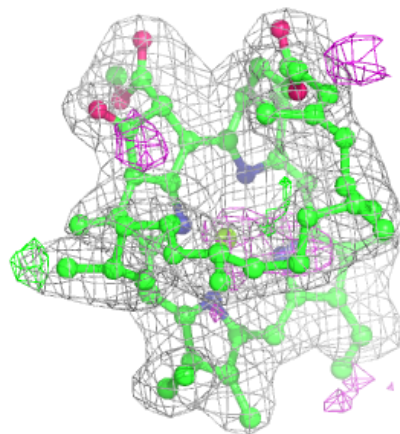
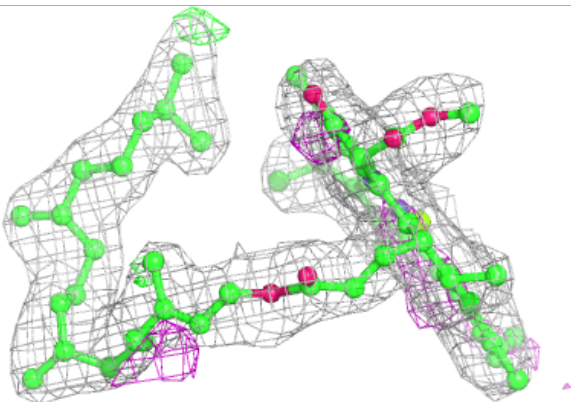
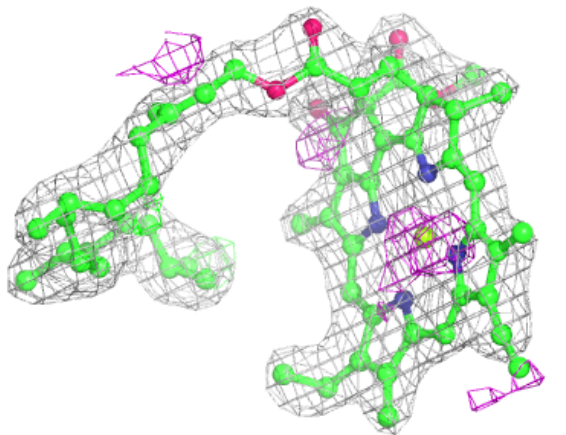
Electron density around CLA b 612:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



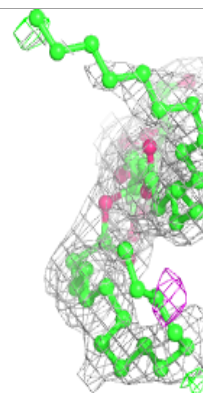
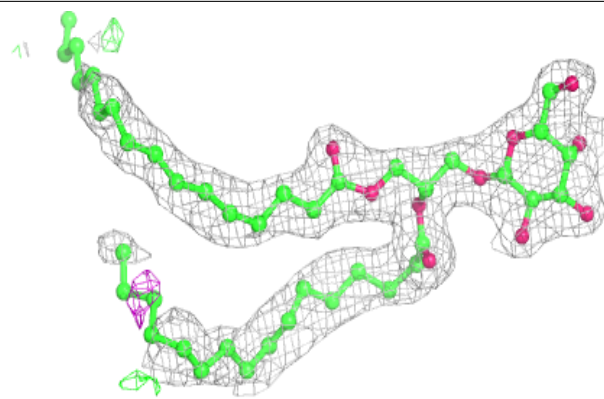
Electron density around CLA c 507:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

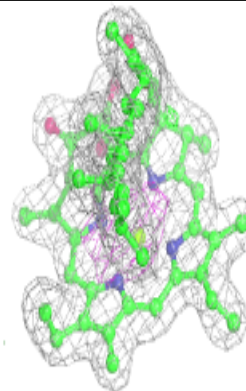
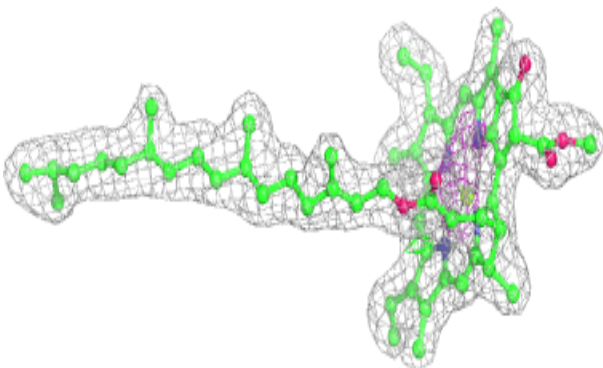
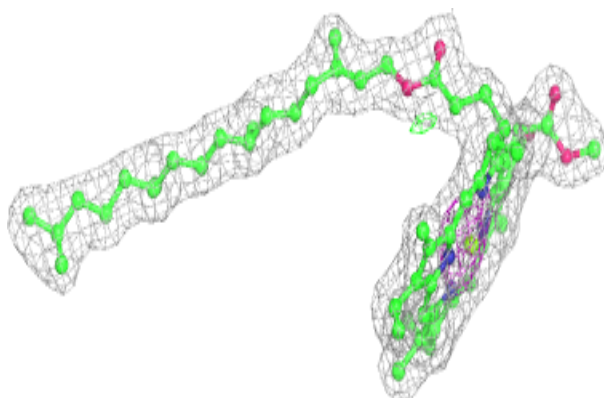


Electron density around LMG D 412:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

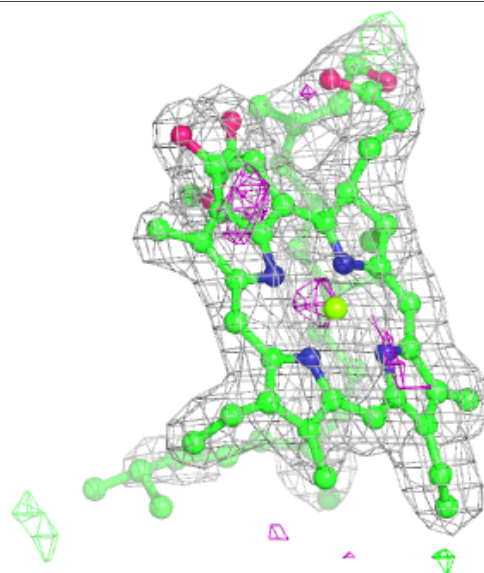
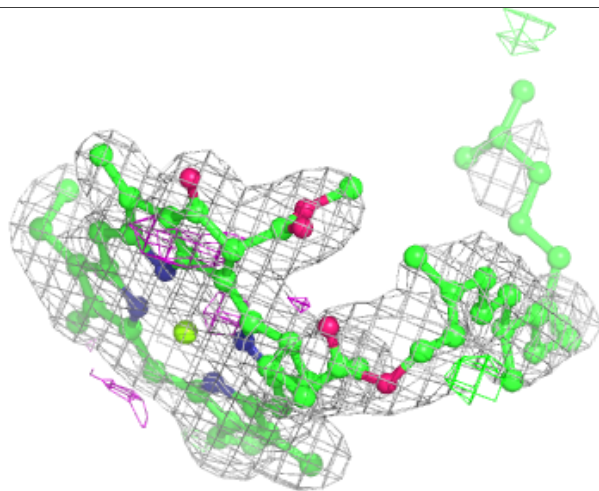
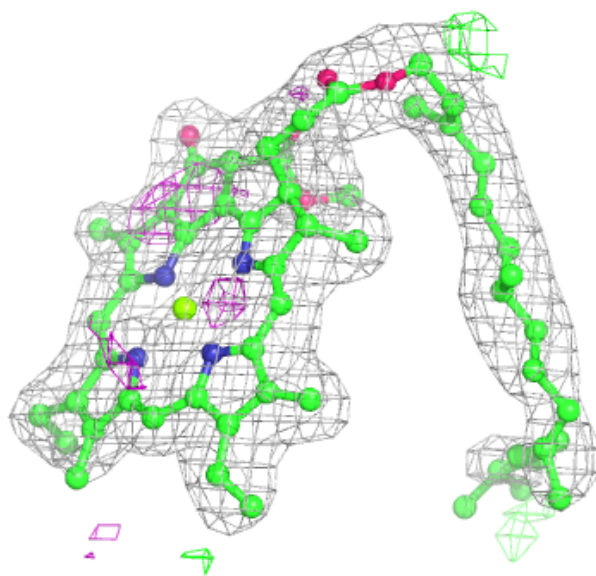
**Electron density around CLA b 617:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



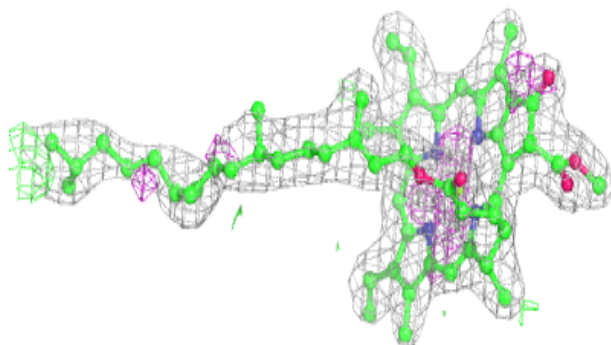
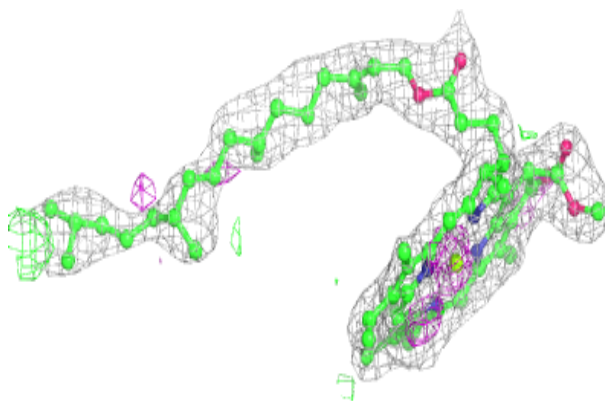
Electron density around CLA b 626:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



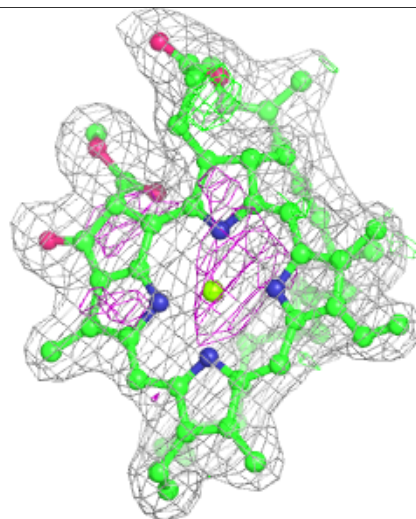
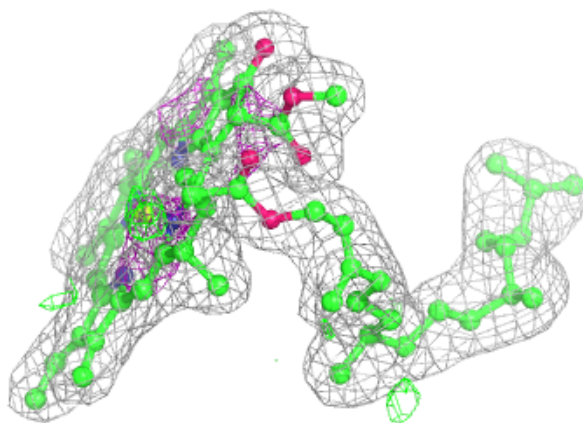
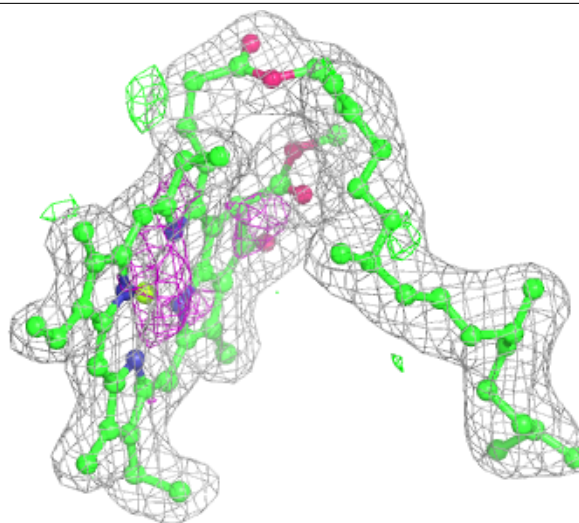
Electron density around CLA C 504:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



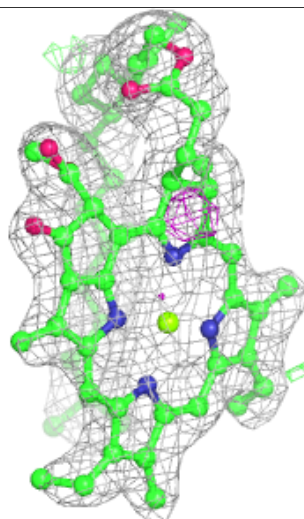
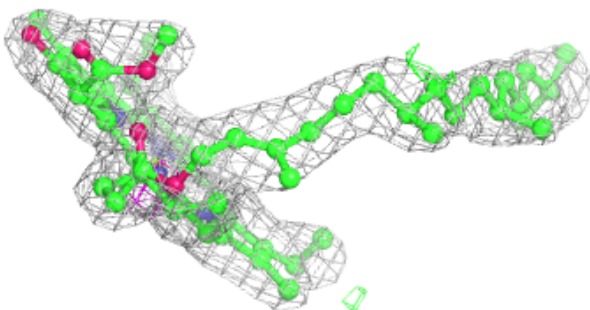
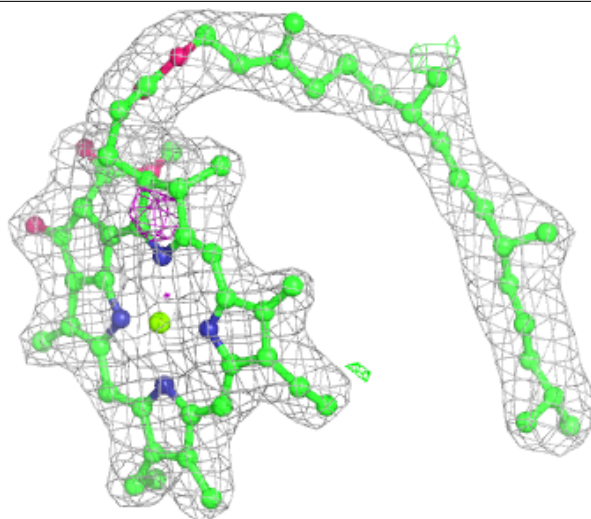
Electron density around CLA B 614:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



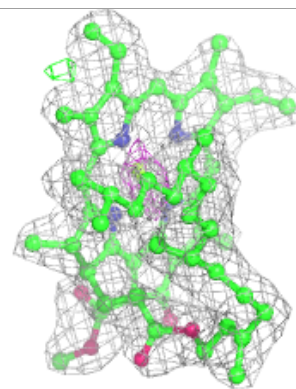
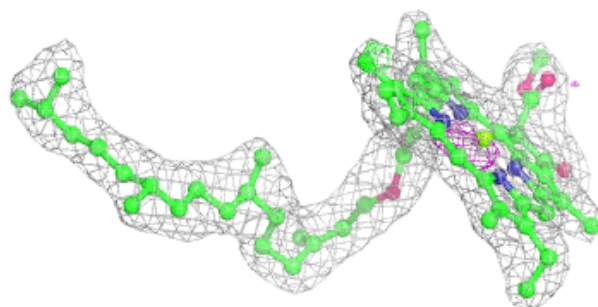
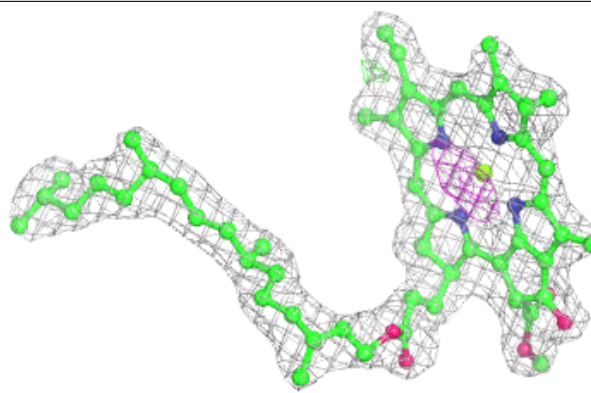
Electron density around CLA C 507:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



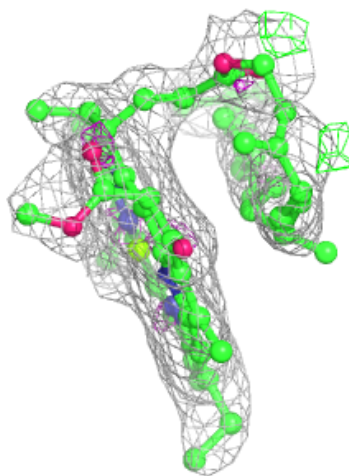
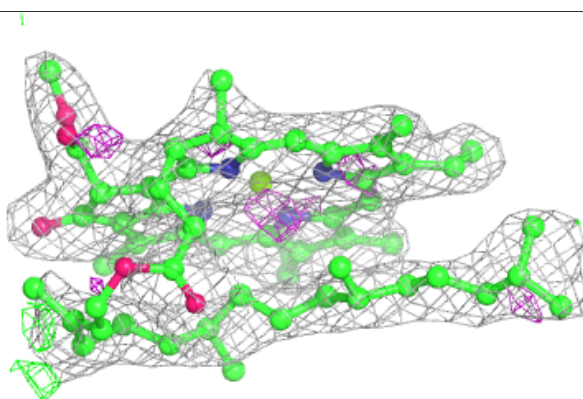
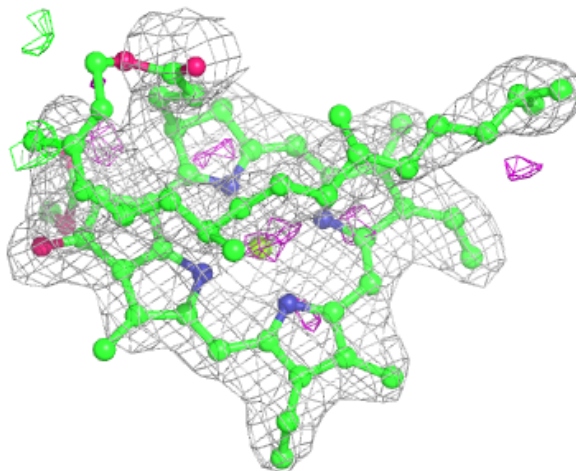
Electron density around CLA C 511:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



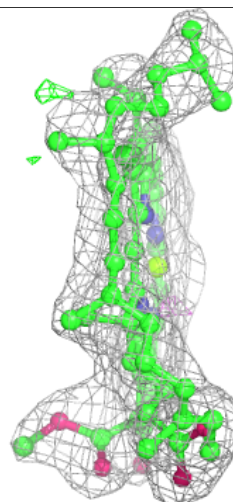
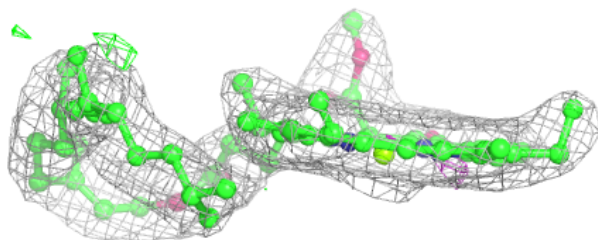
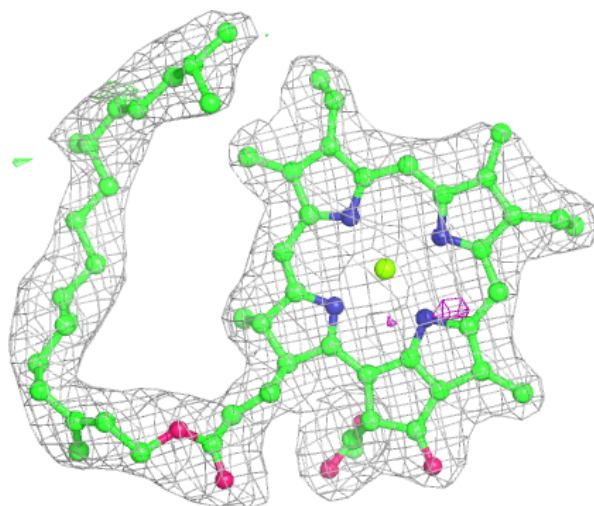
Electron density around CLA b 611:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



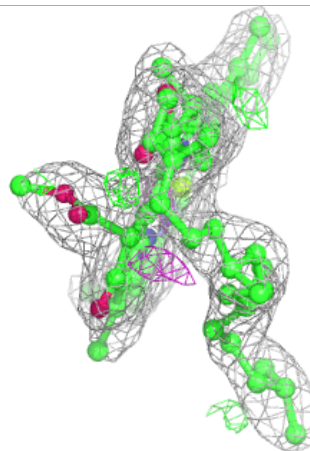
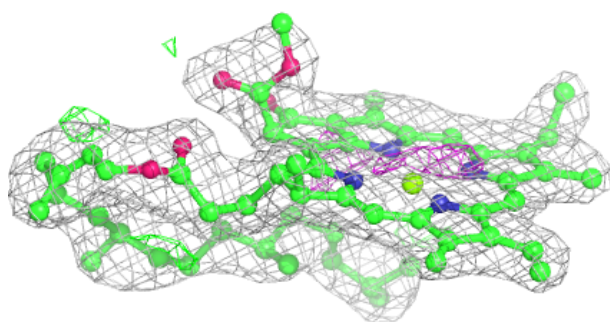
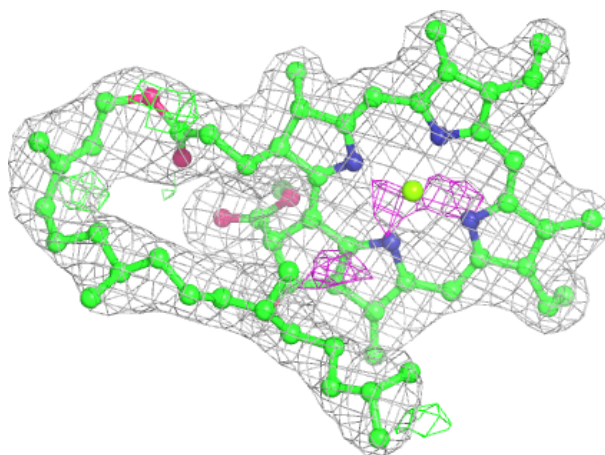
Electron density around CLA C 512:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

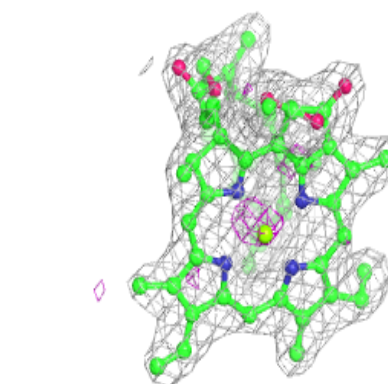
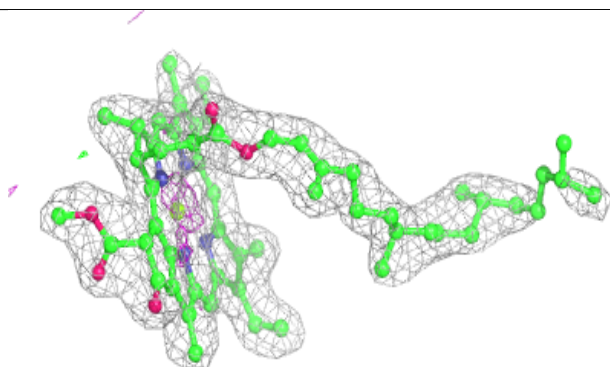
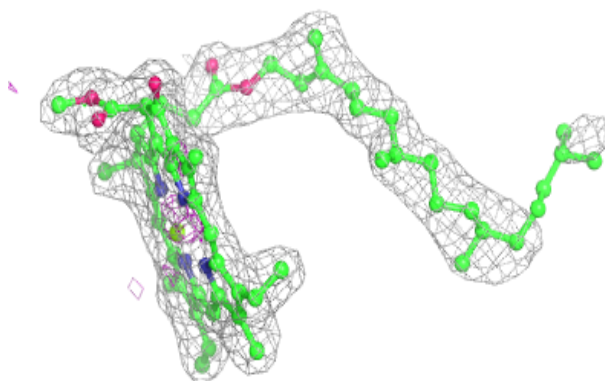


Electron density around CLA C 509:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

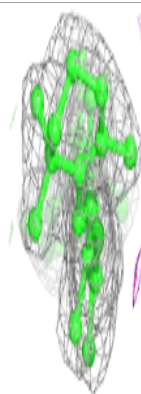
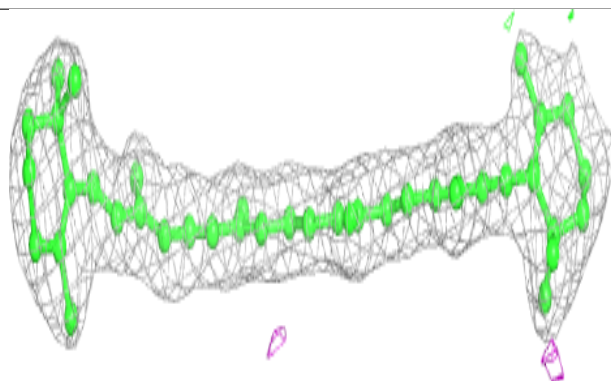
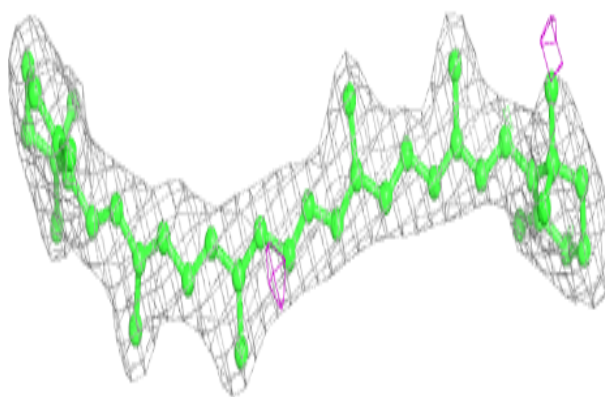
**Electron density around CLA C 508:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

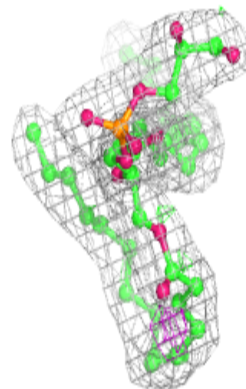
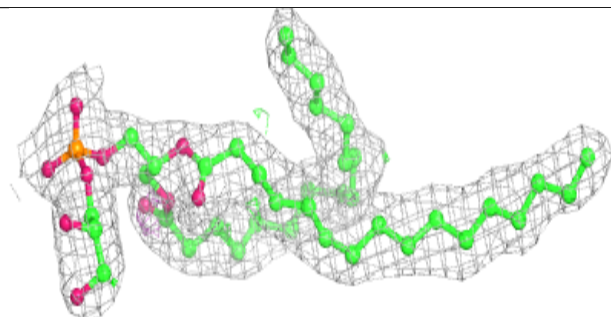
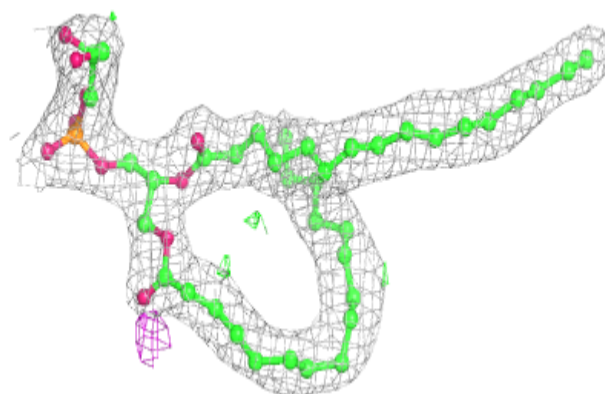


Electron density around BCR h 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

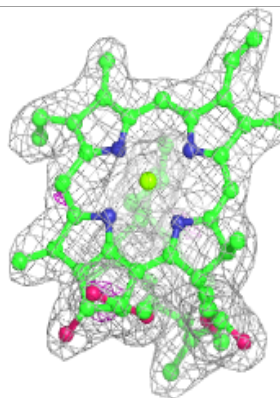
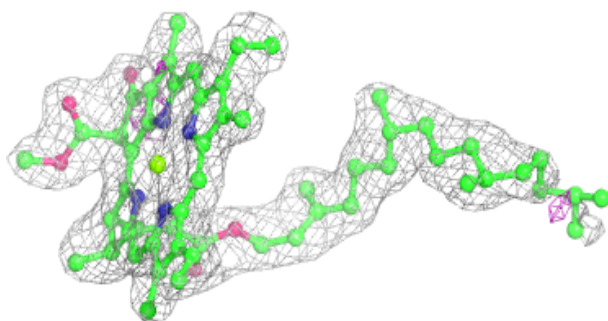
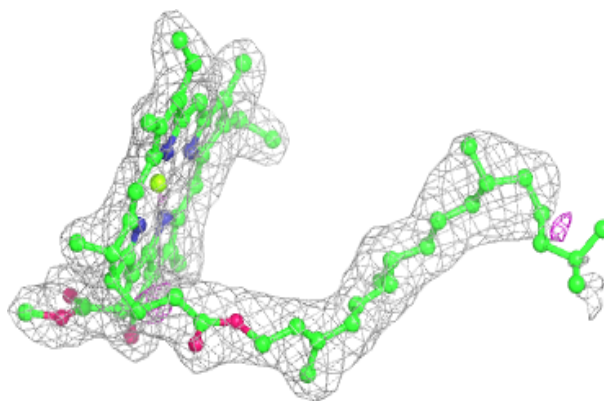
**Electron density around LHG d 406:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

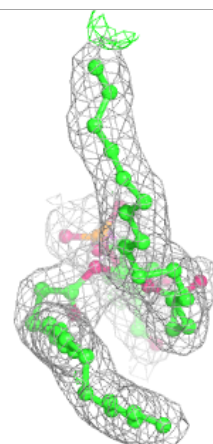
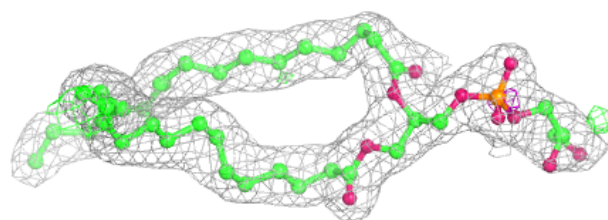
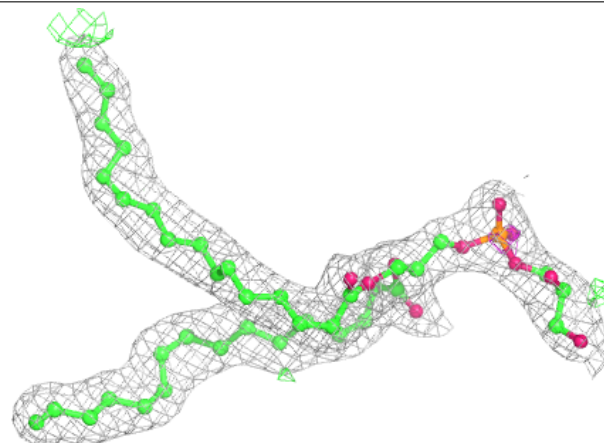


Electron density around CLA c 512:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

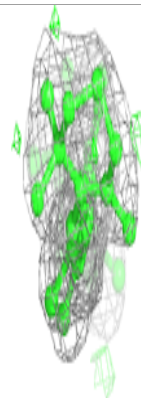
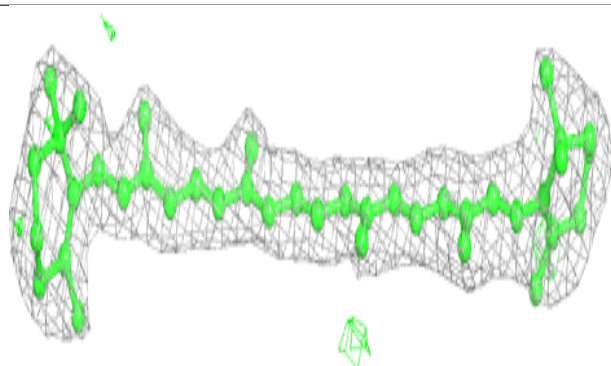
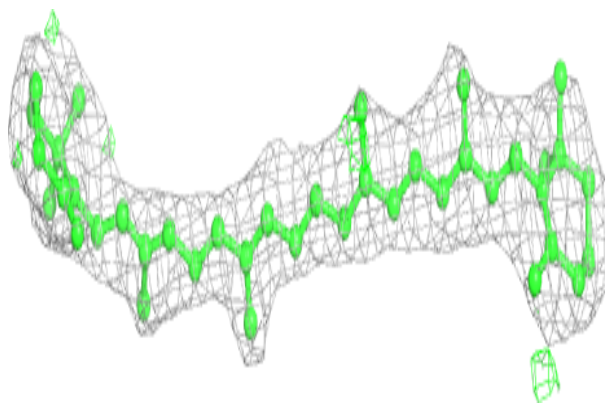
**Electron density around LHG d 407:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

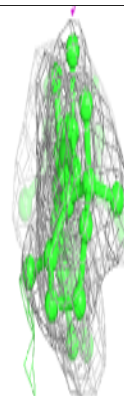
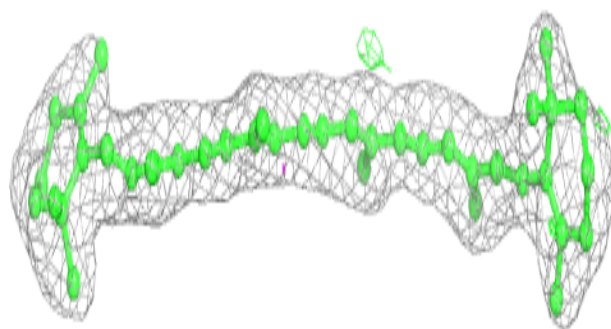
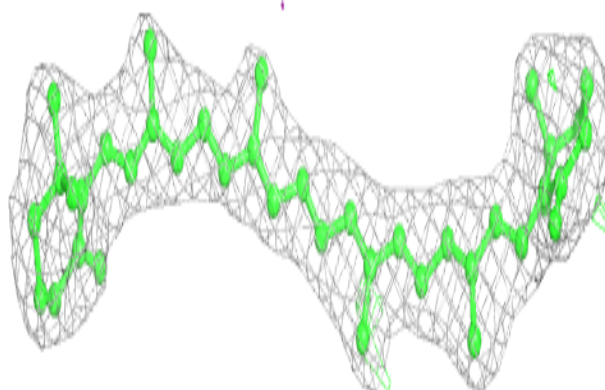


Electron density around BCR c 527:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

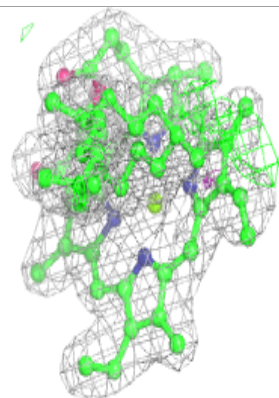
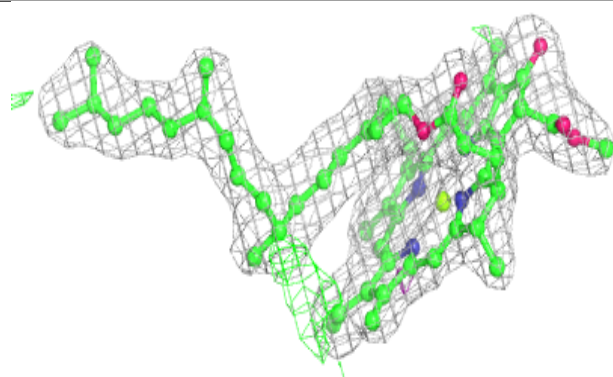
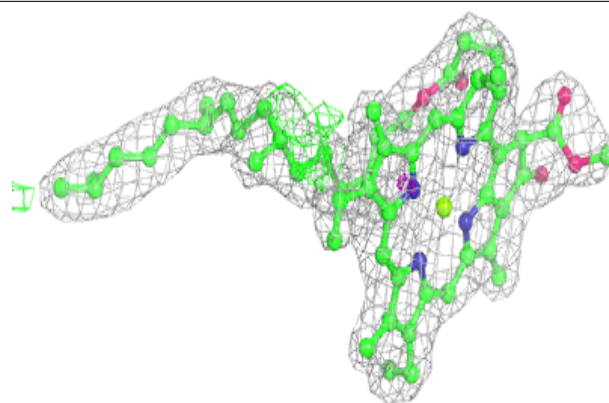
**Electron density around BCR y 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

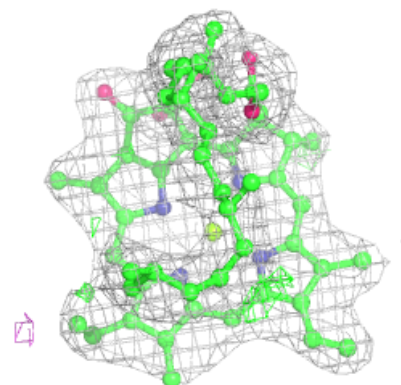
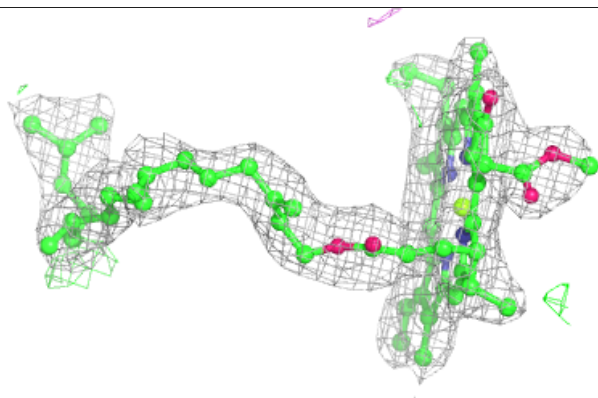
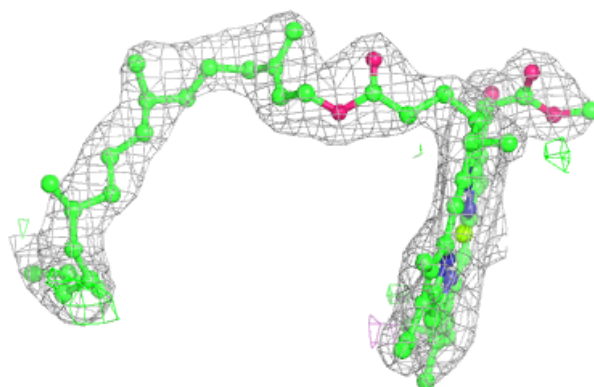


Electron density around CLA c 509:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

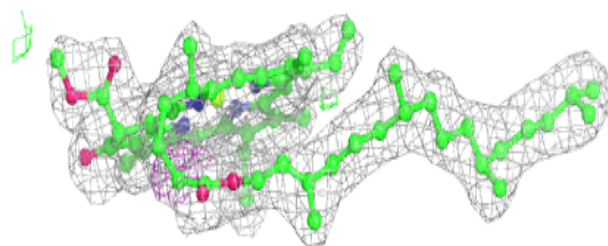
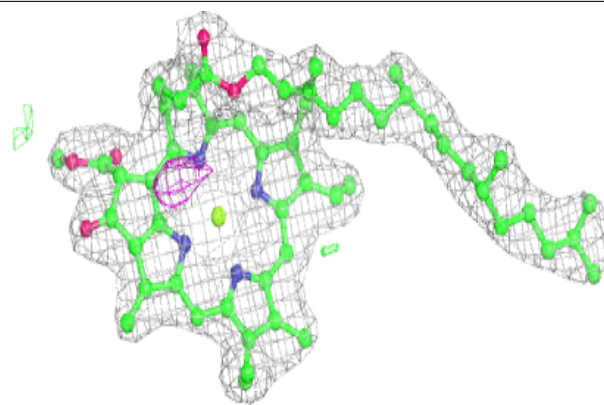
**Electron density around CLA c 510:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

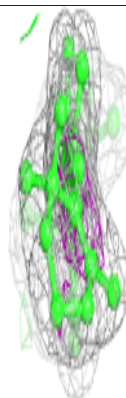
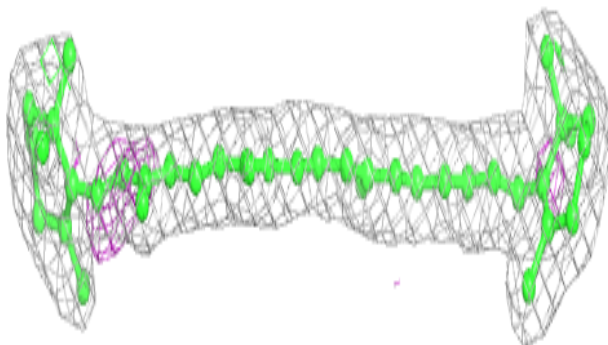
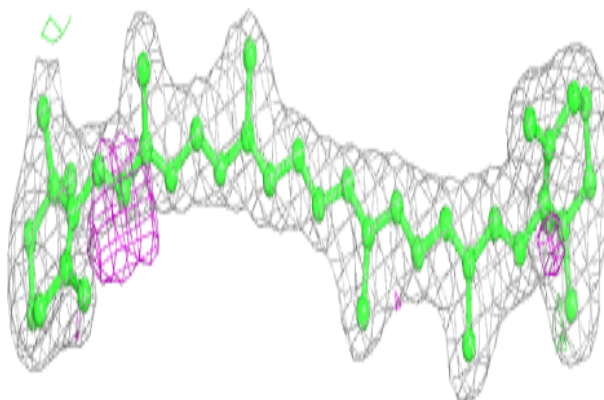


Electron density around CLA c 505:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

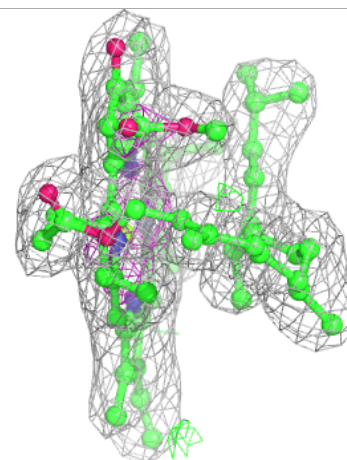
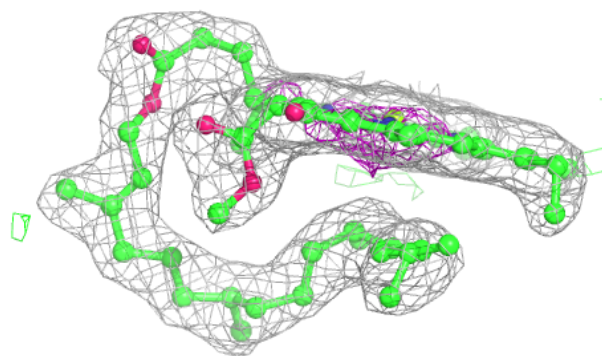
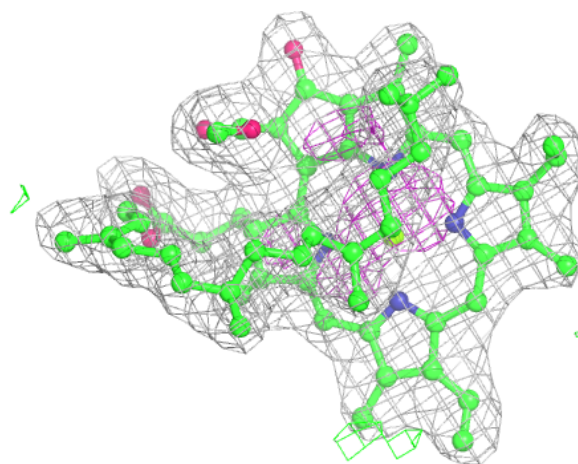
**Electron density around BCR b 628:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



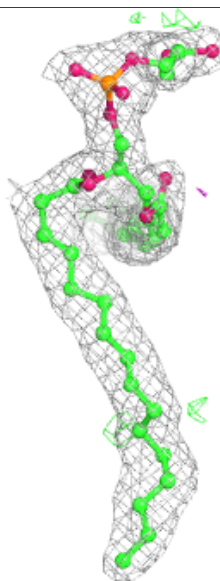
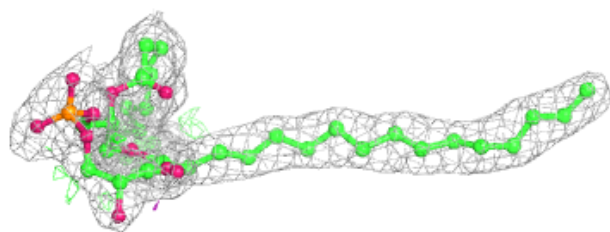
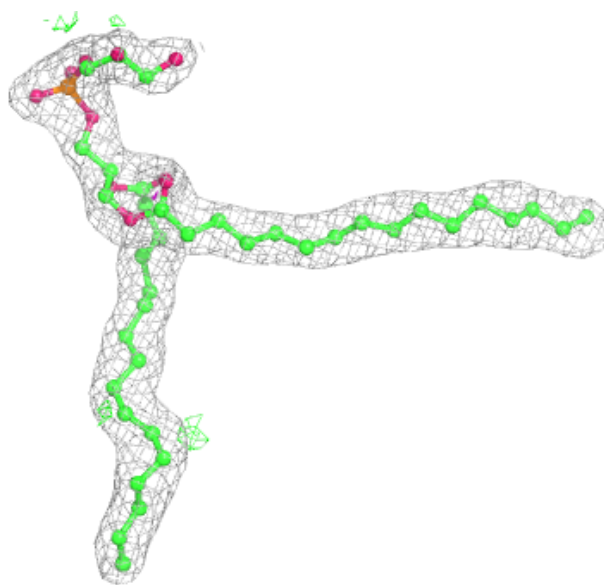
Electron density around CLA c 514:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



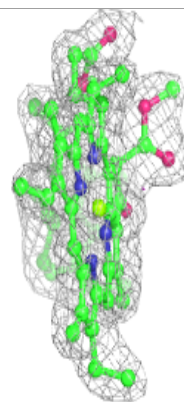
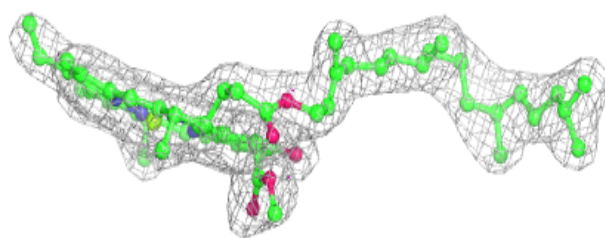
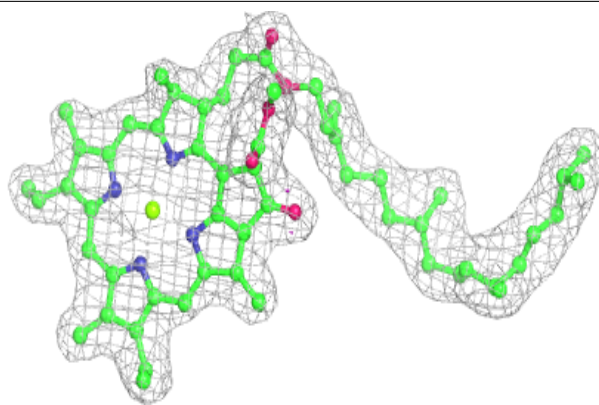
Electron density around LHG 1 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



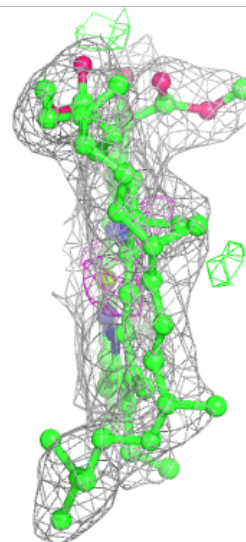
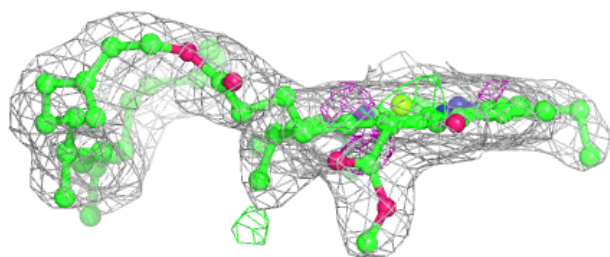
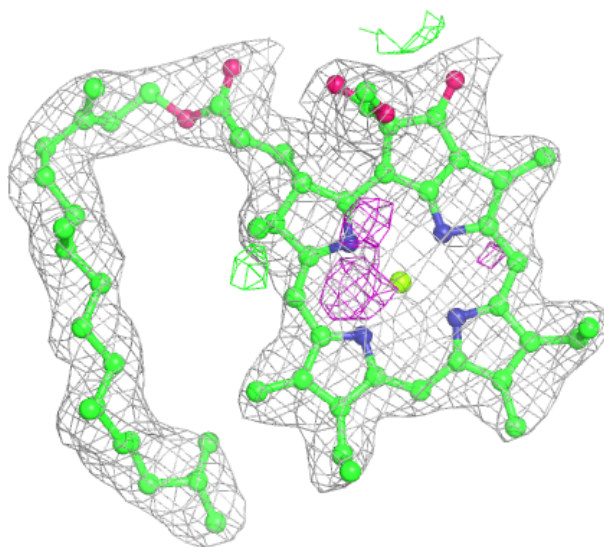
Electron density around CLA B 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



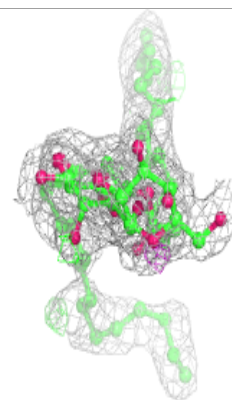
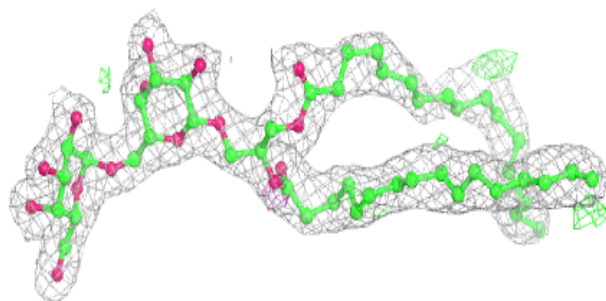
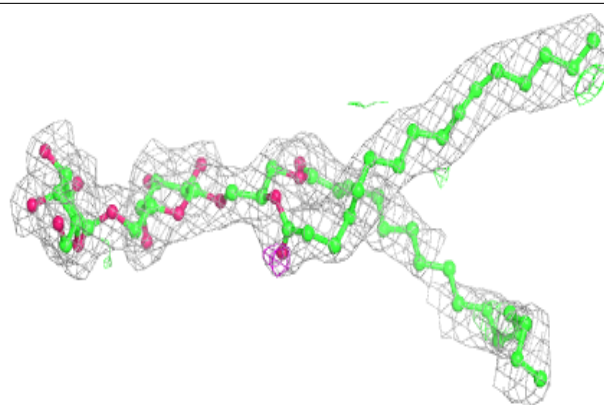
Electron density around CLA c 516:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

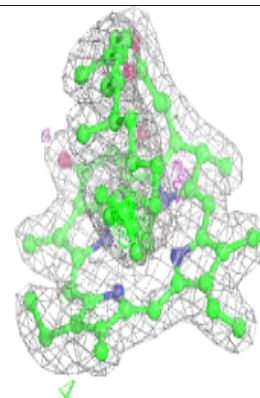
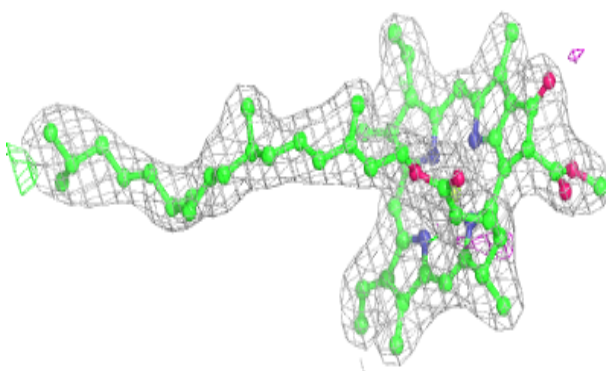
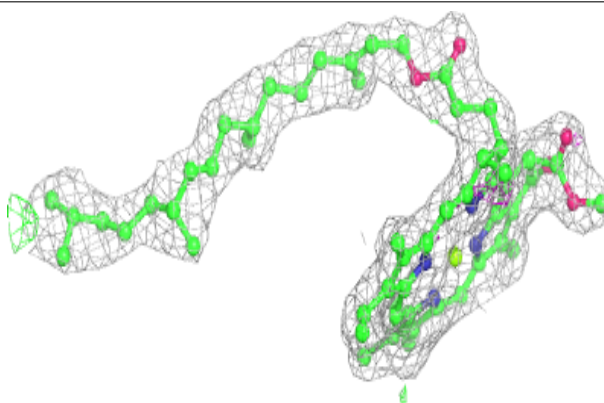


Electron density around DGD c 519:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

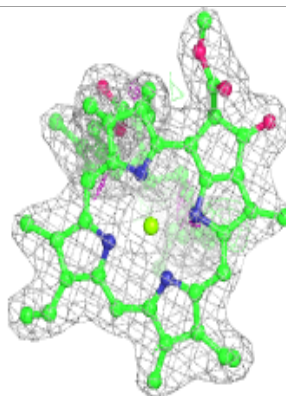
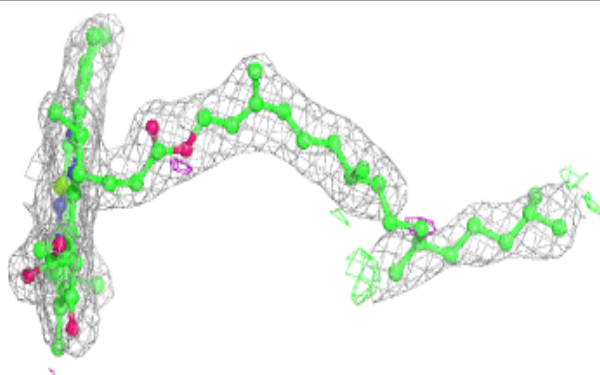
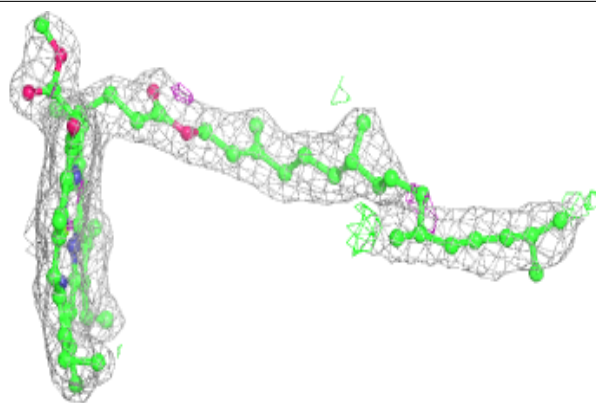
**Electron density around CLA c 508:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

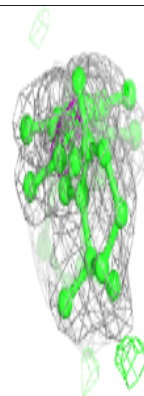
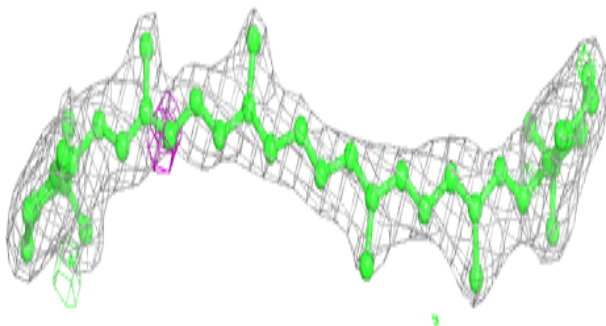
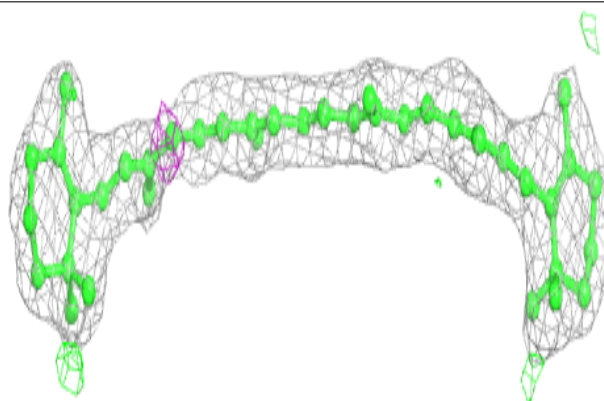


Electron density around CLA B 607:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

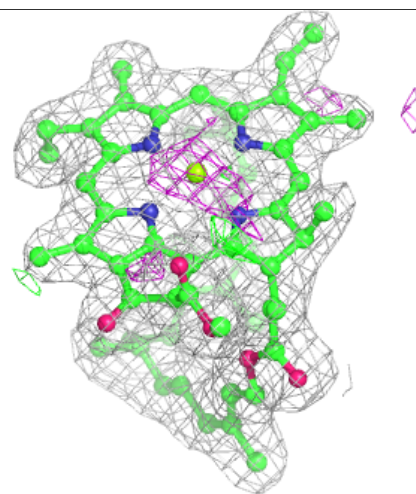
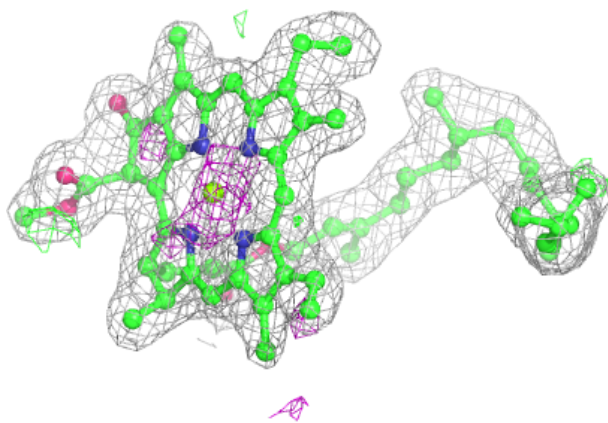
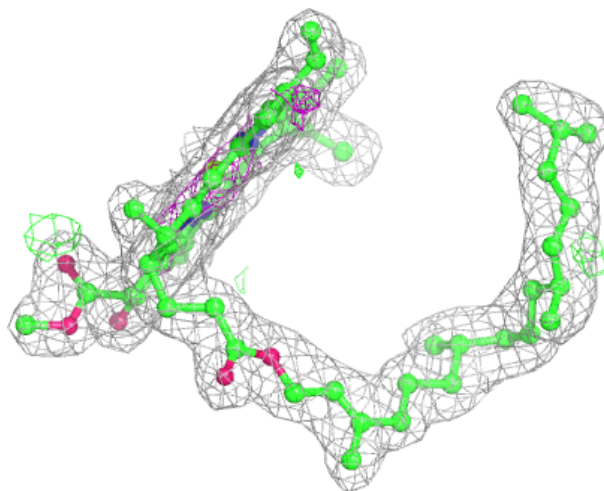
**Electron density around BCR k 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



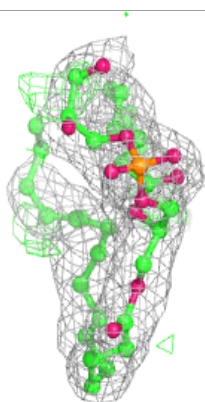
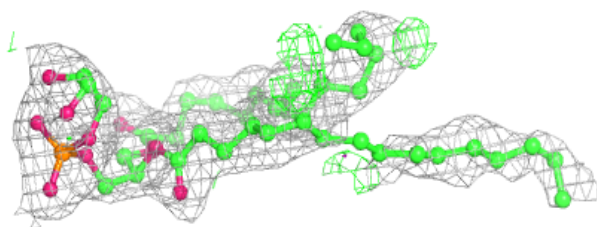
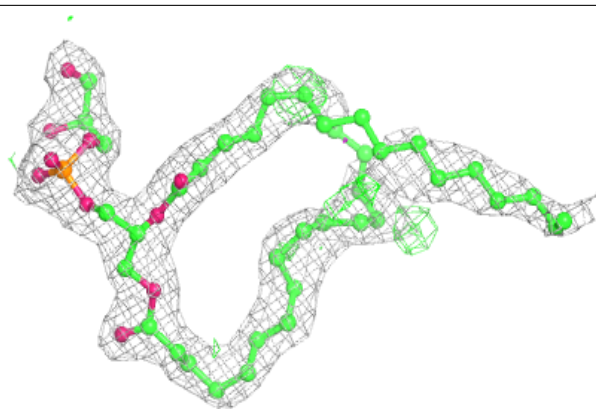
Electron density around CLA b 621:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

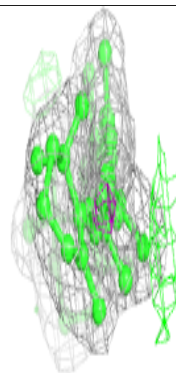
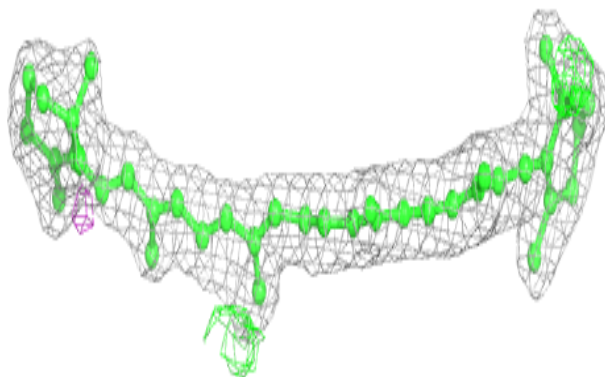
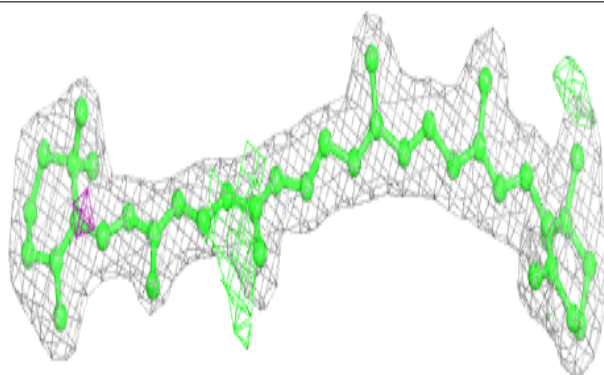


Electron density around LHG d 408:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

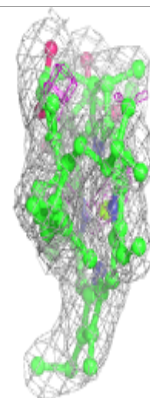
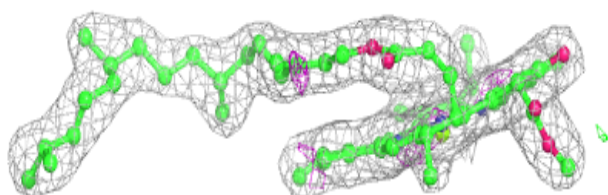
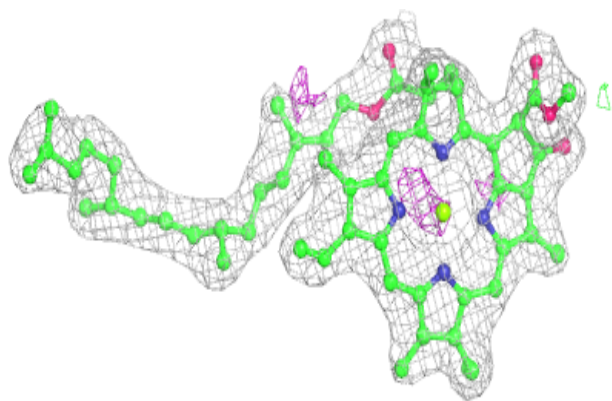
**Electron density around BCR T 103:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

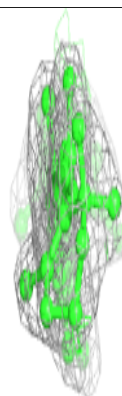
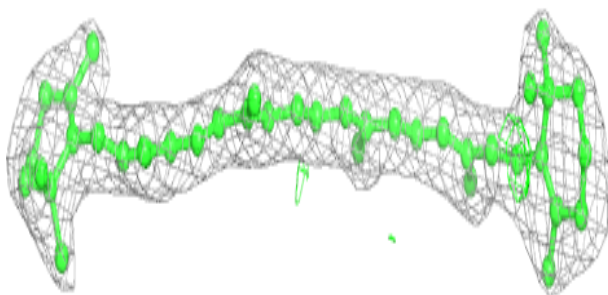
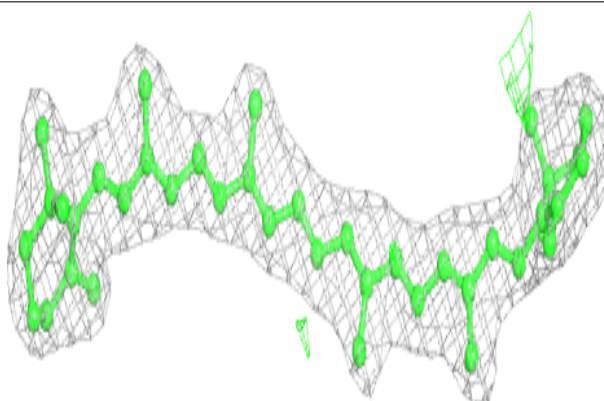


Electron density around CLA b 613:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

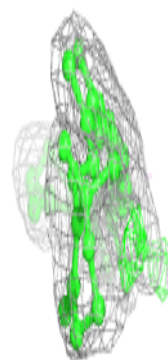
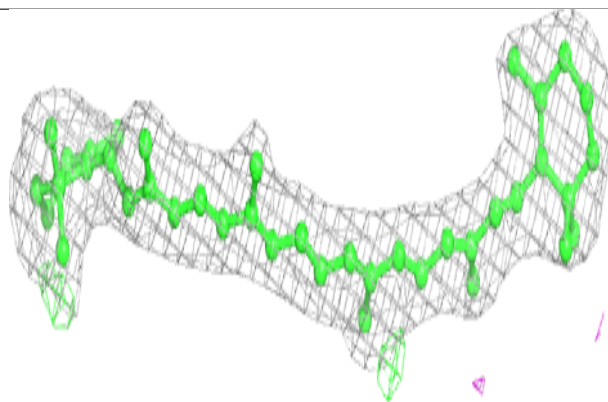
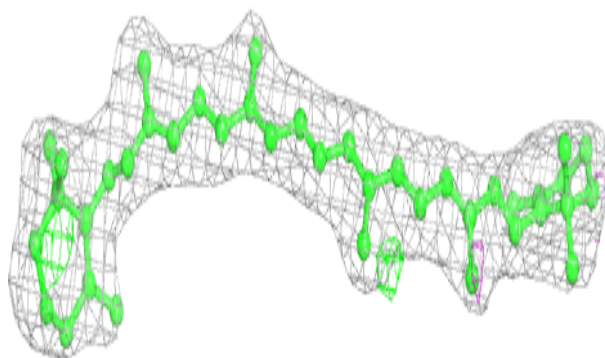
**Electron density around BCR Y 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

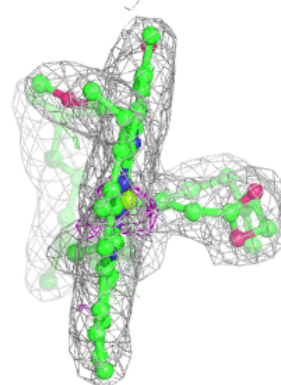
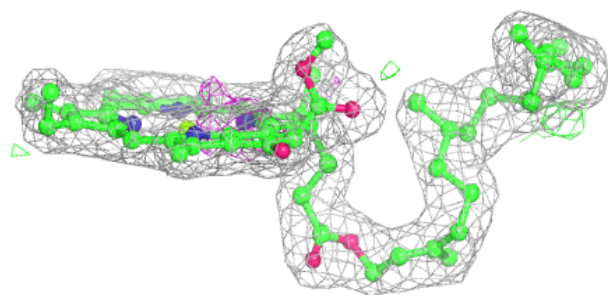
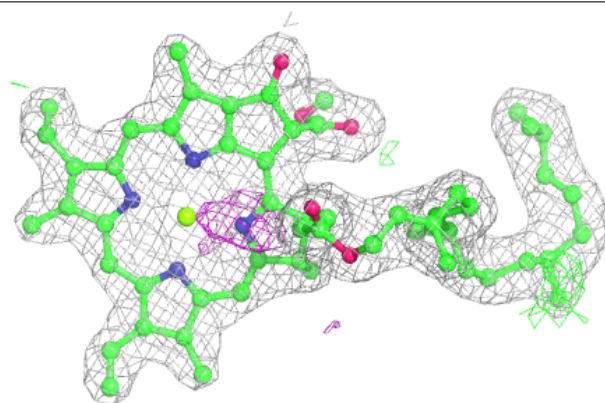


Electron density around BCR d 404:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

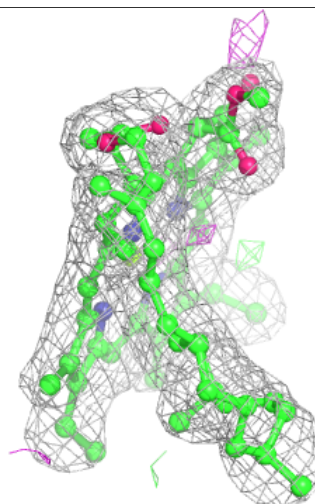
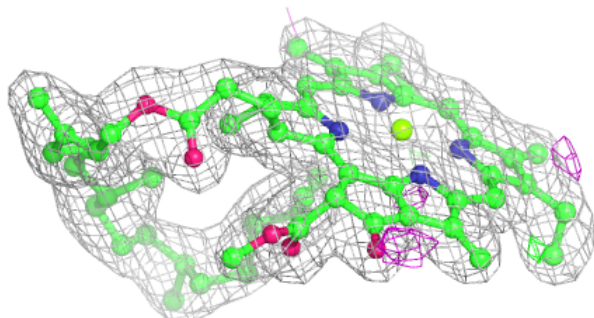
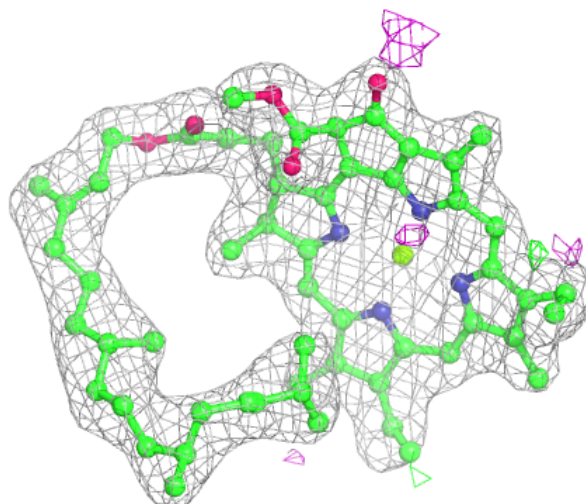
**Electron density around CLA b 622:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



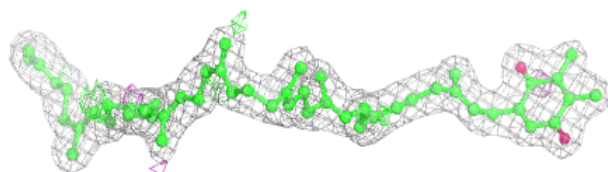
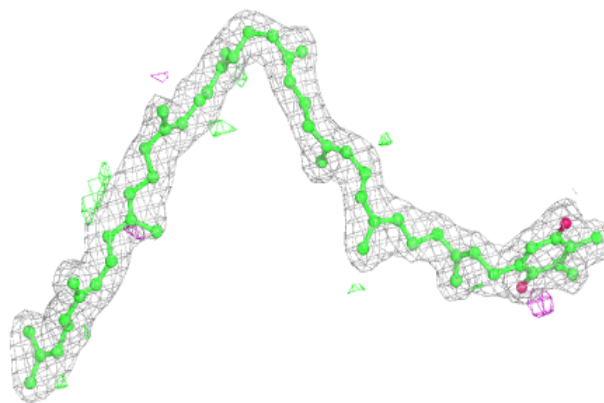
Electron density around CLA B 616:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

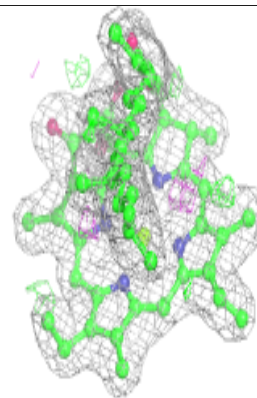
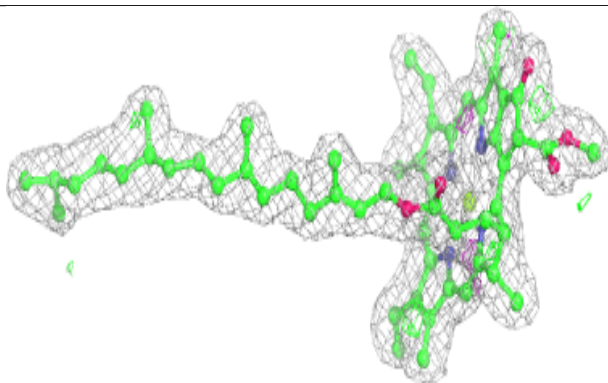
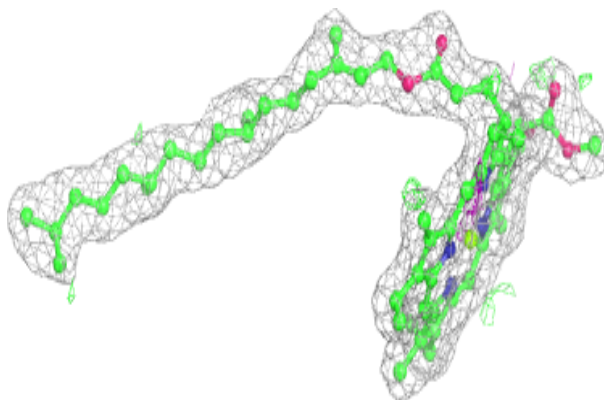


Electron density around PL9 D 405 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

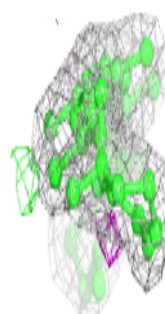
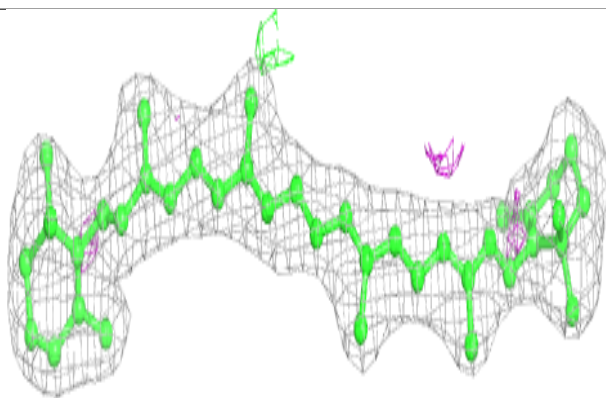
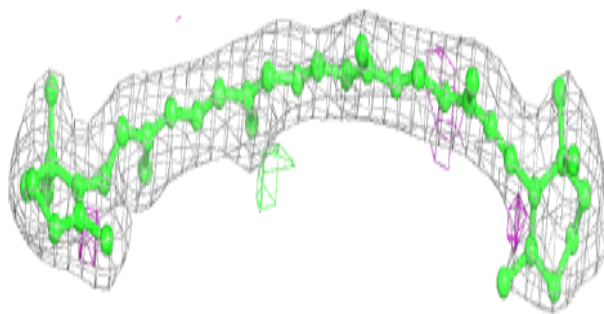
**Electron density around CLA B 608:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

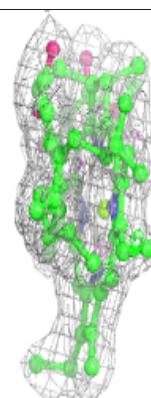
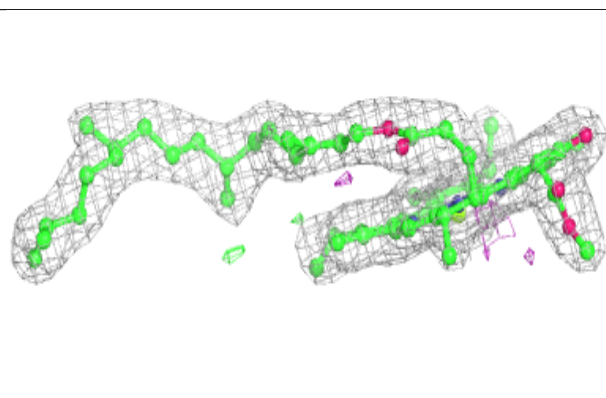
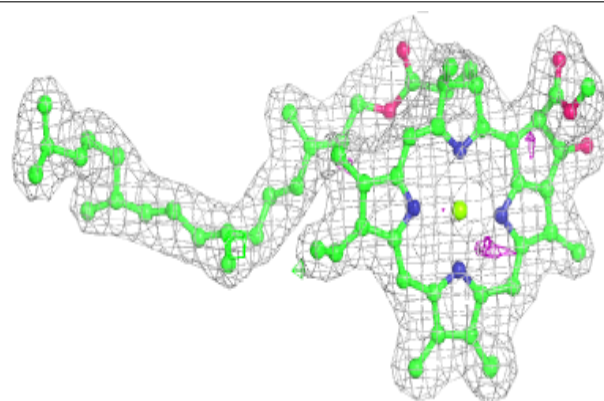


Electron density around BCR D 404:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

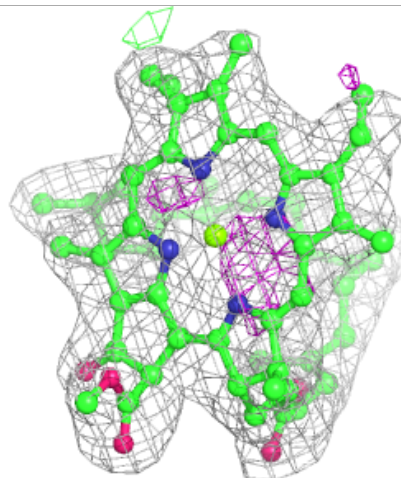
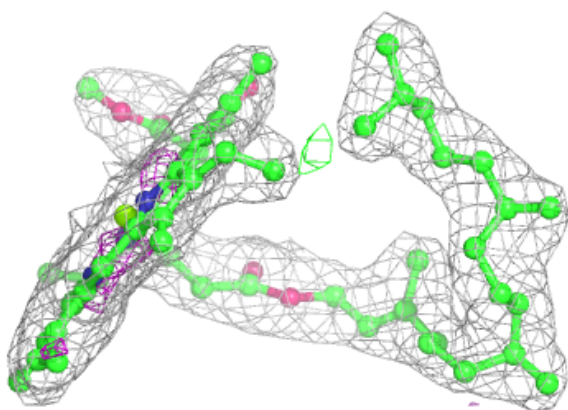
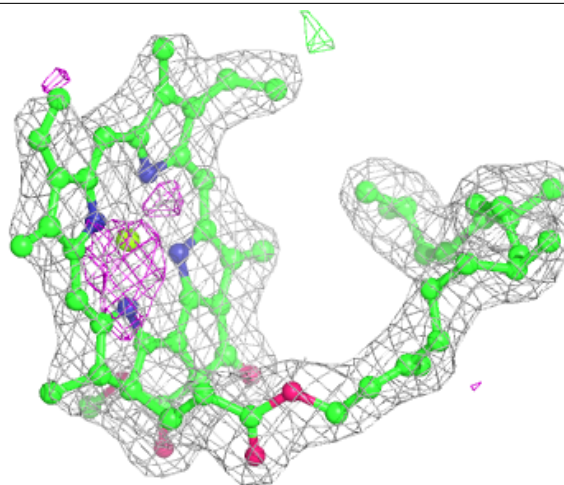
**Electron density around CLA B 604:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



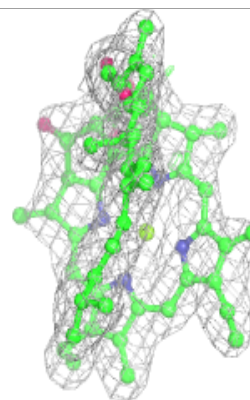
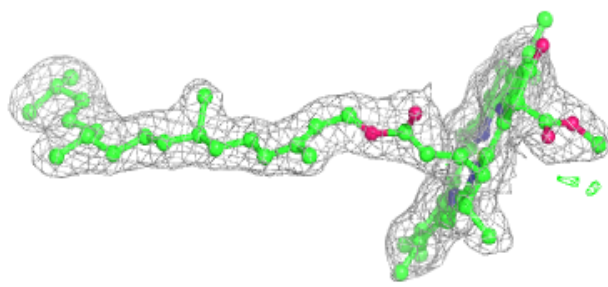
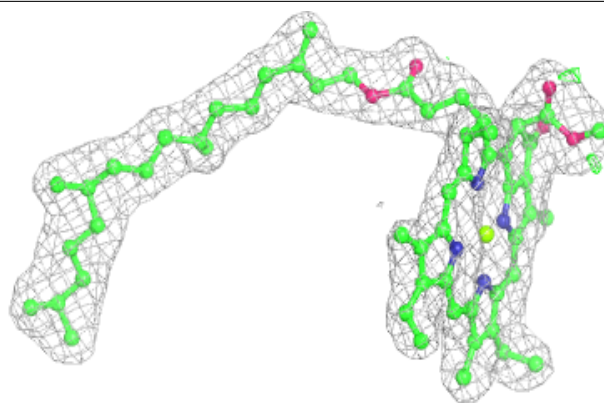
Electron density around CLA C 503:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



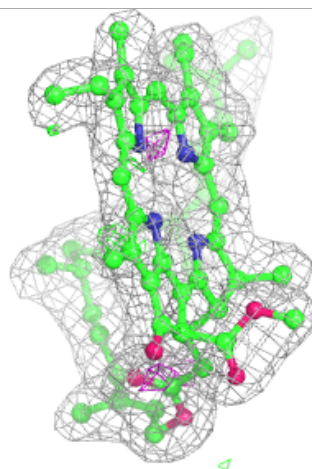
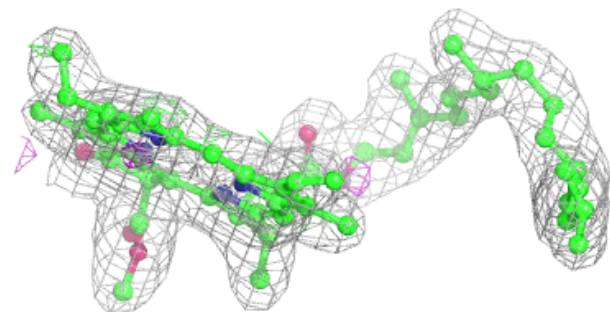
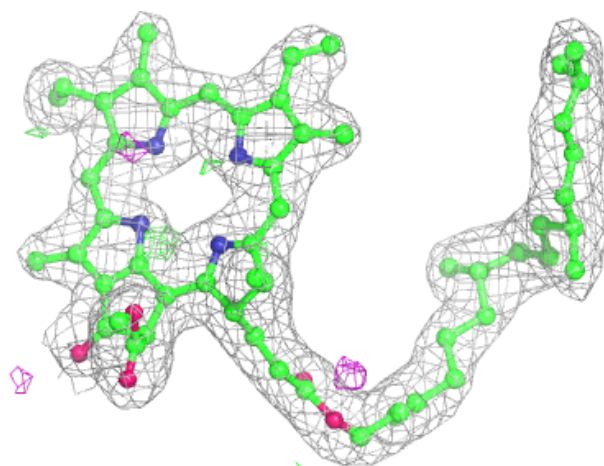
Electron density around CLA B 610:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



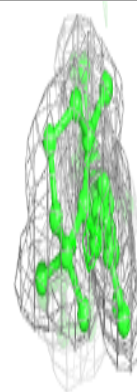
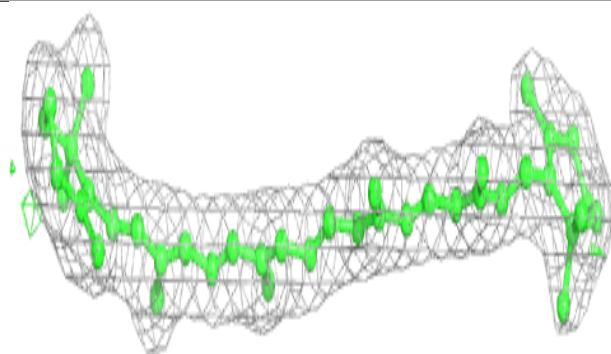
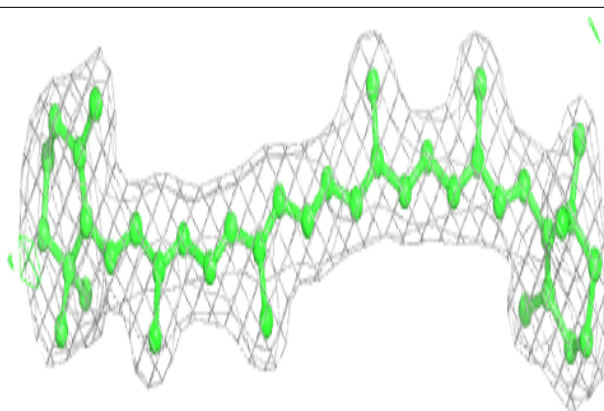
Electron density around PHO a 420 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



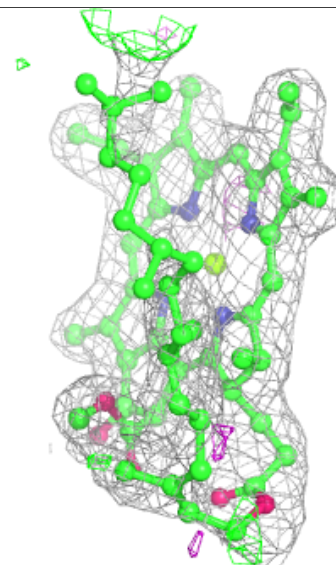
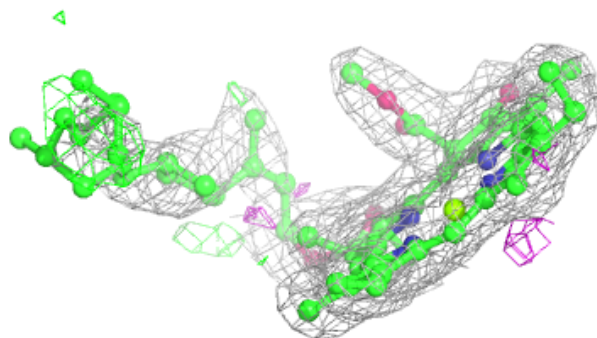
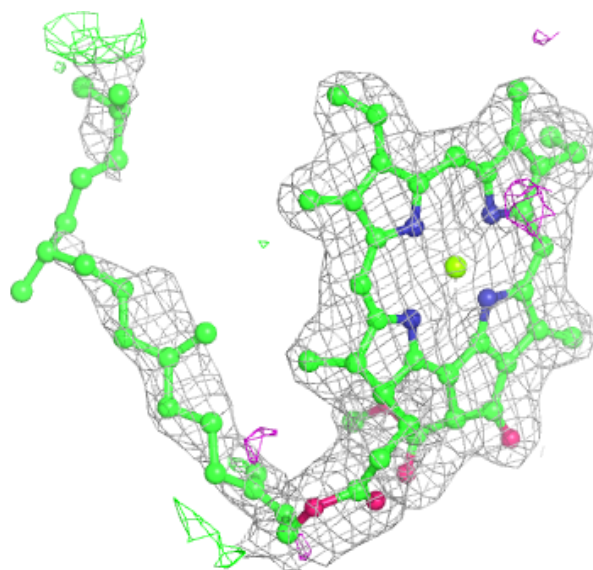
Electron density around BCR B 620:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



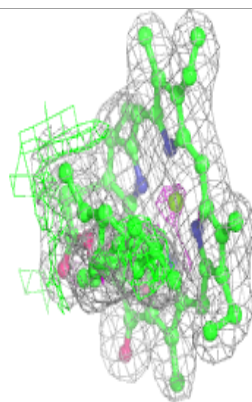
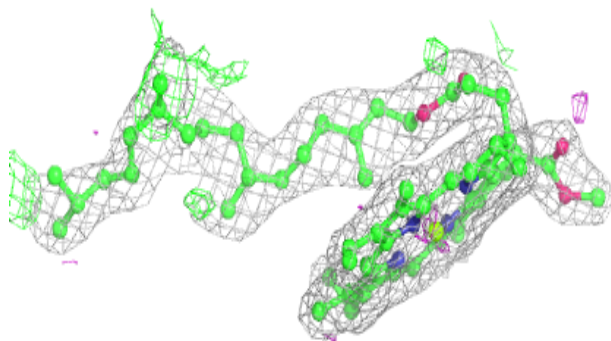
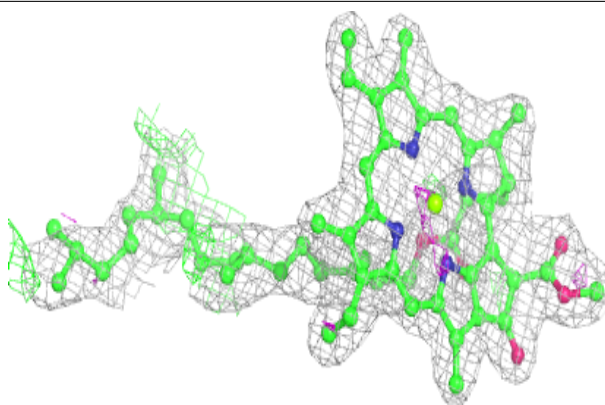
Electron density around CLA B 617:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

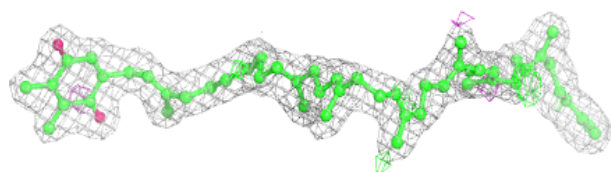
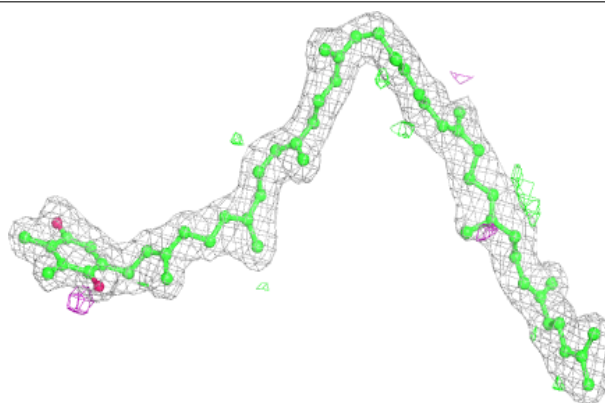


Electron density around CLA b 624:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

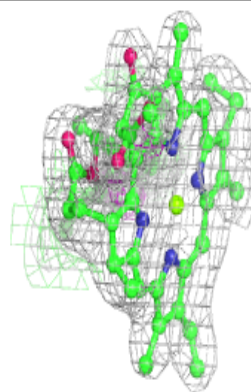
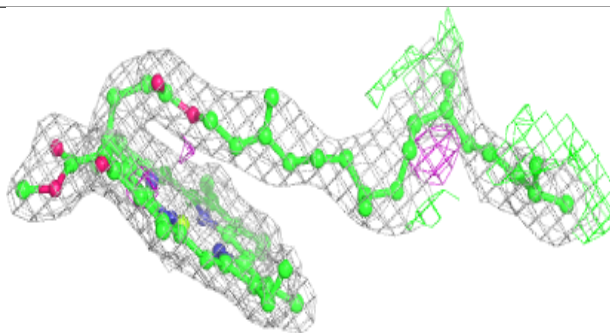
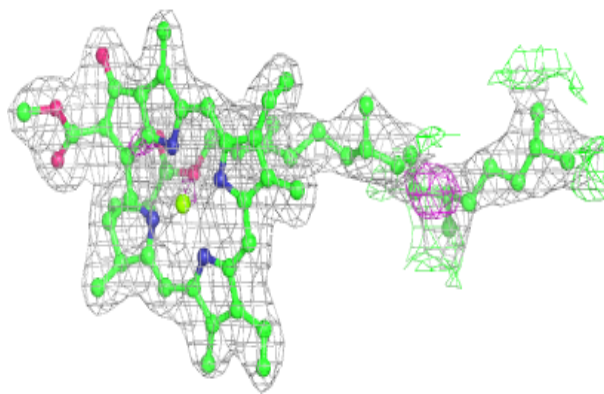
**Electron density around PL9 D 405 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



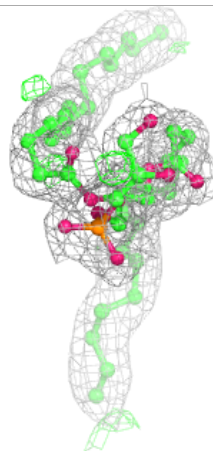
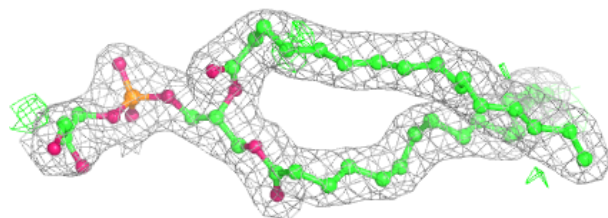
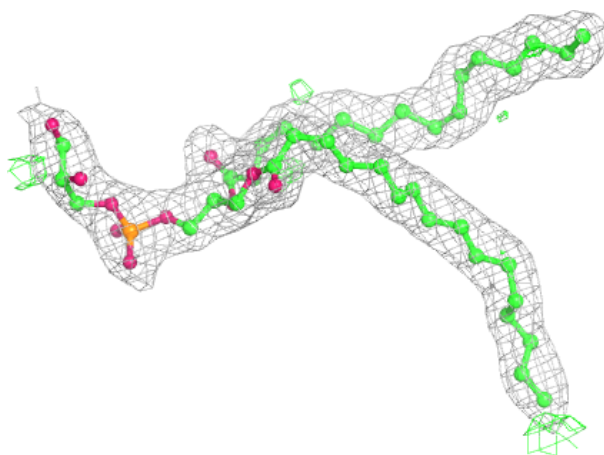
Electron density around CLA B 615:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



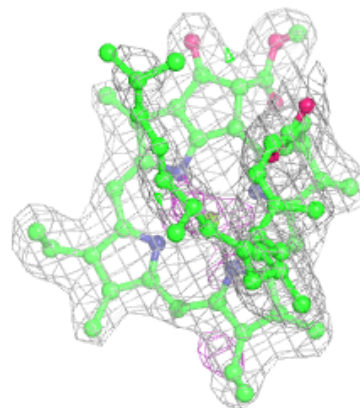
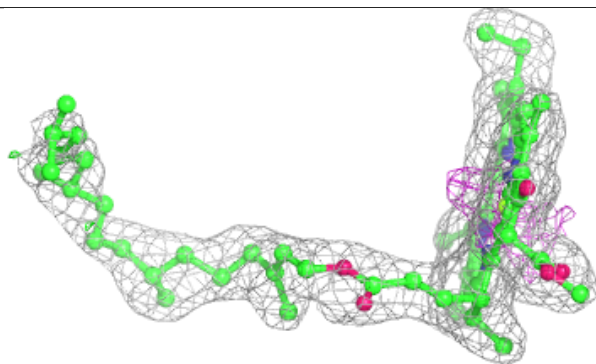
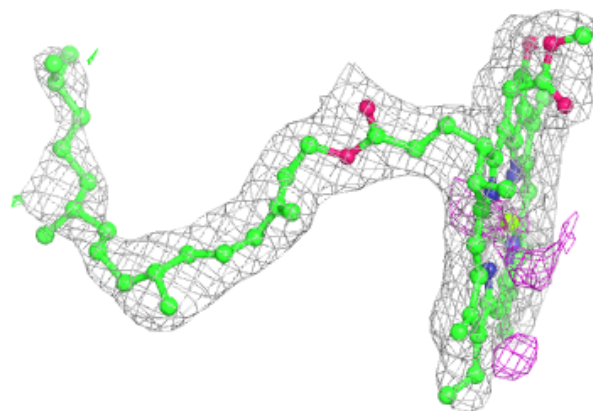
Electron density around LHG D 408:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

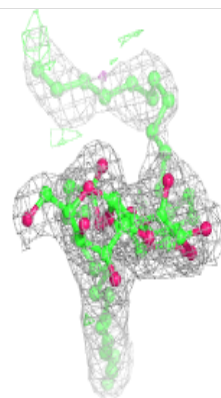
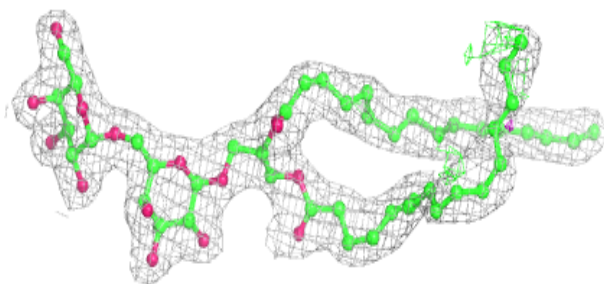
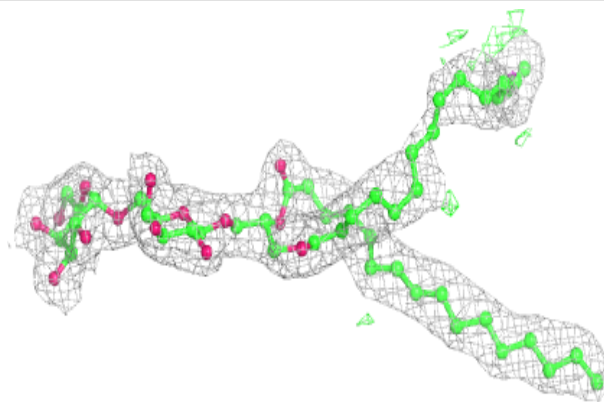


Electron density around CLA D 403:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

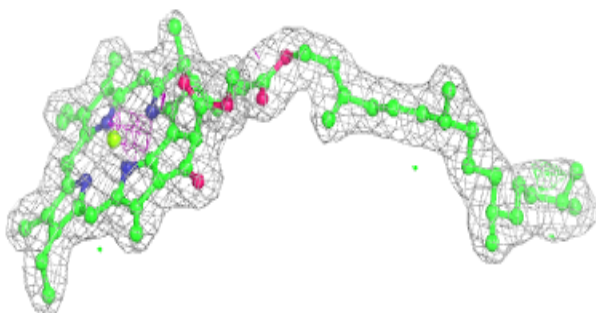
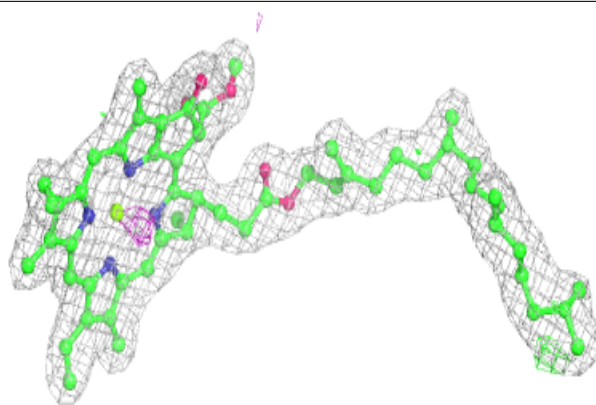
**Electron density around DGD C 516:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

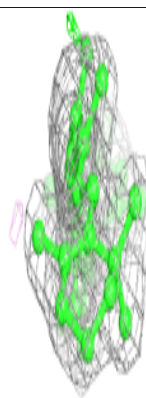
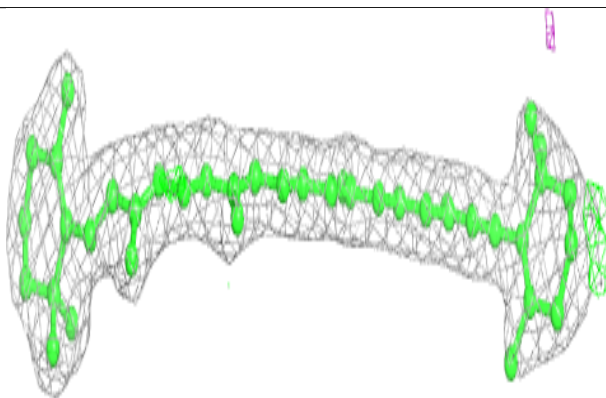
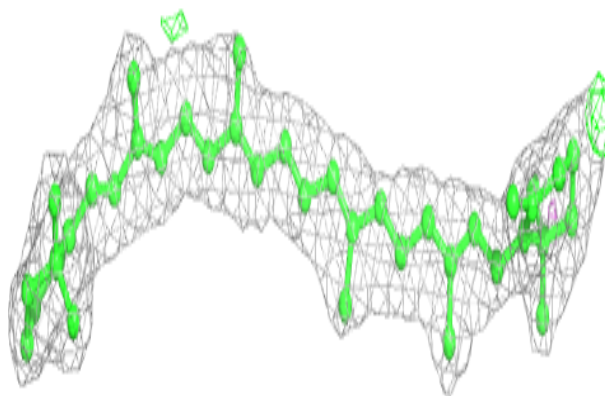


Electron density around CLA a 409:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

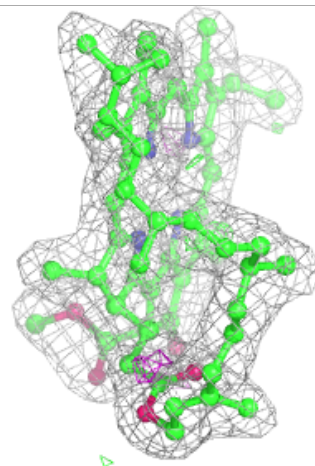
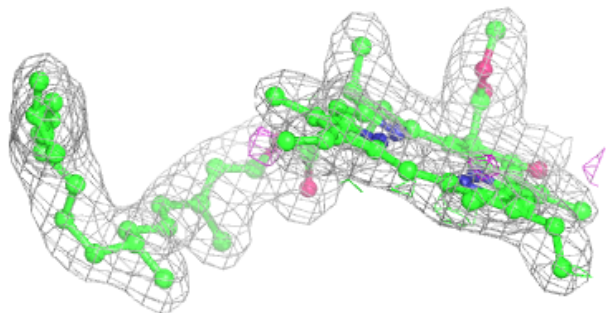
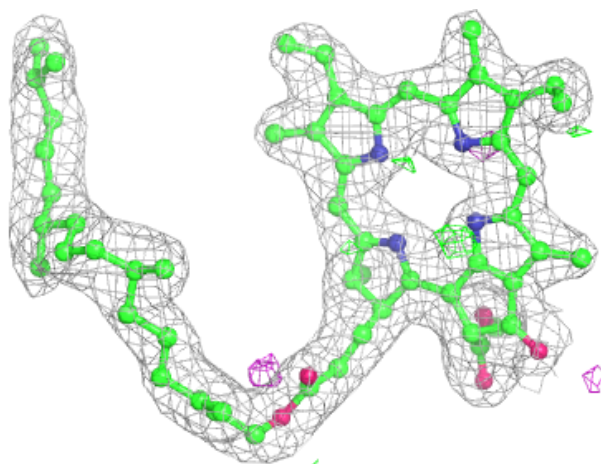
**Electron density around BCR H 102:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



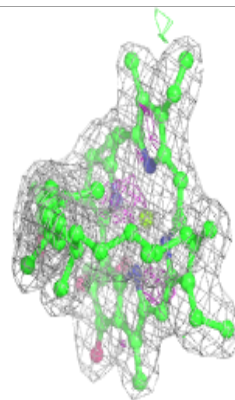
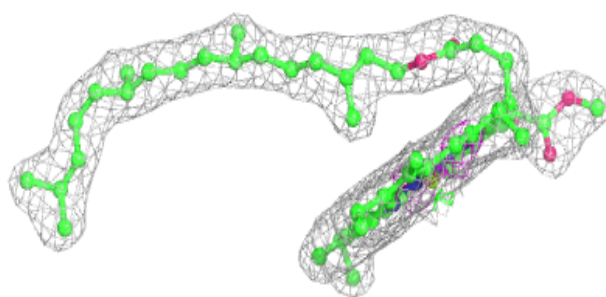
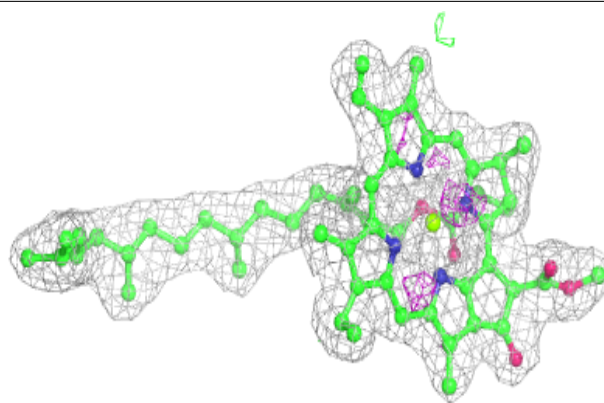
Electron density around PHO a 420 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

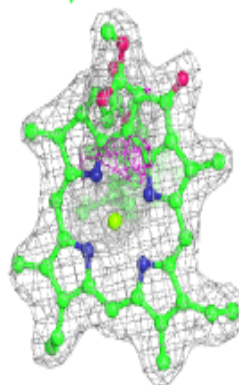
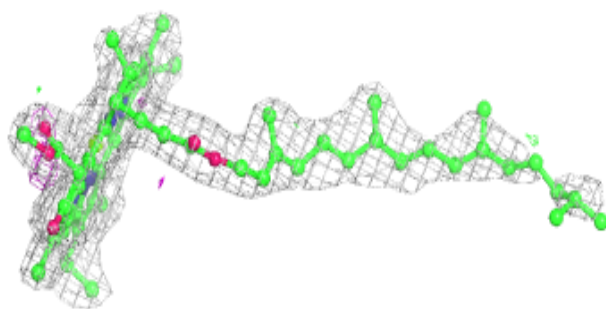
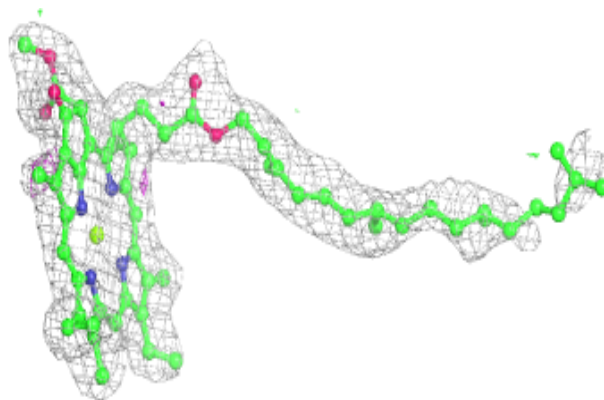


Electron density around CLA b 618:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

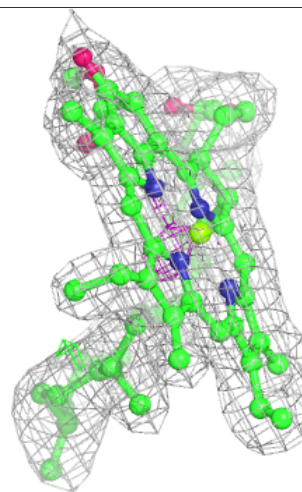
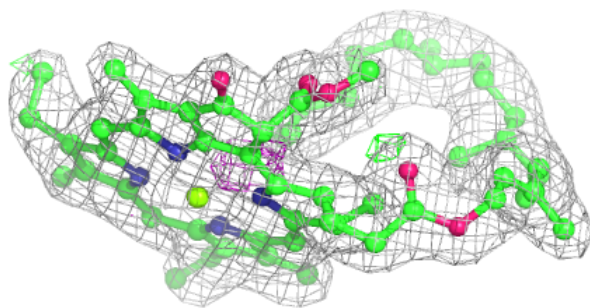
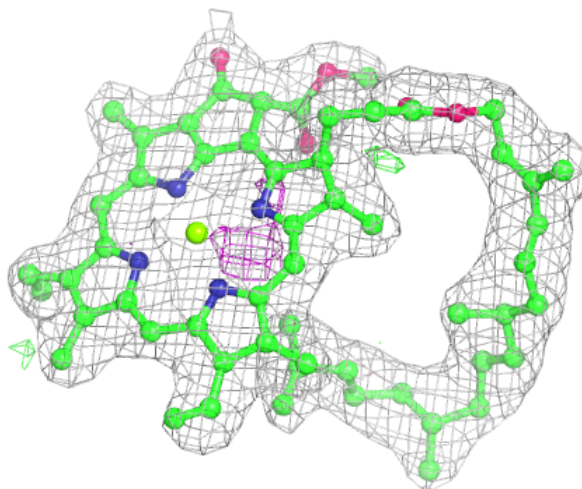
**Electron density around CLA d 403:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



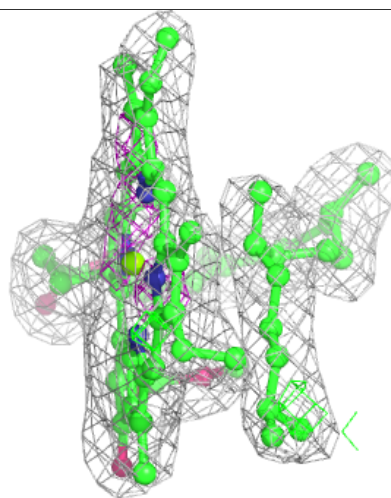
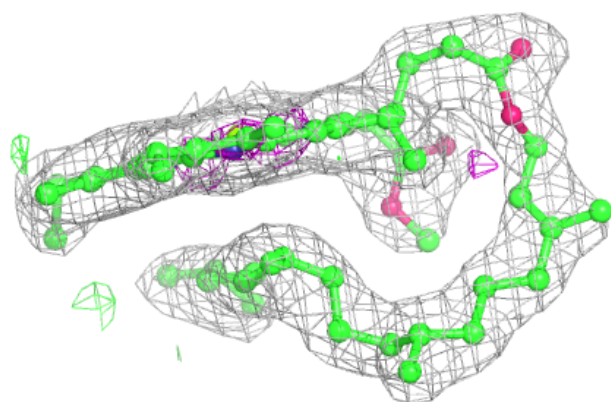
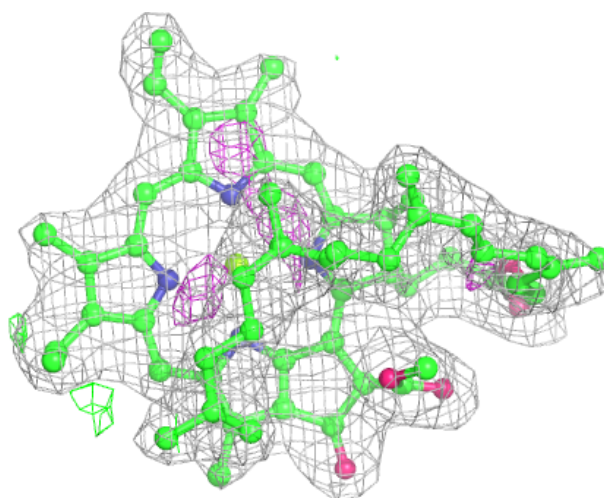
Electron density around CLA b 625:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



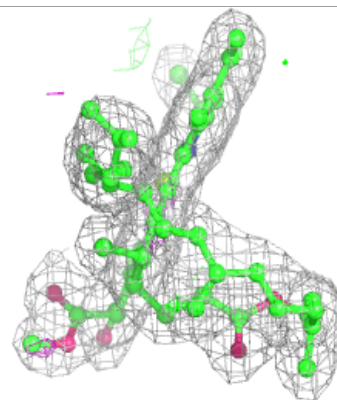
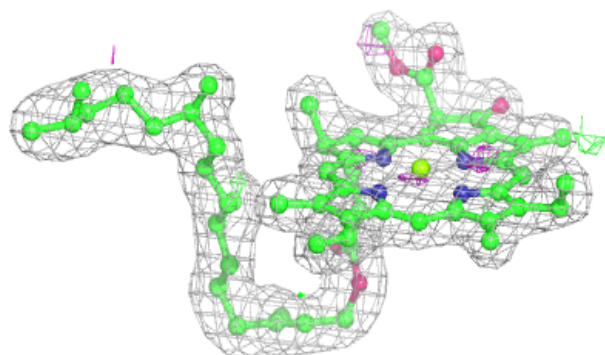
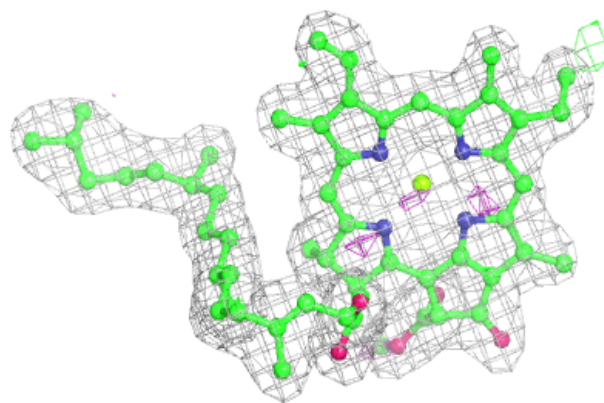
Electron density around CLA C 510:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

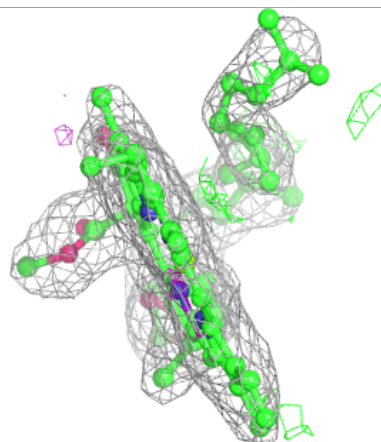
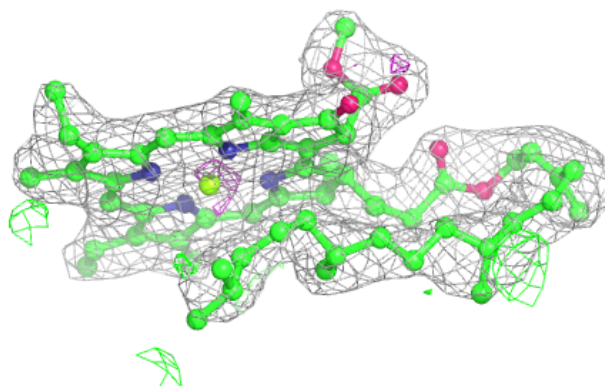
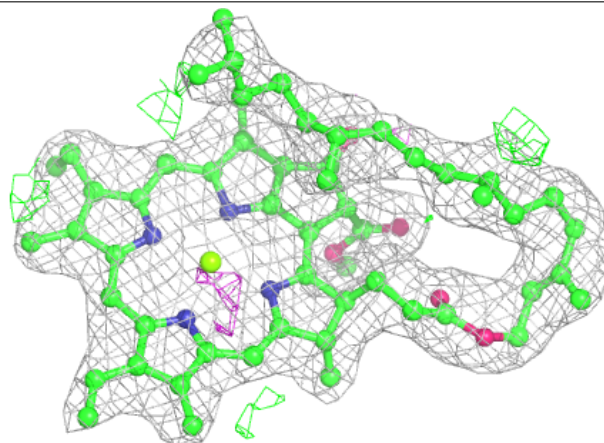


Electron density around CLA d 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

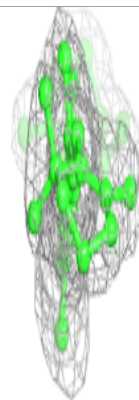
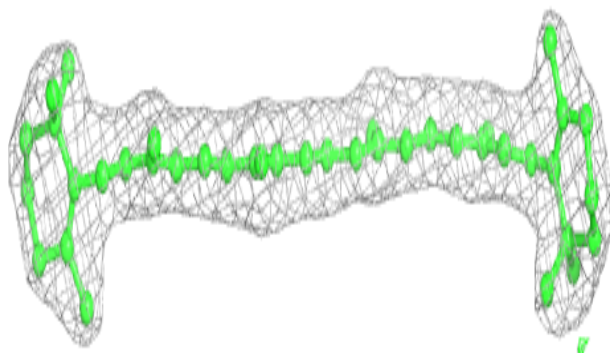
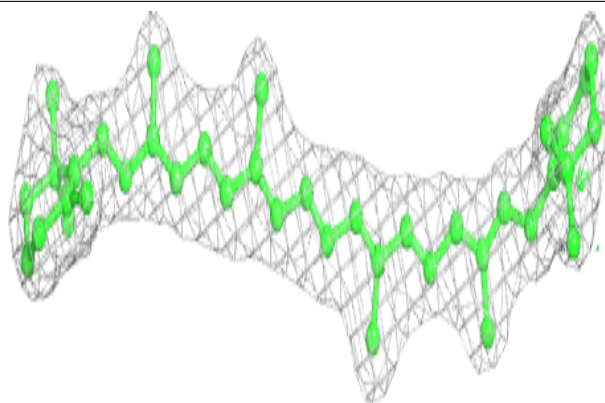
**Electron density around CLA c 513:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



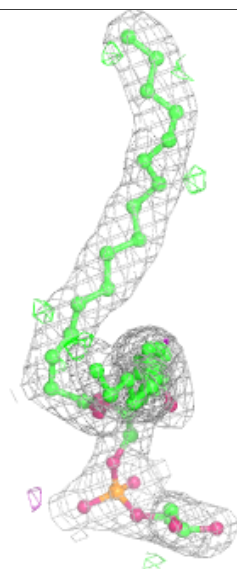
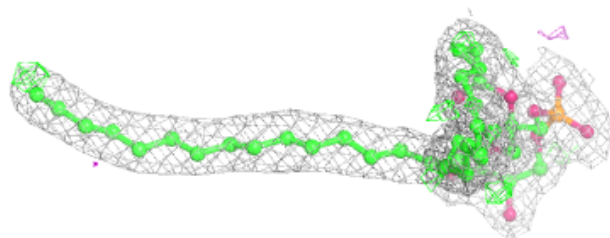
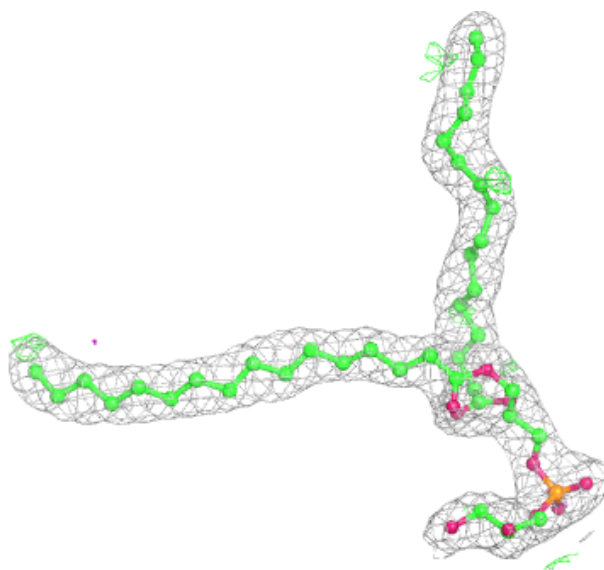
Electron density around BCR c 518:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



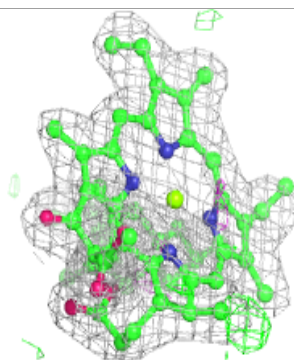
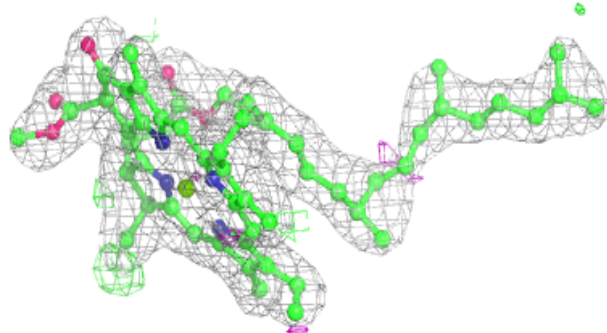
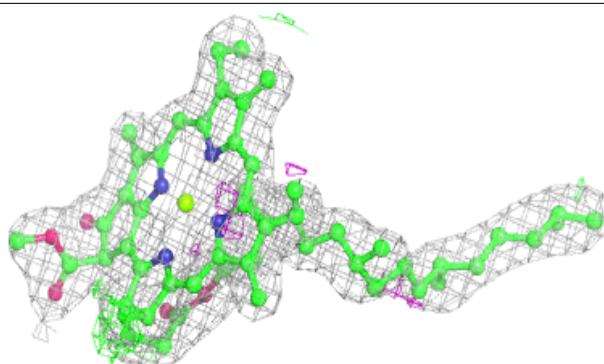
Electron density around LHG L 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

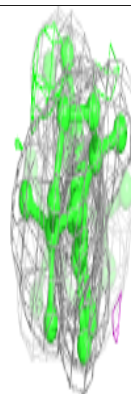
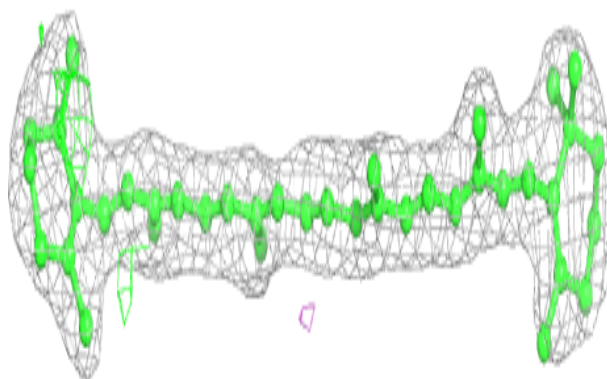
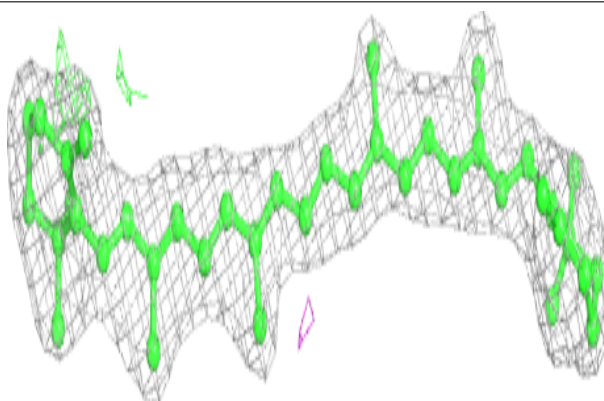


Electron density around CLA C 505:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

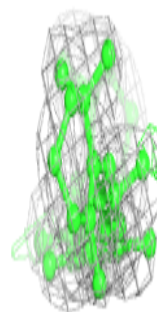
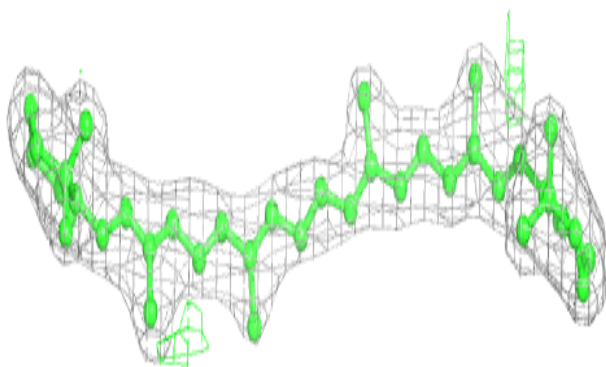
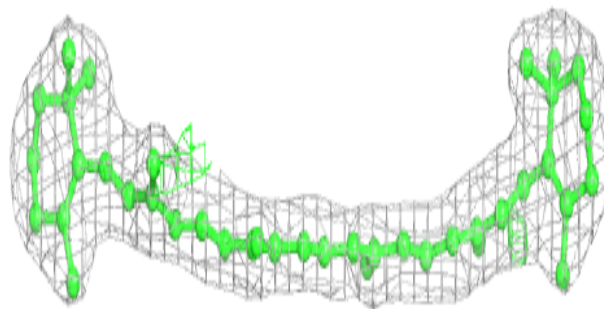
**Electron density around BCR C 514:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

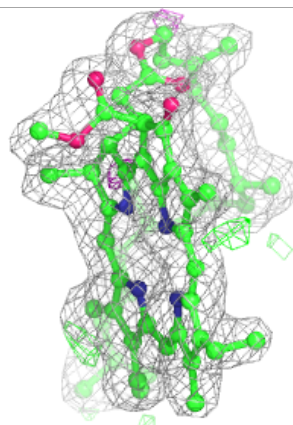
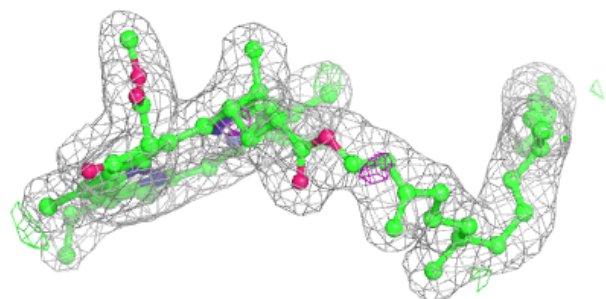
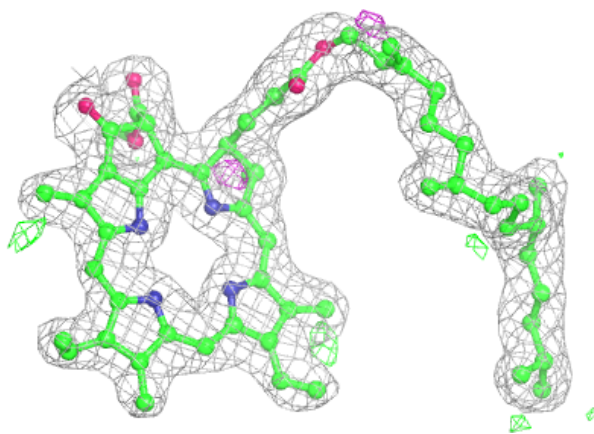


Electron density around BCR K 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

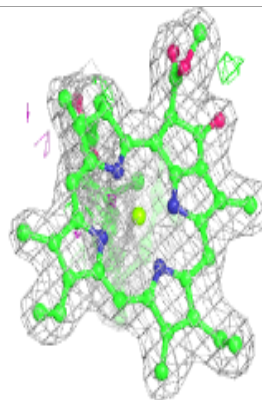
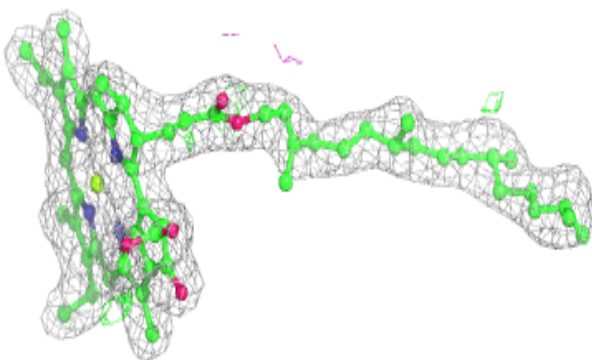
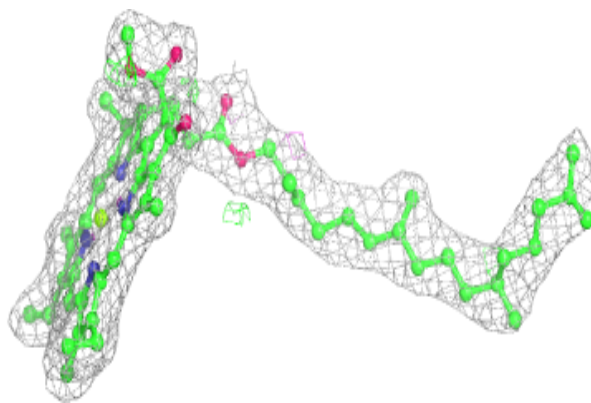
**Electron density around PHO A 409 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

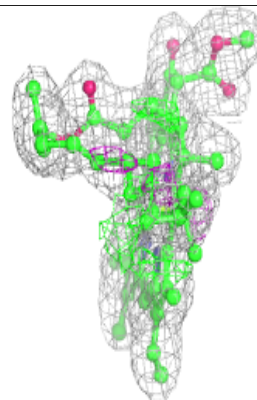
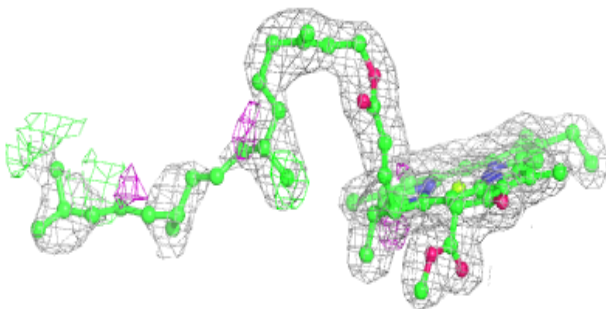
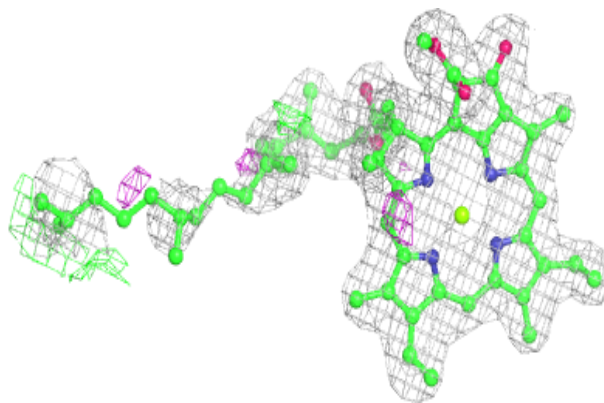


Electron density around CLA b 614:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

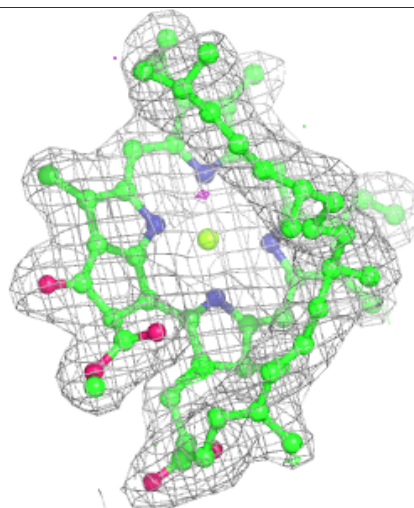
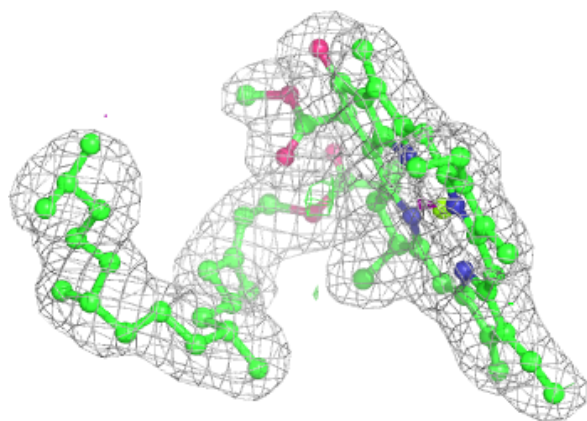
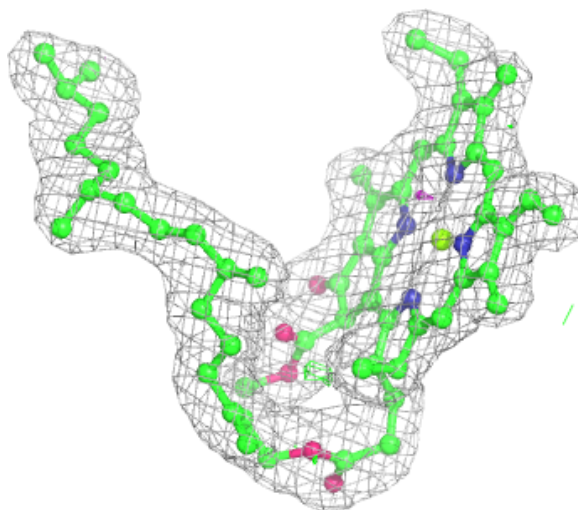
**Electron density around CLA a 410:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



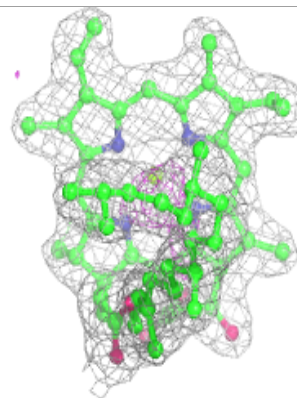
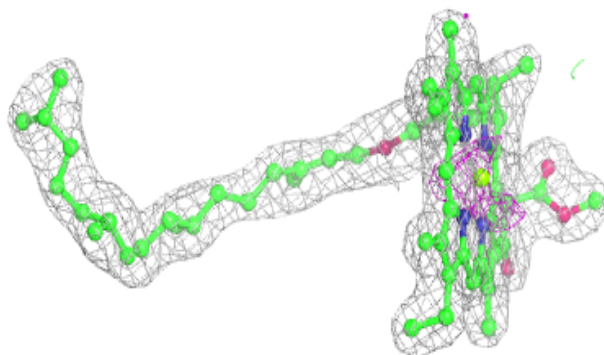
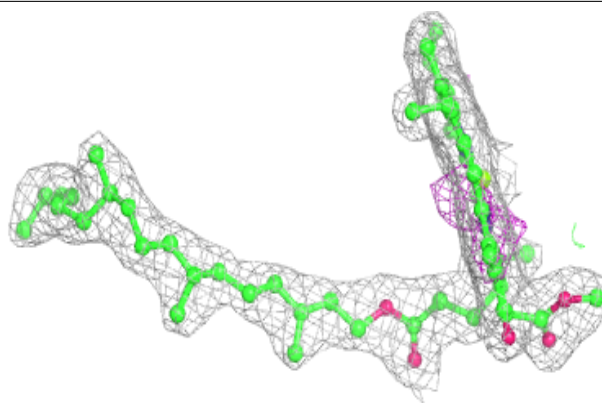
Electron density around CLA b 623:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

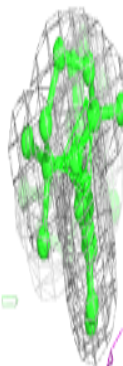
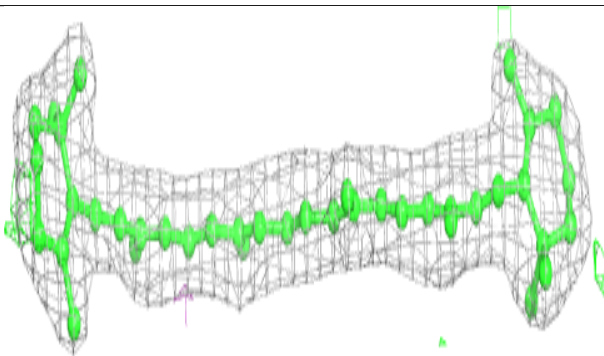
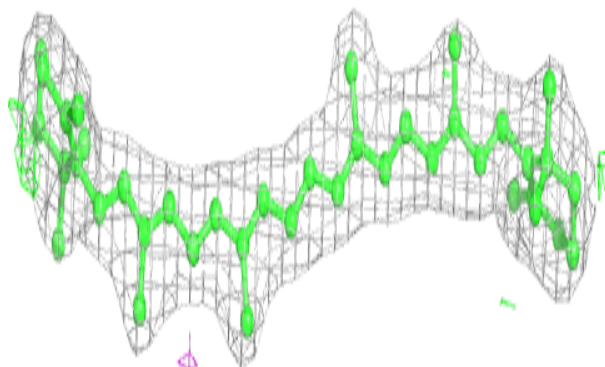


Electron density around CLA b 615:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

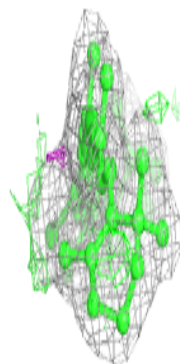
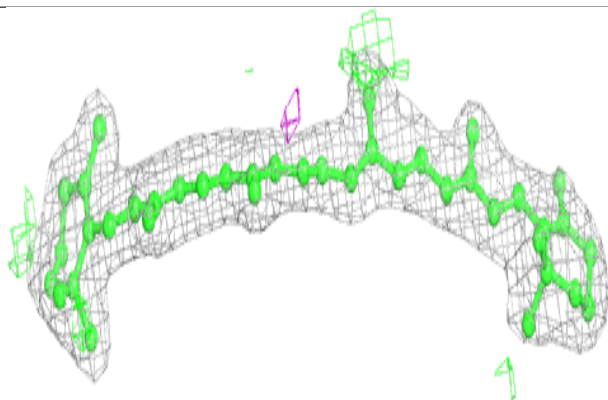
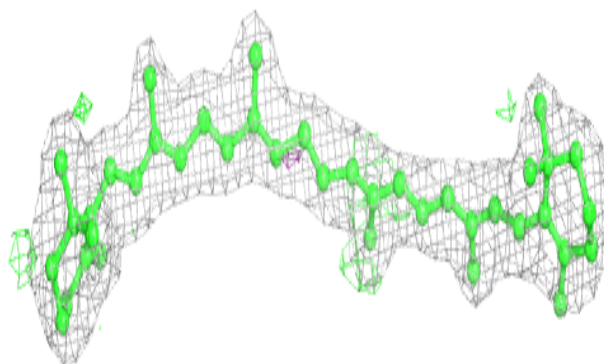
**Electron density around BCR C 515:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



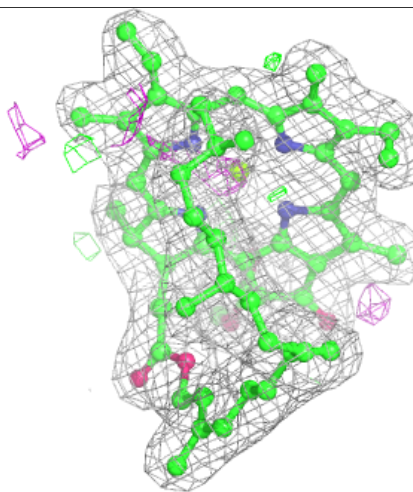
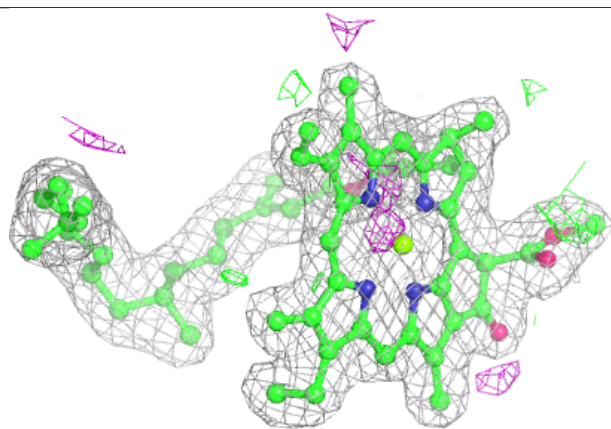
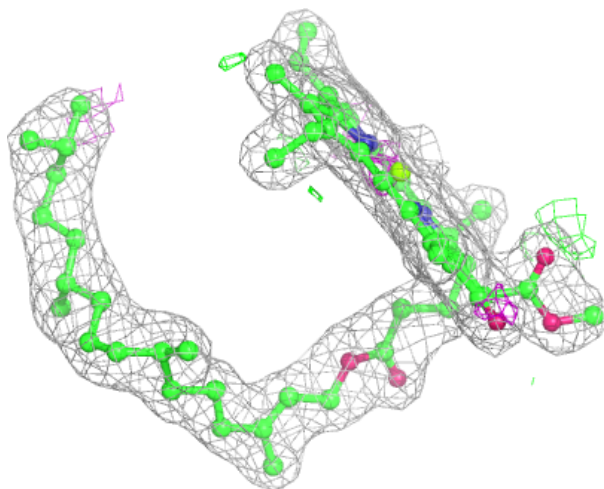
Electron density around BCR t 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



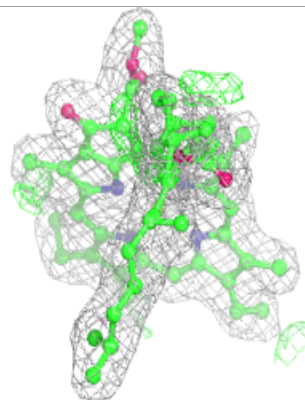
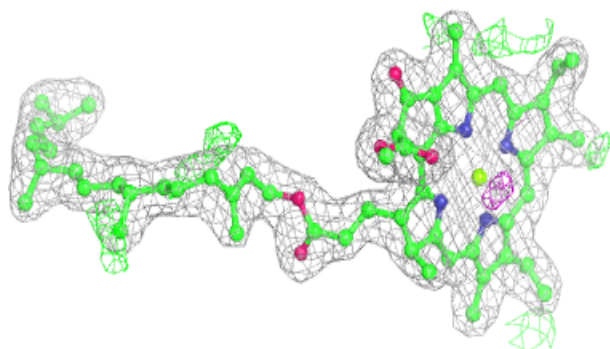
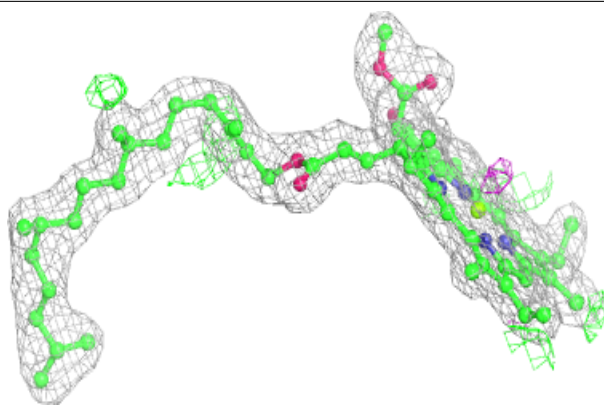
Electron density around CLA B 612:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

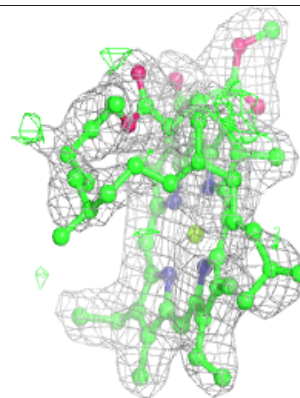
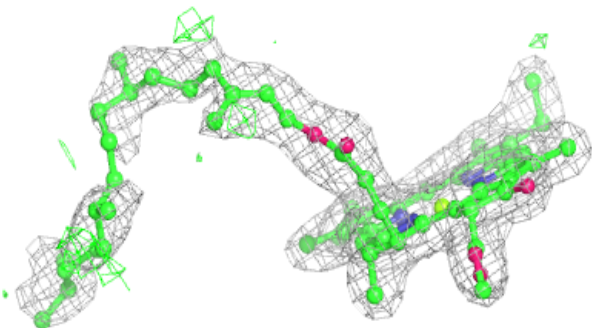
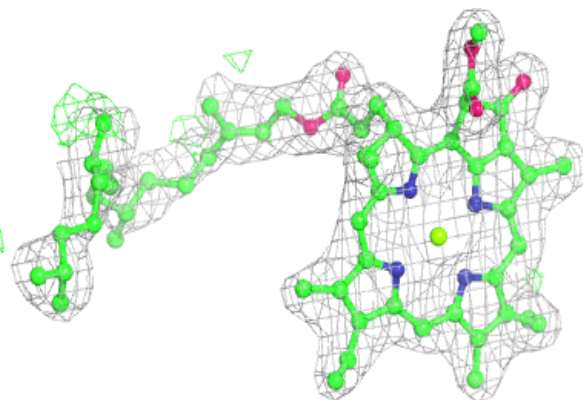


Electron density around CLA D 402:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

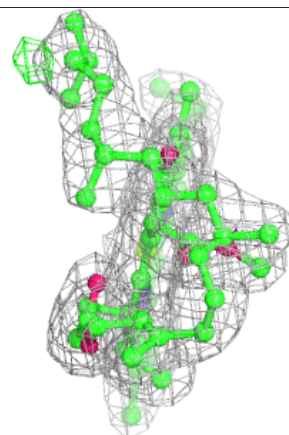
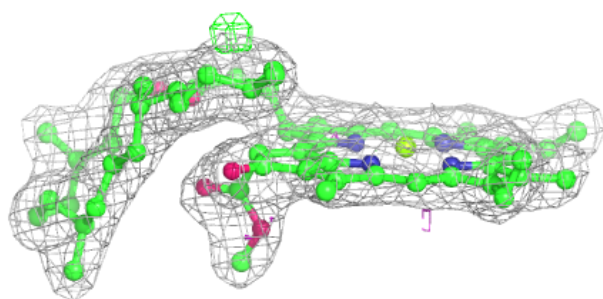
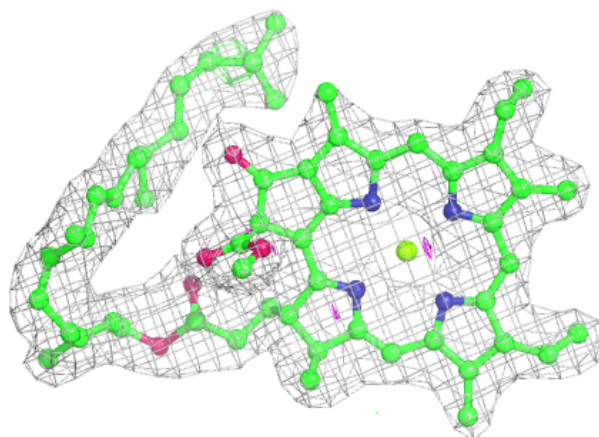
**Electron density around CLA A 410:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

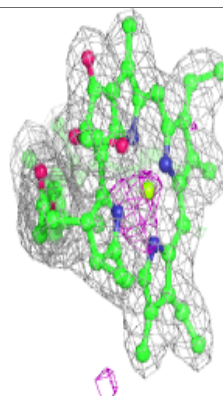
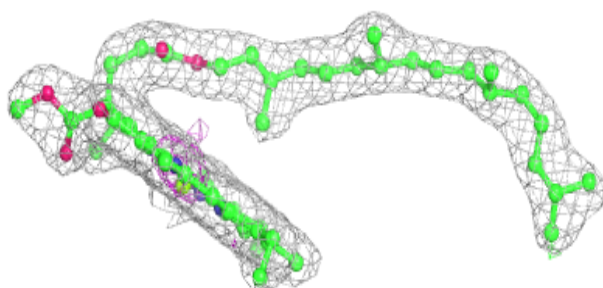
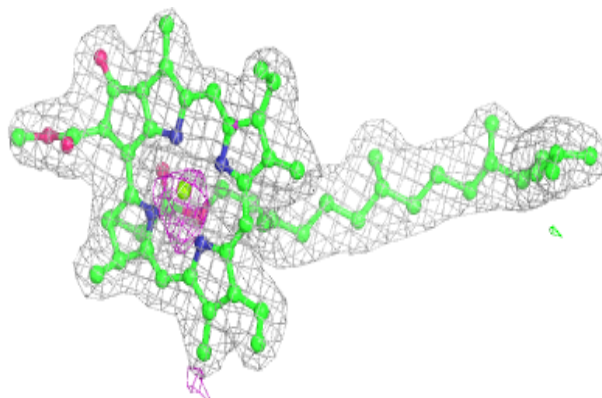


Electron density around CLA b 620:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

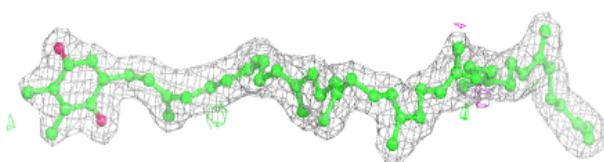
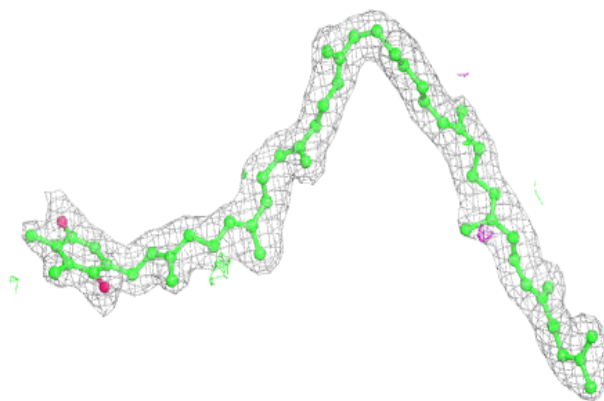
**Electron density around CLA B 609:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

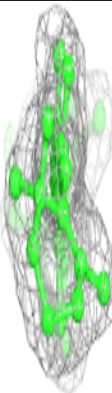
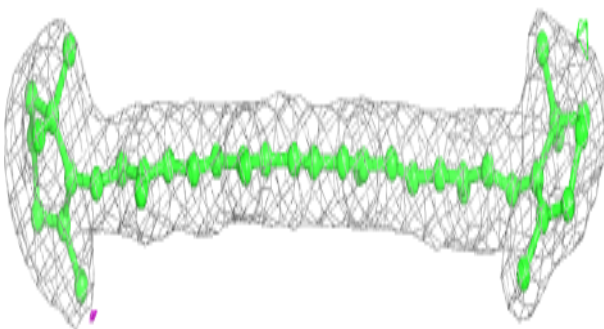
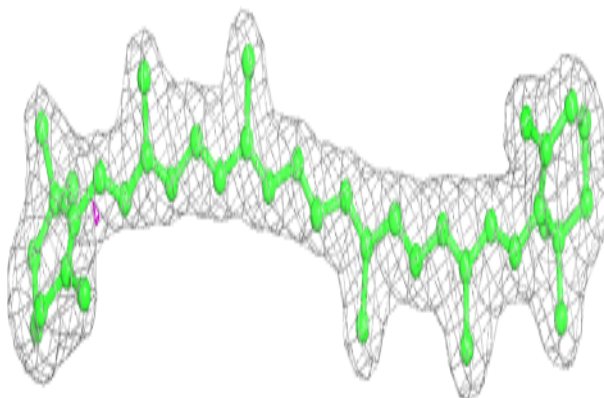


Electron density around PL9 d 405 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

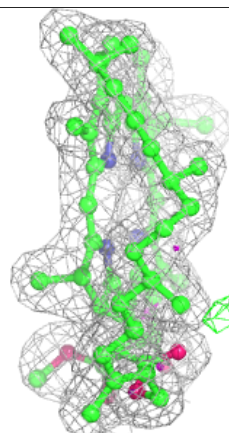
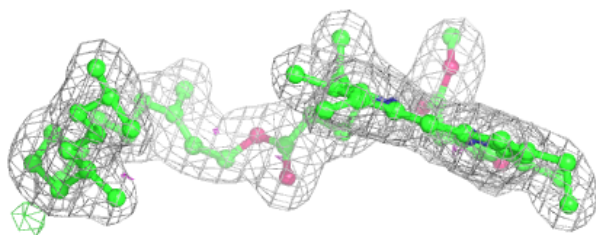
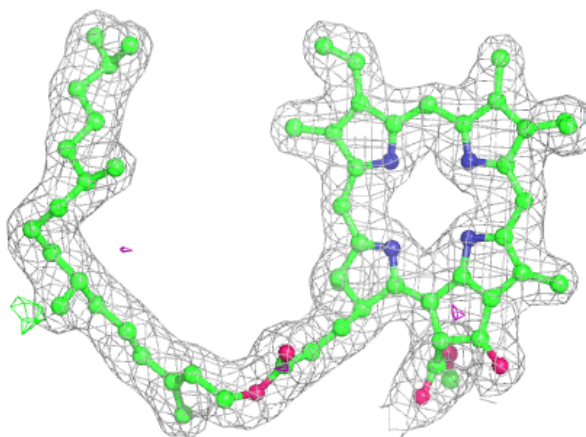
**Electron density around BCR B 619:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

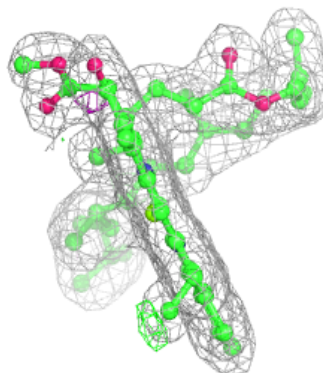
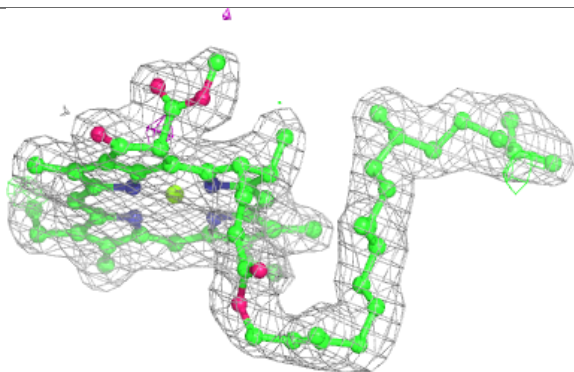
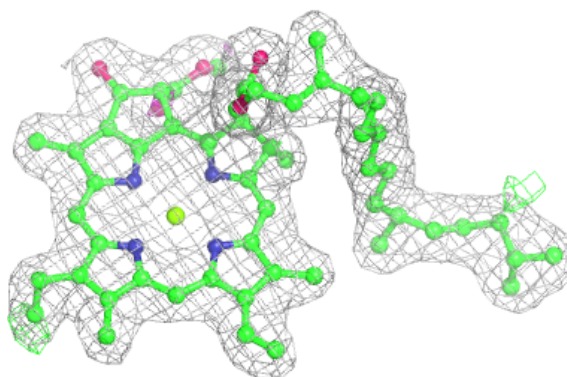


Electron density around PHO A 408:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

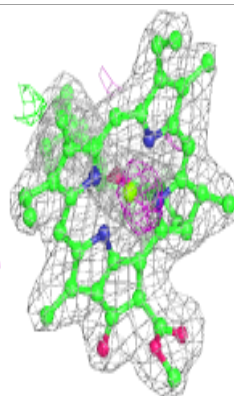
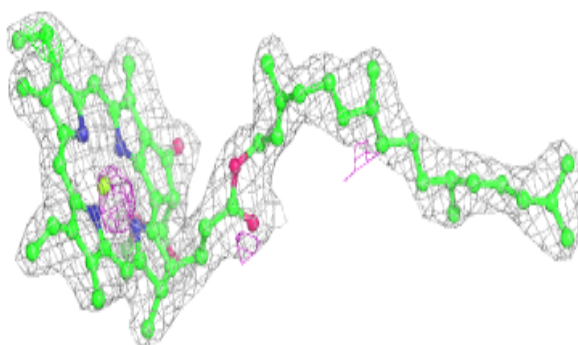
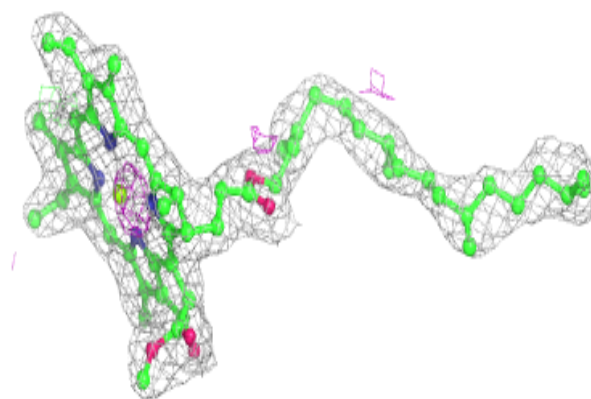
**Electron density around CLA A 406:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

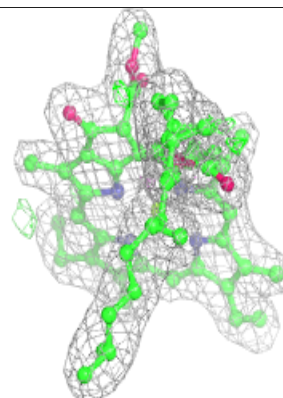
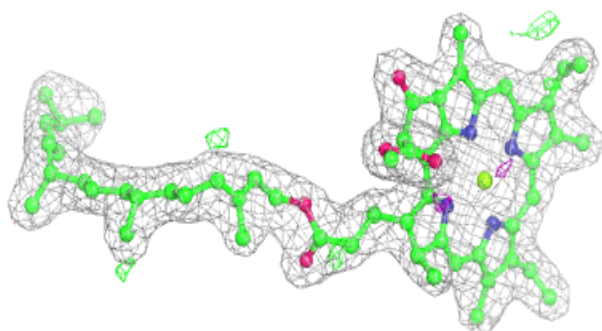
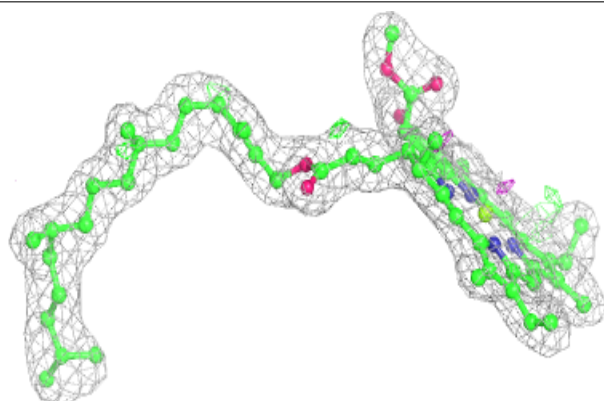


Electron density around CLA c 506:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

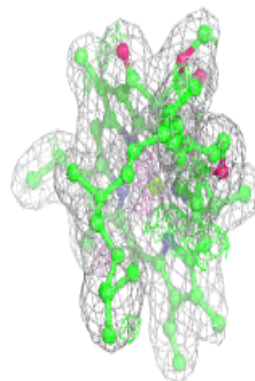
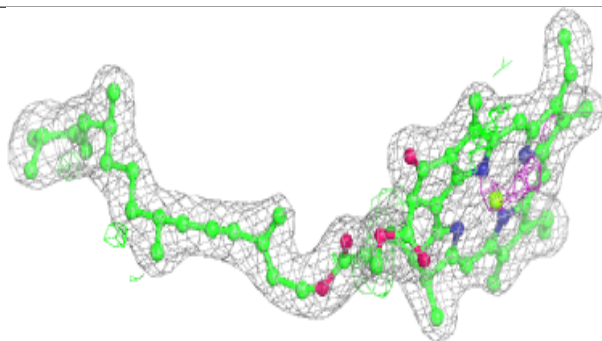
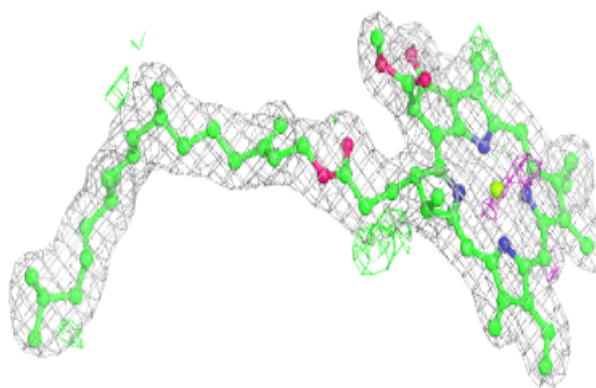
**Electron density around CLA d 402:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

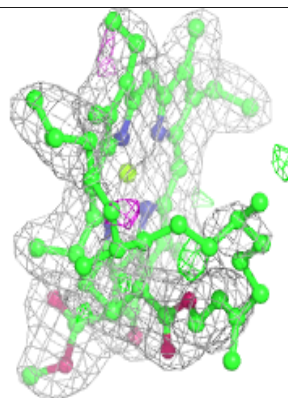
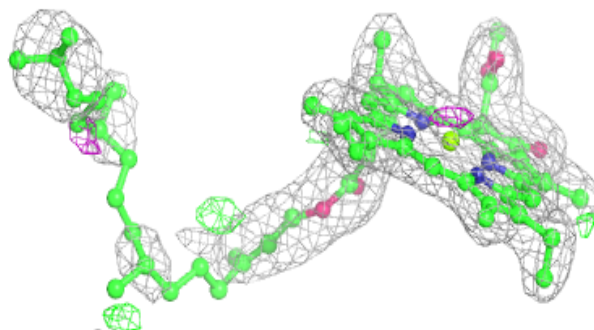
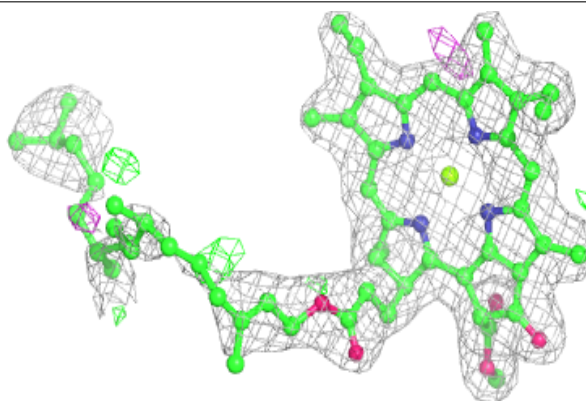


Electron density around CLA A 405:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

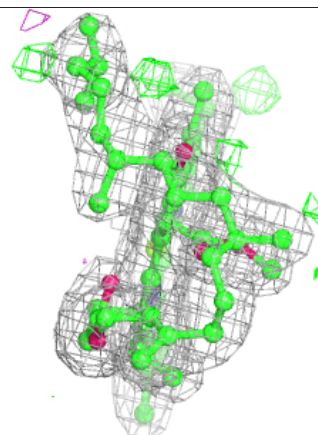
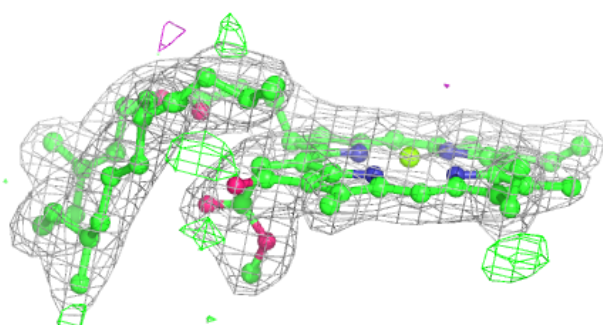
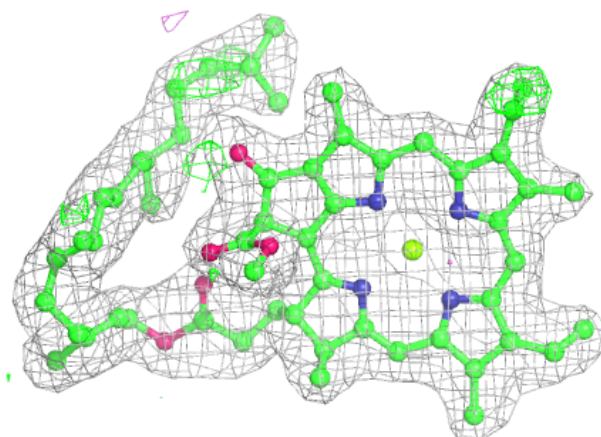
**Electron density around CLA a 412:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

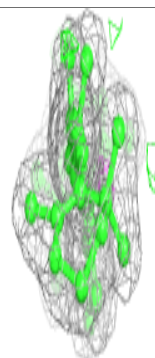
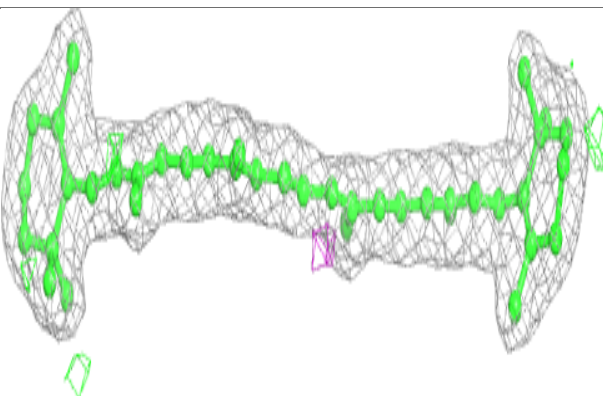
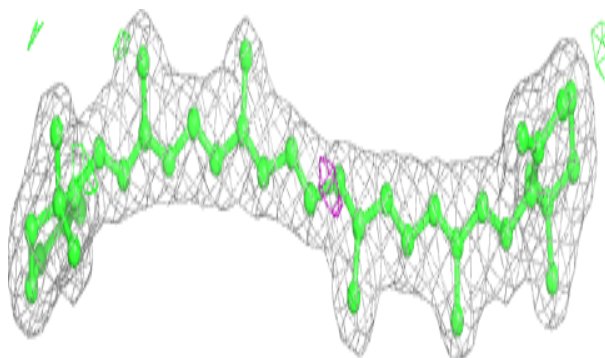


Electron density around CLA B 611:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

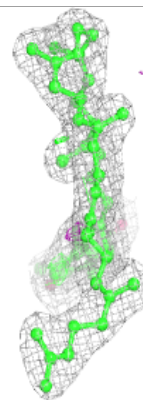
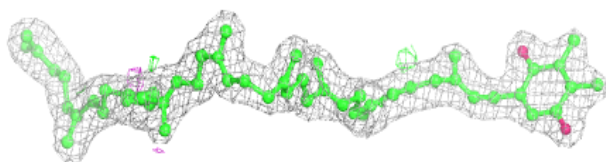
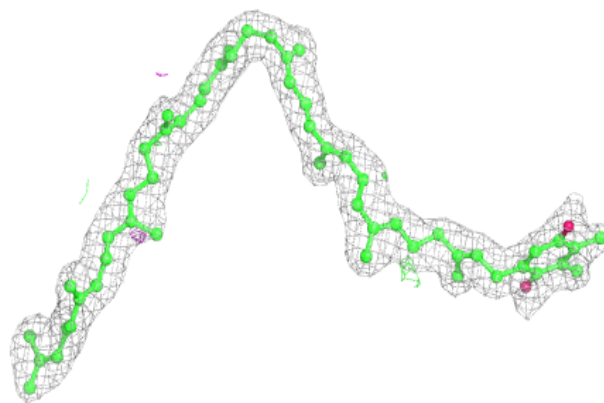
**Electron density around BCR A 411:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

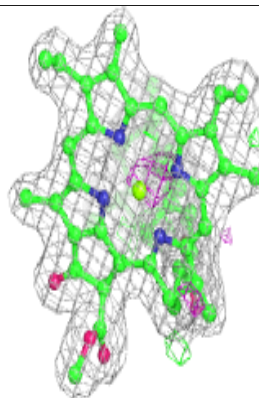
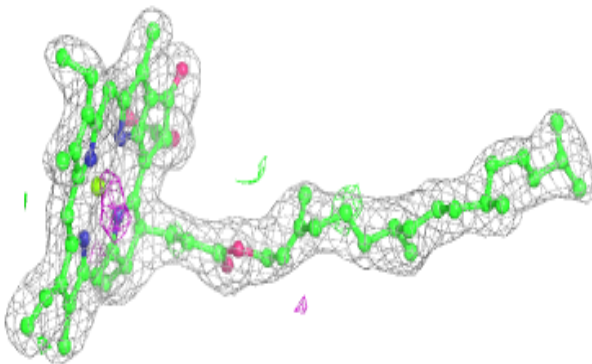
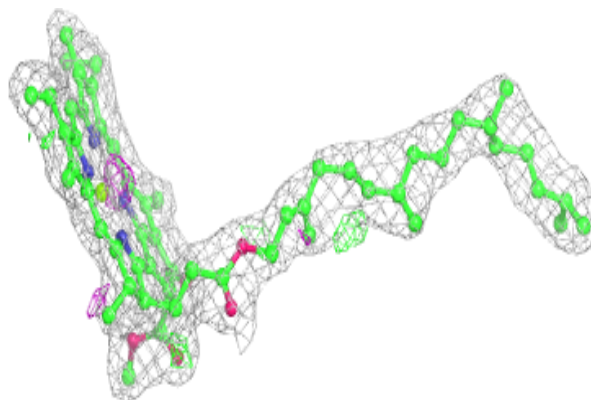


Electron density around PL9 d 405 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

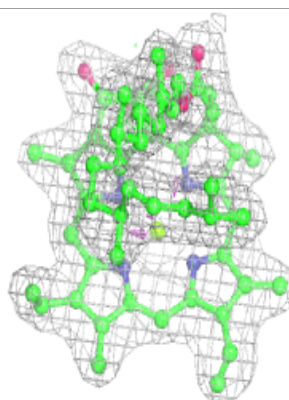
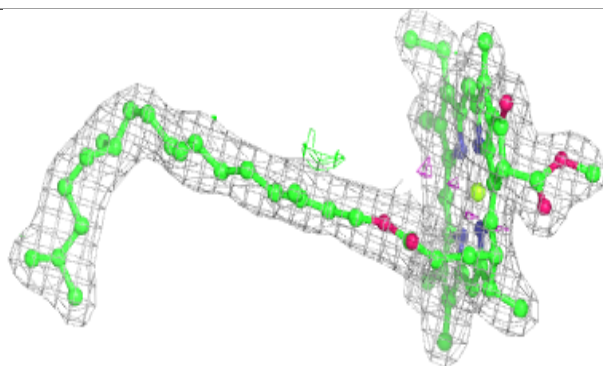
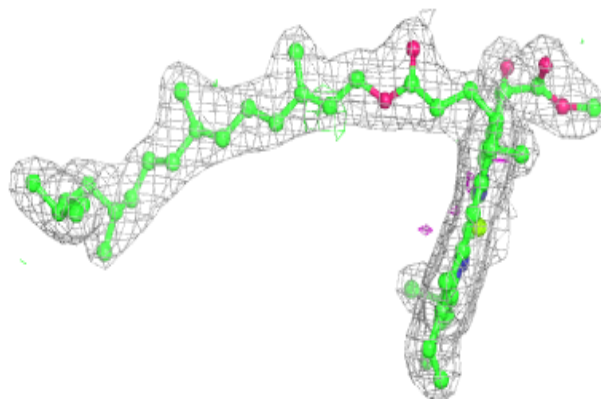
**Electron density around CLA B 605:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



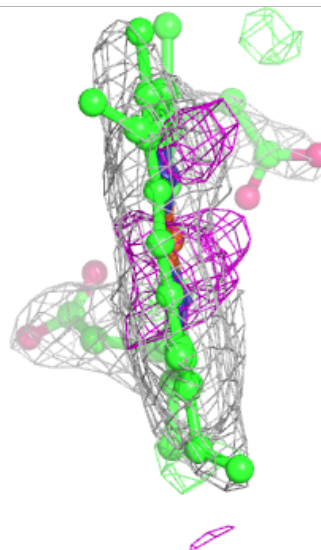
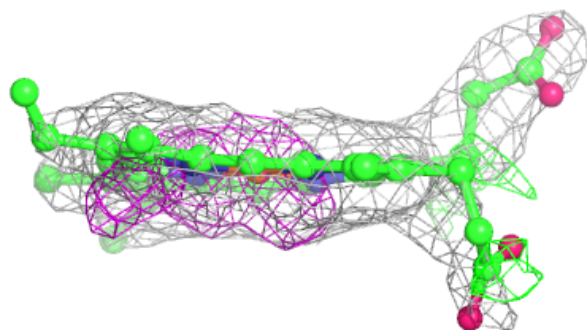
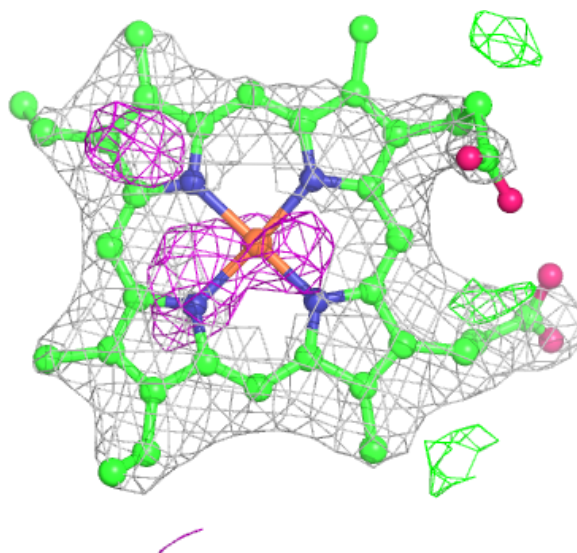
Electron density around CLA B 606:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



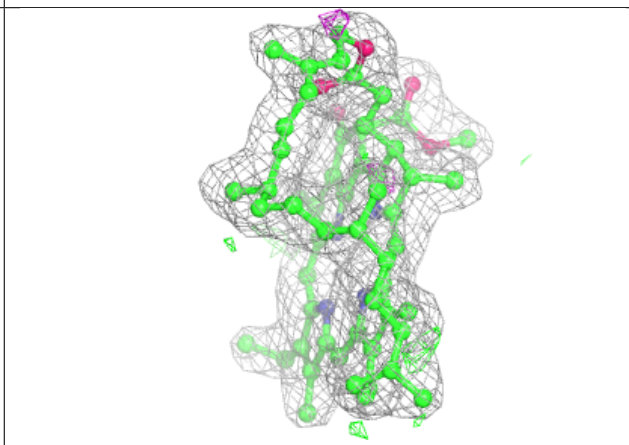
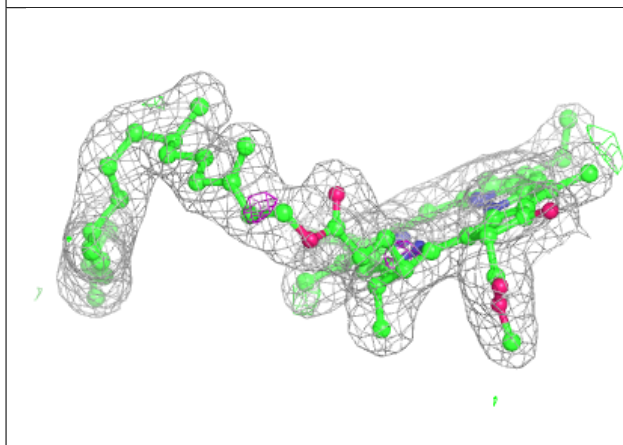
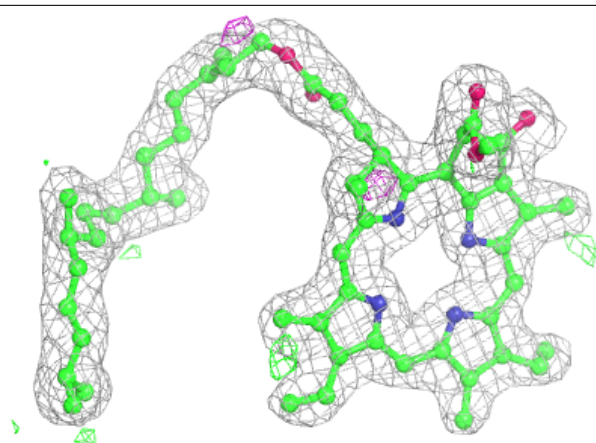
Electron density around HEM e 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

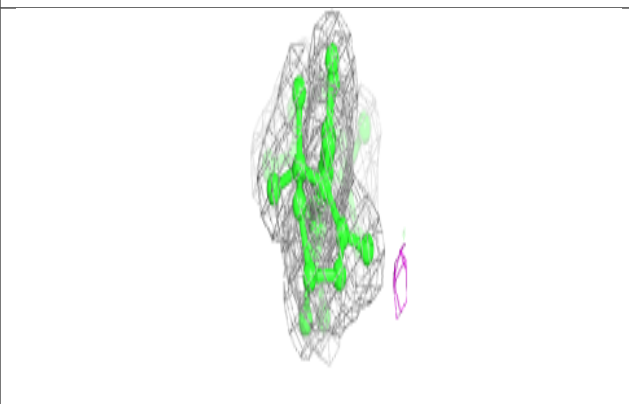
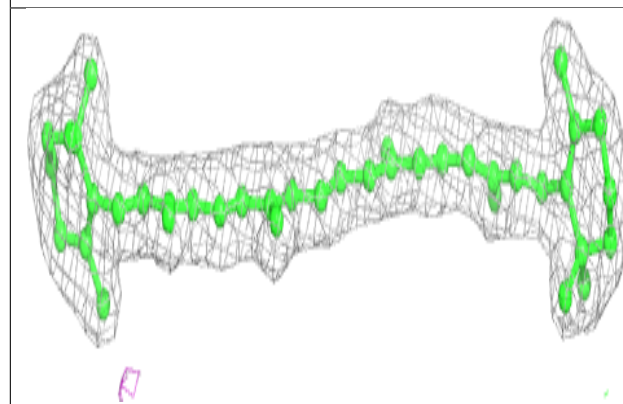
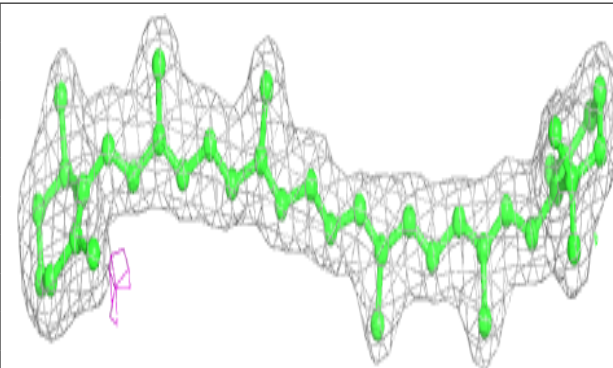


Electron density around PHO A 409 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

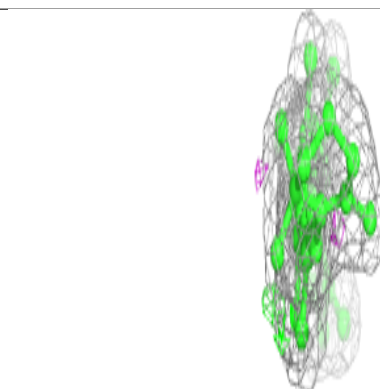
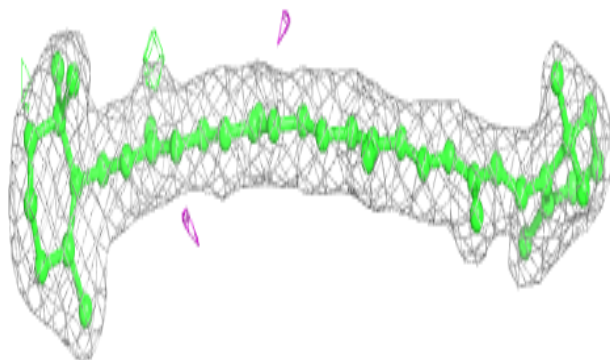
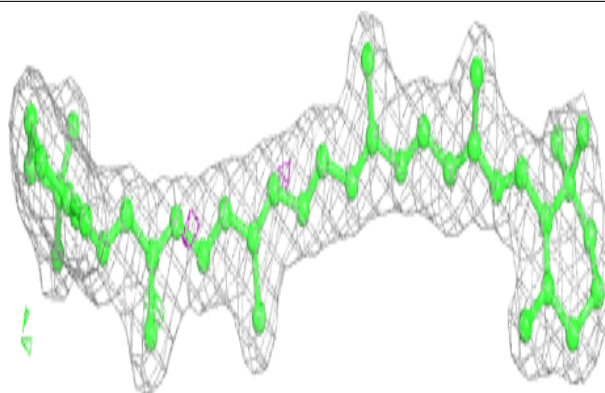
**Electron density around BCR a 413:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

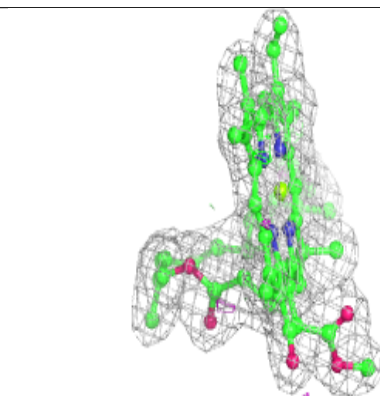
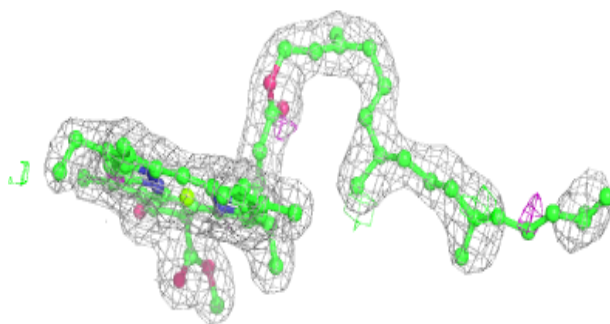
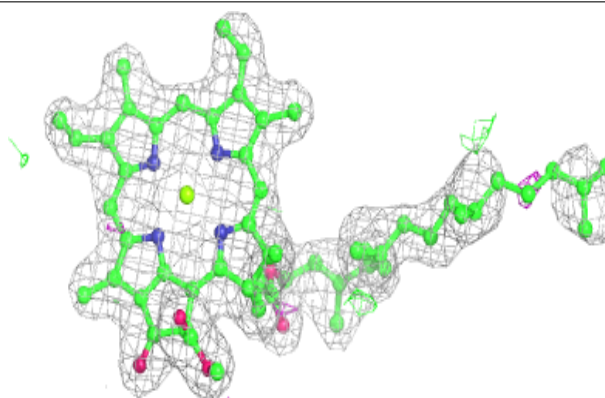


Electron density around BCR b 627:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

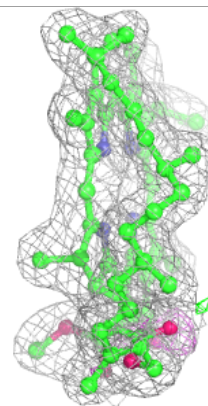
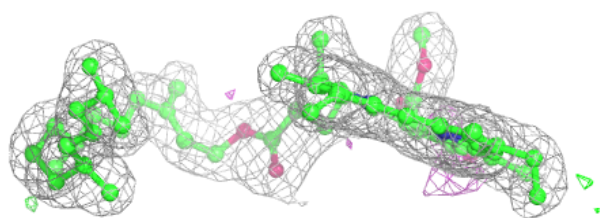
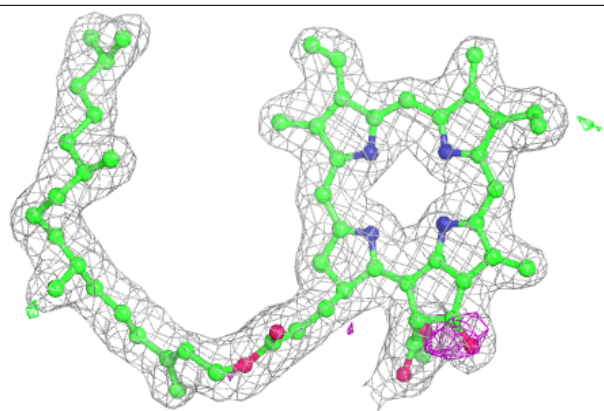
**Electron density around CLA A 407:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

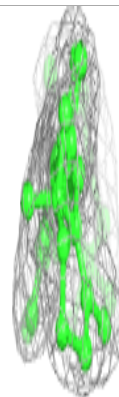
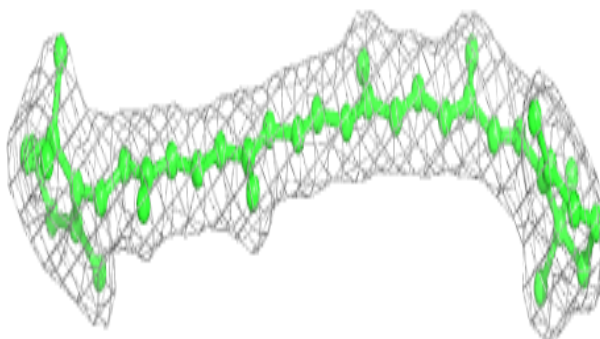
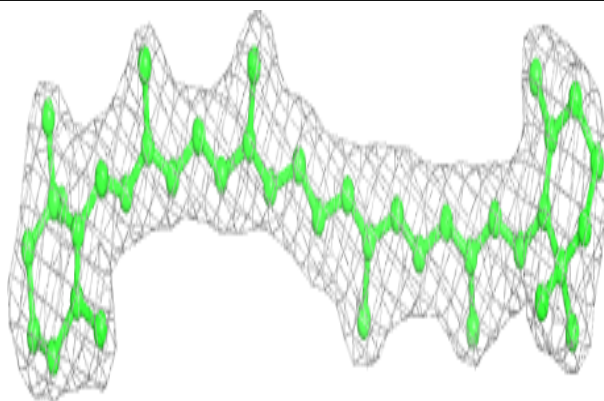


Electron density around PHO a 411:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

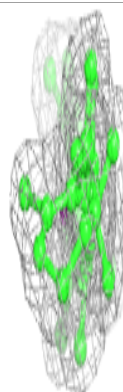
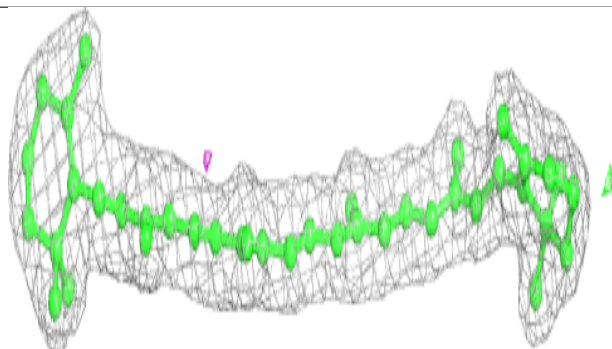
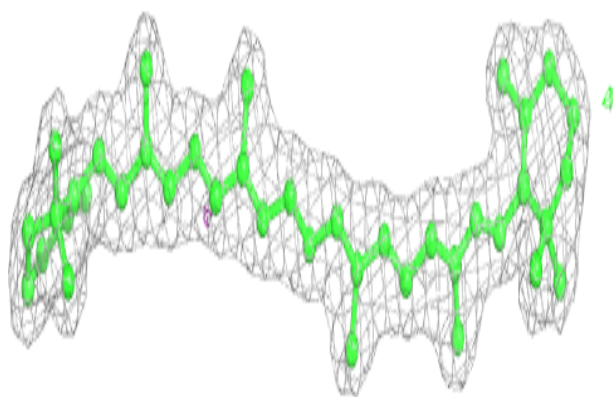
**Electron density around BCR b 629:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

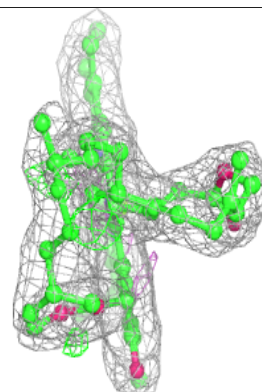
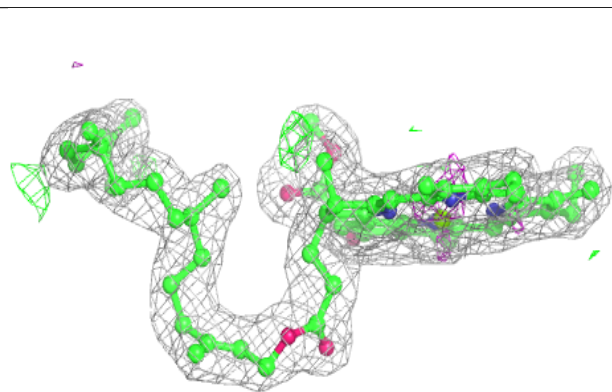
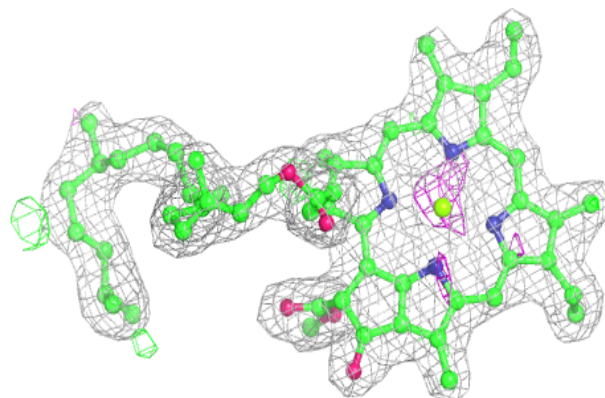


Electron density around BCR B 618:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

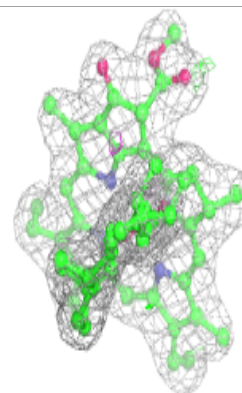
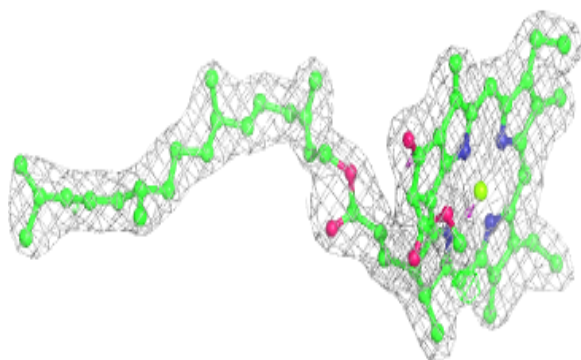
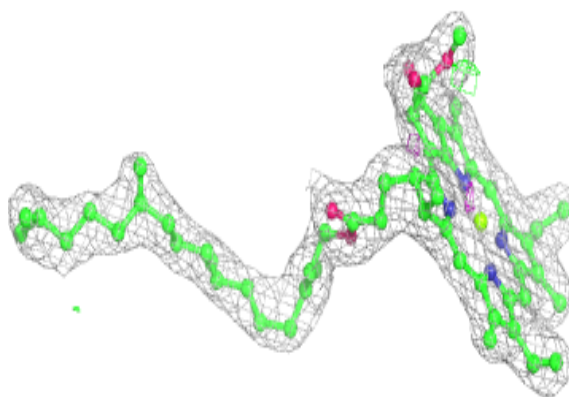
**Electron density around CLA B 613:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



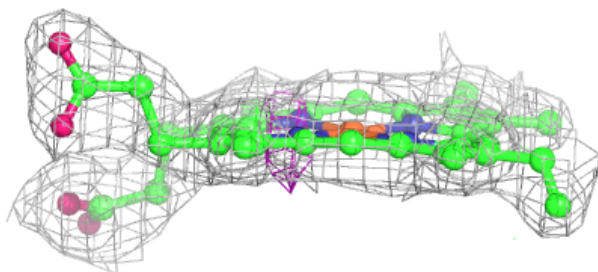
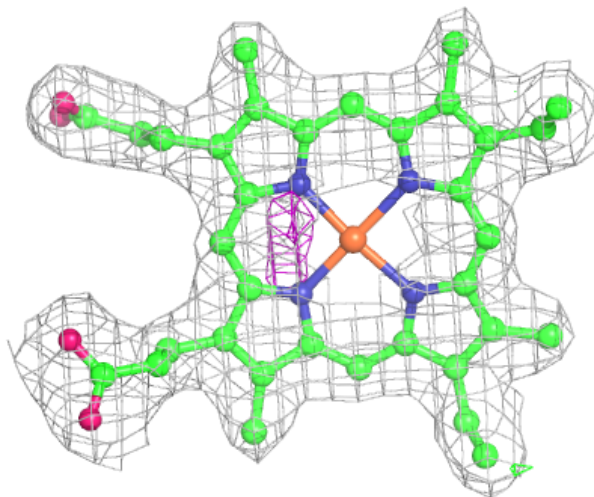
Electron density around CLA C 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



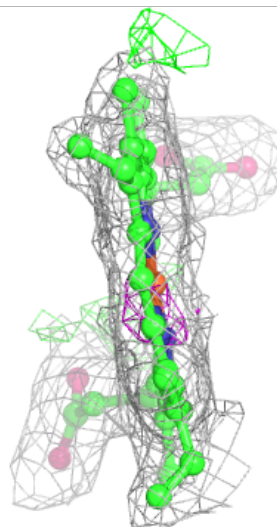
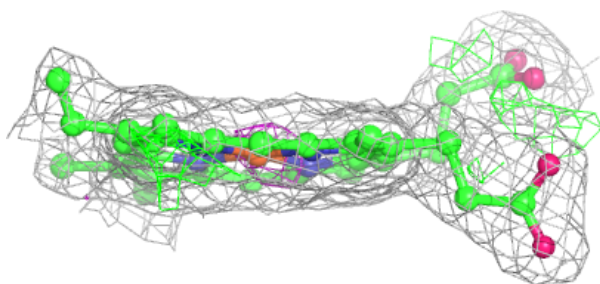
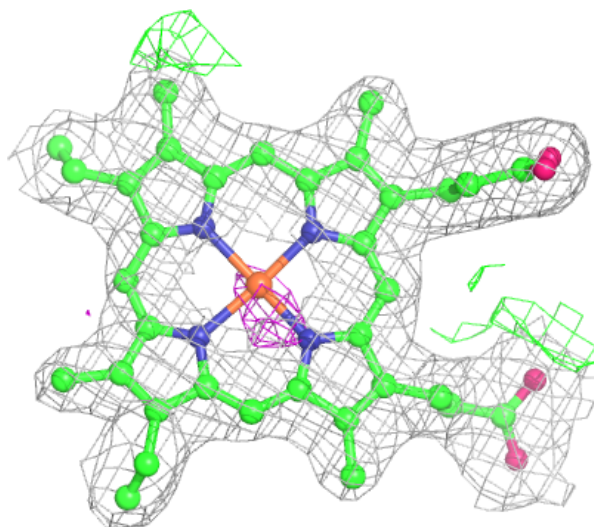
Electron density around HEM v 205:

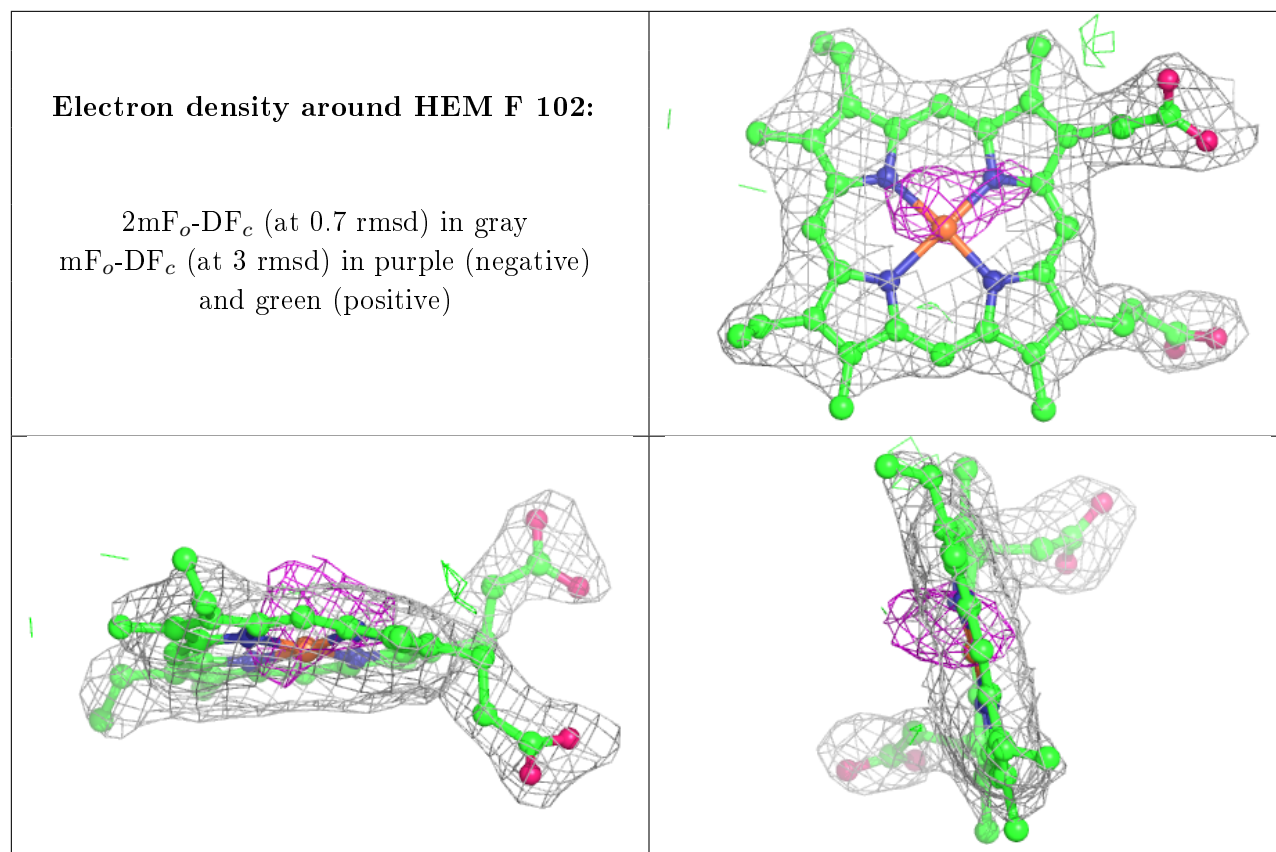
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM V 206:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.